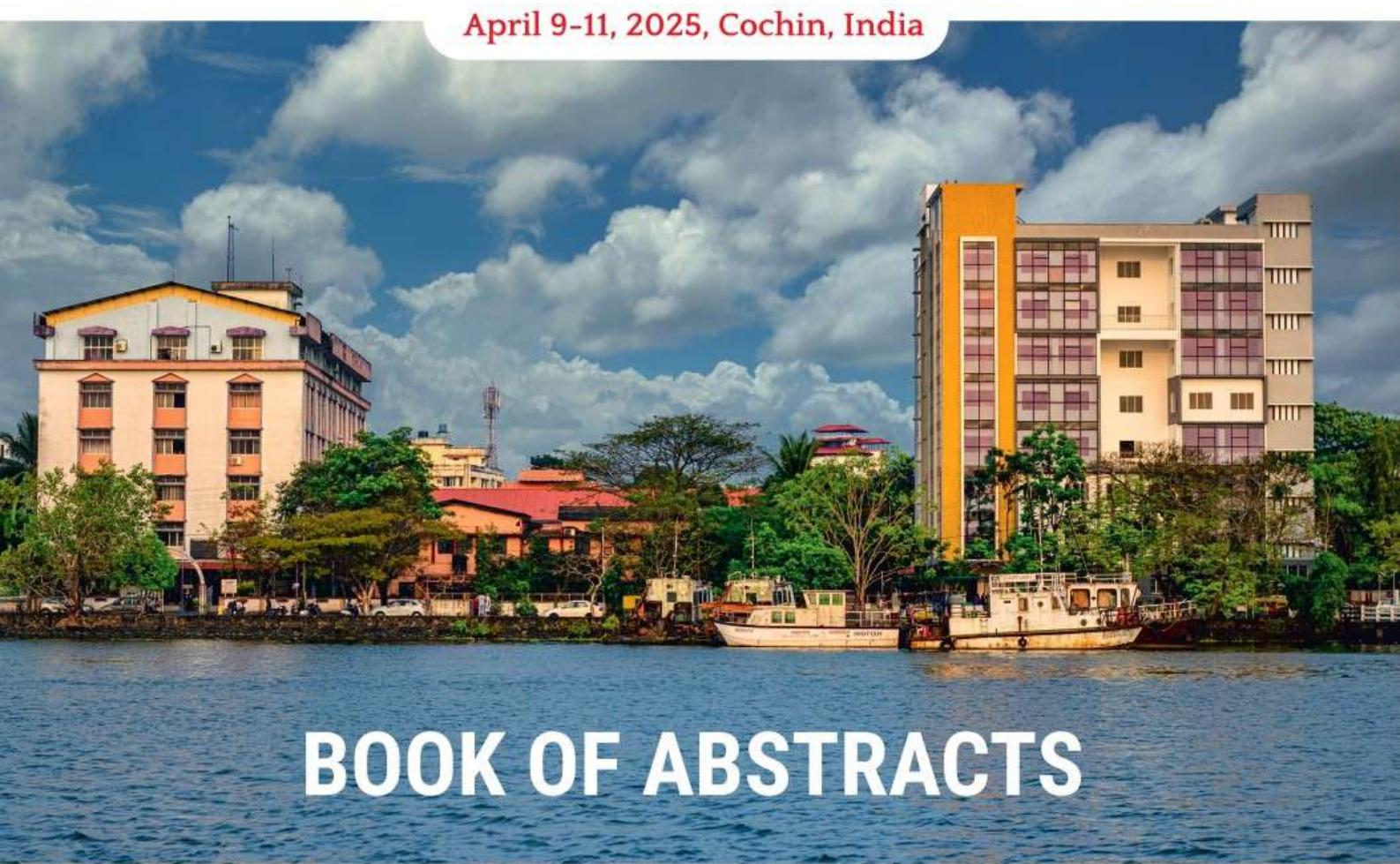




INTERNATIONAL CONFERENCE ON MARINE BIODIVERSITY, GENOMICS AND SUSTAINABLE DEVELOPMENT

ICMBGSD-2025

April 9-11, 2025, Cochin, India



BOOK OF ABSTRACTS

Organized by

Department of Marine Biology, Microbiology and Biochemistry
Cochin University of Science and Technology, Cochin

In Association with

National Centre for Polar and Ocean Research (NCPOR), Goa &
CUSAT-NCPOR Centre for Polar Sciences



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About the Conference

Marine environment covering two third of planet earth exerts huge impact on life on planet earth by moderating the weather extremes, supporting immense biodiversity, ensuring food security and providing huge resources of conventional (oil and gas) and non-conventional energy (OTEC, wave and wind energy) resources. However, the increasing CO₂ concentrations in the atmosphere and resultant global warming has started impacting the weather and climate patterns, biodiversity and livelihood of people in the coastal belt. Dissolution of significant quantities of CO₂ into the sea water is also causing ocean acidification which is impacting the coral reefs, considered as the rainforests of the sea and many forms of calcareous shell forming organisms. Scientific advancements in biology have also resulted in the development of Genomics as a major tool for conservation of marine biodiversity and harnessing the potentialities in a positive manner. Application of genomics is now ranging from resolving taxonomic ambiguity to higher end biotechnological applications, drug discovery and sustainable development.

It is in this backdrop Dept. of Marine Biology, Microbiology and Biochemistry (DMMB) decided to organize this International Conference on Marine Biodiversity, Genomics and Sustainable Development (ICMBGSD 2025). DMMB is the leading department in Cochin University of Science and Technology (CUSAT) and an integral part of the highly interdisciplinary School of Marine Sciences (SMS). SMS, CUSAT is one of its kind's marine sciences schools in the country, which all other branches of marine sciences such as Marine Geology and Geophysics, Physical Oceanography, Chemical Oceanography and Atmospheric Sciences under the same umbrella. Over the years, DMMB, CUSAT has built up great strength in marine biology studies in various disciplines such as marine biodiversity (several new species were discovered by the faculty and researchers from this department), ecotoxicology, marine biotechnology, aquaculture, planktonology and fisheries. ICMBGSD 2025 is organized in association with National Centre for Polar and Ocean Research (NCPOR) and CUSAT-NCPOR Centre for Polar Sciences (CNCPS).

In order to cover the wide-ranging topics, the focal themes of the conference are selected to include Marine Biodiversity and Conservation; Sustainable Fisheries,

Aquaculture and Blue Economy; Marine Biotechnology and Genomics; Marine Natural Products and Drug Discovery; Polar Biology, Ecology, Climate Change and Ocean Health; and Marine Microbiology and Anti-Microbial Resistance. We have roped in the leading international researchers for plenary lectures under each of the focal themes. The response to the conference was overwhelming with nearly 200 abstracts submitted for presentation under oral and poster sessions. Considering the looming threat of climate change on marine ecosystems, ICMBGSD 2025 assumes lot of significance. We hope the deliberations during the conference will find a way out to develop sustainable strategies; both the traditional knowledge and the higher-end genomics-based tools, for harnessing the vast marine biodiversity of the oceans for the benefit of mankind. DMMB, CUSAT extend a warm welcome to all the delegates of ICMBGSD 2025 and wish a very productive, science filled days during the conference.

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About the organizers

Department of Marine Biology, Microbiology and Biochemistry, CUSAT:

The Department of Marine Biology, Microbiology and Biochemistry is the academic continuation of the original Department of Marine Biology and Fisheries, established in 1938 under the University of Travancore for promoting marine research and fisheries investigations. It is one of the five departments, under the School of Marine Sciences of the University that has a unique national and international relevance in our sojourn for exploring the oceans and its services to mankind. The M.Sc. course in Marine Biology began in 1958 along with multidisciplinary research in various aspects of biological oceanography. The department has well equipped laboratories sophisticated instruments and the research carried out in the time-period department has created significant new knowledge in the area of marine biology. There is an excellent output in terms of research publications, books and monographs from the faculty members of the department, since its inception. The department is recognized under DST-FIST, KSCSTE-SARD, UGC-SAP programmes and also the Centre for Excellence in Marine Biology under the Kerala State plan scheme. Several national, International and state-level research projects are being implemented in the thrust areas of marine biology for enhancing our understanding and knowledge of marine ecosystems for the welfare of society.

National Centre for Polar and Ocean Research (NCPOR), Goa:

The National Centre for Polar and Ocean Research (NCPOR), is an autonomous research and development institution under the Ministry of Earth Sciences, Government of India. As the nation's leading centre for Polar and Ocean research, NCPOR is responsible for the planning, execution, and coordination of all Indian scientific expeditions to Antarctica, the Arctic, and the Southern Ocean. The centre's research programs encompass a broad spectrum of scientific disciplines, including glaciology, atmospheric sciences, marine biology, and paleoclimatology. NCPOR operates India's permanent research stations in

Antarctica and the Arctic, providing crucial platforms for long-term scientific observations and data collection. The centre also plays a vital role in managing and archiving polar data, fostering international collaborations, and contributing to global efforts to understand and address the challenges of climate change. With its state-of-the-art laboratories and experienced researchers, NCPOR is at the forefront of polar and ocean science, providing valuable insights into the Earth's dynamic systems.

CUSAT-NCPOR Centre for Polar Sciences (CNCPS):

Under the academic and research collaboration between Cochin University of Science and Technology (CUSAT), Kerala, and the National Centre for Polar and Ocean Research (NCPOR), Goa, CNCPS at School of Marine Sciences, CUSAT encourages and promotes joint academic and research programs in the areas of Marine Biology, Marine Geology, Marine Geophysics, Physical Oceanography, Chemical Oceanography and Atmospheric Sciences.

Dr. R. BINDU
MINISTER FOR
HIGHER EDUCATION & SOCIAL JUSTICE
GOVERNMENT OF KERALA



Thiruvananthapuram

Date 21/03/2025

•—————
Celebrating Marine Conservation
•—————•



The International Conference on Marine Biodiversity, Genomics, and Sustainable Development (ICMBGSD 2025) represents a significant milestone in our pursuit of scientific innovation and sustainable practices related to our oceans. Organized by Cochin University of Science and Technology (CUSAT) in collaboration with the National Centre for Polar and Ocean Research (NCPOR), this conference emphasizes the critical importance of marine biodiversity conservation for ecological balance, sustainable fisheries, and the preservation of invaluable genetic resources.

The sustainable use of marine resources is essential not only for environmental integrity but also for the economic well-being of coastal communities and global food security. The advancement of marine genomics offers transformative potential by enabling deeper insights into marine life and facilitating the development of biotechnological applications across various fields.

Particularly significant for Kerala's higher education sector, CUSAT's Marine Biology Department has a rich legacy of over 90 years in marine sciences. This even reinforces Kerala's position as a leading hub for marine research, creating invaluable opportunities for collaboration among students, researchers, and global experts.

The conference serves as a vital platform for meaningful dialogue and cooperative efforts to protect our oceans for future generations, and we anticipate that the outcomes will contribute significantly to global ocean sustainability initiatives while enhancing Kerala's academic contributions in this vital area.

Warm regards,

A handwritten signature in blue ink, appearing to read "Bindu".

Dr. R. Bindu

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(Re-accredited by NAAC with 'A+' Grade)

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Foreword



It is with great pride and pleasure that I present this Book of Abstracts for the International Conference on Marine Biodiversity, Genomics, and Sustainable Development (ICMBGSD2025), organized by the Department of Marine Biology, Microbiology, and Biochemistry, in association with the National Centre for Polar, and Ocean Research (NCPOR), Goa, and the CUSAT-NCPOR Centre for Polar Sciences.

Marine biodiversity plays a fundamental role in maintaining ecosystem balance, supporting fisheries, and providing crucial resources for medicine, biotechnology, and climate regulation. The sustainable utilization of marine resources is imperative for ensuring long-term ecological and economic benefits, particularly for coastal communities and industries dependent on marine ecosystems. Scientific advancements in "OMICS" have opened new avenues for understanding biodiversity, conserving fragile ecosystems, and discovering novel bioactive compounds with pharmaceutical and industrial applications. This conference serves as a significant platform to explore these dimensions and foster global collaborations for ocean sustainability.

The School of Marine Sciences, CUSAT, has been at the forefront of marine science research and education in India, with a rich legacy spanning over 90 years. The school has made significant contributions to oceanographic research, air-sea interactions and climate change, marine biodiversity conservation, and sustainable resource management, reinforcing Kerala's and India's standing as a hub for research excellence in marine sciences. The Department of Marine Biology, Microbiology, and Biochemistry has played a pivotal role in advancing interdisciplinary research, exploring new frontiers in marine biodiversity, marine biotechnology and genomics, and equipping future generations with the skills and knowledge necessary to tackle emerging challenges in marine sciences.

This conference provides a unique opportunity for scientists, researchers, academicians, students, and industry professionals to exchange ideas, share ground-breaking research, and foster collaborations that will shape the future of, marine biodiversity conservation, sustainable utilization, and genomics applications. On behalf of Cochin University of Science and Technology, I extend my heartfelt congratulations to the Department of Marine Biology, Microbiology, and Biochemistry on this remarkable occasion. I am confident that this conference will inspire new collaborations, cultivate young scientific talent, and contribute significantly to global efforts in marine conservation and sustainable resource management.

Wishing you all a fruitful and inspiring conference.

Prof. (Dr.) Junaid Bushiri
Vice-Chancellor
Cochin University of Science and Technology
Kochi-22

PREFACE

Welcome to the International Conference on Marine Biodiversity, Genomics, and Sustainable Development (ICMBGSD 2025). We are overwhelmed by the tremendous response to the call for abstracts for presentation in ICMBGSD 2025 on topics ranging from marine biodiversity to higher end applications of genomics. Sustainable utilization of the marine resources is a key area which also attracted a good number of abstracts. This abstract book is a compilation of all the abstracts received for oral and poster presentations as well those from keynote and invited speakers. This will serve as ready reference for all those participating in the ICMBGSD 2025.

The health of our oceans is obviously linked to the delicate balance of marine biodiversity and the complex mechanisms of marine genomics. As climate change intensifies, understanding these vital components becomes paramount for ensuring sustainable development. This conference, organized by the Department of Marine Biology, Microbiology and Biochemistry in association with the National Centre for Polar and Ocean Research (NCPOR), Goa, and the CUSAT-NCPOR Centre for Polar Sciences, has brought together leading scientists, researchers, and stakeholders to address the complex challenges facing our marine ecosystems.

The presentations and discussions contained within this volume delve into critical areas, including the impact of environmental changes on marine biodiversity, the application of genomics in marine conservation, and the development of sustainable practices for resource management. This compilation of abstracts serves as a valuable resource for researchers, policymakers, and environmentalists, highlighting innovative research and fostering interdisciplinary discussion. We believe that the insights shared here will inspire future investigations and contribute to the development of effective strategies for safeguarding our oceans.

The enthusiastic participation of students and researchers from various disciplines, as evidenced by the substantial number of abstracts submitted, underscores the importance of this conference. These abstracts represent a diverse range of research ideas and approaches, reflecting the dynamic nature of marine science.

We extend our sincere gratitude to all keynote speakers, presenters, and participants for their valuable contributions, particularly to the international delegates who travelled great distances to attend this conference. We also acknowledge the unwavering support and meticulous efforts of the faculty, research scholars and staff of the Department of Marine Biology, Microbiology and Biochemistry, the National Centre for Polar and Ocean Research (NCPOR), Goa, and the CUSAT-NCPOR Centre for Polar Sciences, whose collaborative work has been instrumental in the success of this conference.

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Plenary Talks



PL-1

MARINE BIODIVERSITY CONSERVATION AND SUSTAINABLE BLUE ECONOMY: CHALLENGES AND STRATEGIES FOR INDIA

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The ocean has long been perceived as an infinite source of resources, space, and economic growth. The Sustainable Blue Economy (SBE) provides a framework to balance economic progress with environmental conservation and social well-being, encompassing fisheries, aquaculture, marine transportation, tourism, ocean energy, and marine biotechnology. A well-managed SBE can unlock multiple environmental, social, and economic benefits while advancing Sustainable Development Goals (SDGs), particularly SDG 14 (Life Below Water). Despite its critical role in addressing the triple planetary crisis of climate change, biodiversity loss, and pollution, SDG 14 remains one of the most underfunded global goals. Many nations are striving to develop their ocean economies while aligning with international commitments such as the Global Biodiversity Framework and the Paris Agreement. A primary challenge lies in integrating biodiversity conservation into economic policies, ensuring responsible management of marine genetic resources (MGRs), and fostering effective governance frameworks for sustainability. Governance mechanisms play a crucial role in achieving a Sustainable Blue Economy by bridging science, policy, and community-driven approaches. The Sustainable Blue Economy Initiative promotes a balance between economic activities and ecological resilience, safeguarding marine and coastal resources for future generations. Key strategies include marine spatial planning, ecosystem-based management, and community-led conservation models, which help protect biodiversity while supporting economic livelihoods. This initiative also underscores the importance of capacity building and knowledge-sharing, incorporating both scientific expertise and traditional ecological knowledge to create innovative solutions. One of the critical risks in blue economy development is "ocean grabbing," where large corporate entities monopolize marine resources, often excluding local communities from economic benefits. Ensuring inclusivity requires participatory governance that blends top-down policy frameworks with bottom-up, community-led initiatives. Sustainable technologies such as renewable ocean energy, circular economy models, and clean marine technologies can



drive the transition toward a low-carbon, resource-efficient future. This paper examines the challenges and opportunities associated with marine biodiversity conservation and the development of a Sustainable Blue Economy in India. Through case studies, it highlights place-based approaches that consider regional history, ecological context, and socio-economic conditions. By adopting best practices at both local and global levels, India can align marine conservation efforts with economic growth, promoting a socio-ecological transformation crucial for achieving climate resilience and biodiversity goals. A well-structured Sustainable Blue Economy can address environmental, economic, and social challenges while restoring, protecting, and maintaining resilient marine ecosystems. It fosters economic opportunities that are both inclusive and sustainable. This paper advocates for a paradigm shift in marine resource management, transitioning from fragmented sectoral approaches to a holistic, ecosystem-based governance model that ensures ocean-based economies contribute effectively to global sustainability while preserving marine biodiversity for generations to come.

Keywords: Sustainable Blue Economy, Marine Biodiversity Conservation, Ocean Governance, Climate Resilience, Sustainable Development Goals, Marine Genetic Resources



PL-2

THE IMPORTANCE OF GEOGRAPHY IN MARINE AND MEDICINAL PLANT NATURAL PRODUCTS DRUG DISCOVERY

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Natural products have always played an important role in clinical pharmacy and drug discovery, from the root of traditional medicine to the dawn of Westernization, through the present. The complex structures of natural products have inspired the development of many modern research techniques and instrumental advances. Progress in the field has also led to the creation of various strategies for discovery, including chemistry-focused, bioactivity-guided, genome mining, and taxonomy prioritization. Emergent from our practice of all of these techniques, which are each still valid and all in use globally, has been the recognition of the great importance of geography in marine and medicinal plant natural products drug discovery. Chemogeographical analysis is a relatively underappreciated and underused tool for natural products drug discovery platforms, yet it can inform decision making in biodiversity collection efforts, efficient targeting for compound isolation, and, interestingly enough, uncovering the ecological and pharmacological functions of natural products. Thus, the so-called reinvestigation, but the comparative study, of seemingly identical taxa from disparate geographies has been shown to yield important discoveries of new bioactive natural products, and the discovery of new bioactive compounds taken in the context of geography has informed the pharmacological functions of some related molecules. This is strongly encouraging of the further ethical and responsible study of both uncharacterized and “previously examined” biodiversity, highlighting also the paramount importance of biodiversity conservation for the future of improving human health outcomes.

Keywords: Biodiversity, Natural products, Drug discovery, Human Health



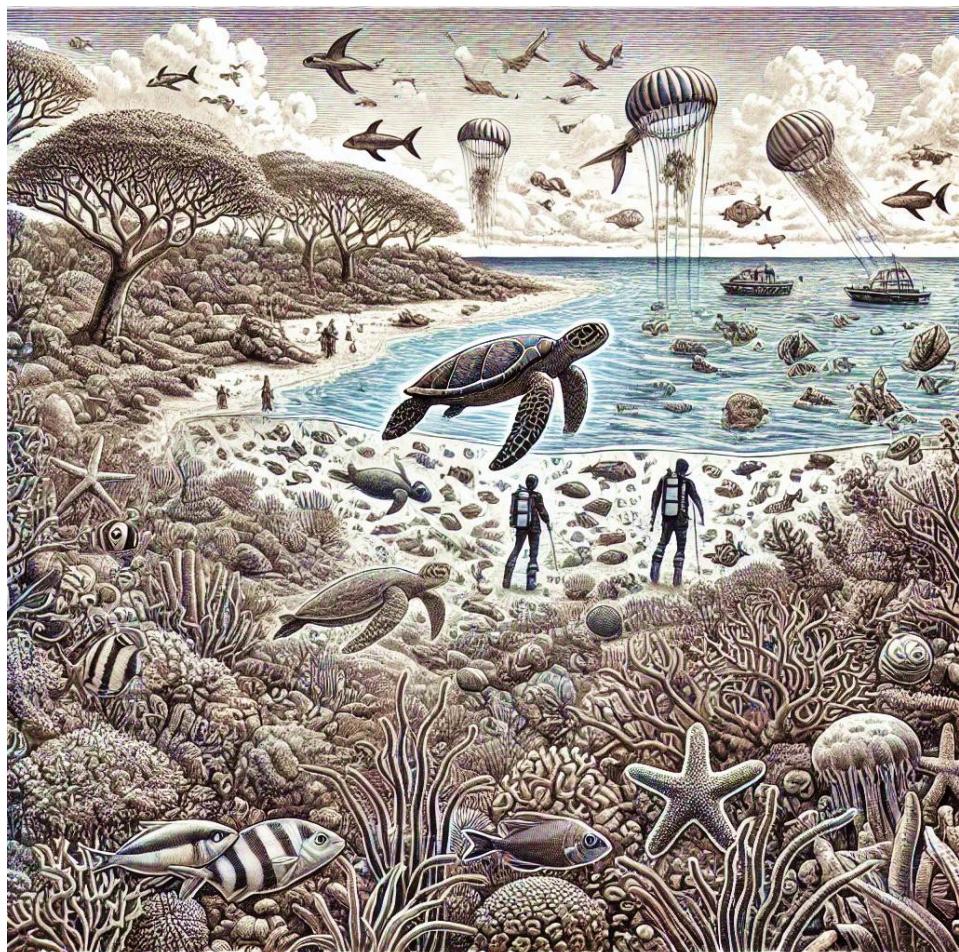
BIOLOGICAL CLOCKS THAT REGULATE LUNAR- AND TIDE SYNCHRONIZED SPAWNING RHYTHM IN MARINE ANIMALS

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Marine organisms have adapted to a multitude of environmental cycles, such as annual, seasonal, lunar/semilunar, daily, and tidal rhythms, and developed biological clocks entrained to these rhythms. However, molecular mechanisms of biological clocks that regulate the lunar- and tide-synchronized rhythms are still unknown. We have been researching molecular clockworks of the semilunar and tide-synchronized spawning rhythm of the grass puffer, *Takifugu alboplumbeus*, because it spawns several hours before high tide only during spring tide (new moon and full moon) in early summer. In the pineal gland, the expression of melatonin receptor genes exhibits ultradian variations with a period of 15 hours in the fish reared under constant darkness. To elucidate the molecular basis of the biological clock that makes this rhythm, a transcriptome analysis was conducted in the pineal gland. The pineal glands of mature male fish were sampled eight times every three hrs. Of approximately 20,000 expressed genes, about 1,100 genes were estimated to fluctuate in expression on 12-15 hour cycles, suggesting the presence of a circatidal clock of a 12.4-hour cycle. It has been revealed in the hypothalamus that there are a number of semilunar genes with peaks or troughs in the expression levels on the day of new moon and full moon in a lunar month. These results suggest that the grass puffer may have circatidal and circadian clocks in the pineal gland, and they may regulate the semilunar gene expression in the hypothalamus because circatidal and circadian clocks only coincide once per semilunar month. Circatidal clock, a novel biological clock, as well as the circadian clock, may play important roles in the precisely-timed daily and semilunar spawning of the grass puffer.

Keywords: Biological clock, Lunar cycle, Tidal cycle, Pufferfish, Reproductive rhythm



Marine Biodiversity and Conservation

Invited Talks



MBC-IT 1

DEEP OCEAN MISSION – EXPLORING THE UNEXPLORED!

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Considering the importance of Ocean for sustainable development of the country, Ministry of Earth Sciences (MoES), Government of India, has launched Deep Ocean Mission in September 2021, aimed at developing technologies to explore deep ocean resources and their sustainable use, growing the country's marine and maritime economy and tackling the climate change and pollution. It was launched as a Central Sector Scheme at an estimated cost of Rs.4077 crore to be implemented in five years from 2021-2026, with six major components. The six major Verticals are, viz. (i). Development of Technologies for Deep Sea Mining, Manned Submersible, and Underwater Robotics, (ii). Development of Ocean Climate Change Advisory Services, (iii). Technological innovation for exploration and conservation of deep-sea biodiversity, (iv). Deep Ocean Survey and Exploration, (v). Energy and Freshwater from the Ocean, and (vi). Advanced Marine Station for Ocean Biology. The activities of the Mission are implemented by Institutes within MoES (NIOT, NCPOR, CMLRE, INCOIS, IITM and NCCR) and the other Ministry's Departments/ Institutes like ISRO, DRDO, DBT, CSIR, BARC, Indian Academic Institutes (IITs, NITs, Universities, etc.) and Industries. The mission also has collaboration with international research institutes. The biology, microbiology and biodiversity vertical of the Mission is being implemented through NIOT and CMLRE in coordination with other collaborating institutes. Several research cruises have been organized near seamounts, resulting in the collection of over 1000 samples representing around 150 distinct species, many of which may be new to science or previously unrecorded in the Indian EEZ. As part of its efforts to isolate deep-sea piezo tolerant and piezophilic microbes, NIOT has isolated and characterised approximately 1300 distinct heterotrophic microbes comprising numerous deep-sea bacteria, actinobacteria, fungal and yeast isolates. Further, deep-sea microbes are explored by metagenomics. This extensive research not only enhances understanding of deep-sea ecosystems, but also establishes a foundation for future explorations and conservation initiatives. The



Government of India's Vision of New India by 2030 highlighted the Blue Economy as one of the ten core dimensions of growth. Deep Ocean Mission is a mission mode project to support the Blue Economy Initiatives of the Government. India's Exclusive Economic Zone spreads over 2.2 million sq. km and the deep sea has much more to offer, which are unexplored.

Keywords: Deep Ocean Mission, Marine Resources, Blue Economy, Biodiversity, Conservation



MBC-IT 2

CHALLENGES AND ADVANCES IN eDNA RESEARCH FOR BIODIVERSITY CONSERVATION

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Environmental DNA (eDNA) refers to the genetic material that organisms leave behind in their environment through various excretions, including skin, scales, waste, and other types of cellular debris. Metabarcoding of eDNA, facilitated by high-throughput sequencing methods, enables the exploration of biodiversity in marine ecosystems without the need for physically intact samples. However, eDNA research faces several challenges, including rapid DNA degradation, the risk of contamination, and the need for standardized procedures to ensure consistent results. Continued advancements in data analysis, the expansion of reference databases, and the development of precise methodologies will be vital in optimizing the use of eDNA for monitoring marine biodiversity and supporting conservation efforts. This lecture will discuss the strengths and weaknesses of eDNA sequencing in the context of marine biodiversity analysis, drawing on examples from our research in the seamounts of the Arabian Sea.

Keywords: Biodiversity, Environmental DNA, Seamounts

Oral Presentations



MBC-O1

DIVERSITY AND COMMUNITY DYNAMICS OF MICROPHYTOBENTHOS IN THE INTERTIDAL MANGROVE ECOSYSTEMS OF THE SOUTHWEST COAST OF INDIA

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The study explores the taxonomic composition, biodiversity patterns, and community structure of microphytobenthos (MPB) across highly productive mangrove habitats of the southwest coast of peninsular India from December 2018 to February 2020. The mangrove ecosystems of Kannur-Payannur (KAN), Kochi-Kadamakudy (KOC1), Kochi-Puthuvype (KOC2), Kochi-Mangalavanam (KOC3), and Kollam-Ayiramthengu (KOL) were selected for the study. A total of 155 MPB species from 71 genera were identified, predominantly diatoms (146 species), followed by cyanobacteria (10 species), and minor contributions from dinoflagellates, euglenophytes, charophytes, and chrysophytes. Pennate diatoms accounted for 59.8% of the total diatom population. Notably, *Psammodictyon panduriforme* was reported for the first time from the Southwest coast of India. Biodiversity indices revealed significant spatial and seasonal variations. The highest species diversity ($H' = 4$) was recorded in KOC1, whereas the lowest diversity ($H' = 1.50$) was found in KOC3, likely due to shading by dense mangrove canopies. MPB abundance peaked in KOC3 ($N = 9.02 \times 10^3$), while KOC2 exhibited the lowest density ($N = 1.64 \times 10^3$). Seasonal fluctuations were evident, with post-monsoon (POM) displaying the highest species diversity ($H' = 3.91$), followed by pre-monsoon (PRM), and the lowest diversity recorded during monsoon (MON, $H' = 2.75$). Statistical analyses confirmed significant seasonal shifts in MPB composition ($p < 0.05$), with diatom-dominated assemblages post-monsoon transitioning to extensive cyanobacterial mats, particularly *Oscillatoria* sp., during monsoon and pre-monsoon. These findings



underscore the intricate interplay between environmental factors and MPB diversity, emphasizing their ecological significance in mangrove ecosystems and the need for conservation efforts in these vulnerable habitats.

Keywords: Benthic microalgae, Benthic diatoms, Mangrove ecosystem, SW coast of India



MBC-O2

HARMFUL DINOFLAGELLATE DISTRIBUTION RELATED TO WATER QUALITY IN COASTAL WATERS OF MALABAR, SOUTH EASTERN ARABIAN SEA

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A dinoflagellate is a single-celled organism that commonly occurs in large numbers in the marine environment. When the environment changes, harmful dinoflagellate algae often emerge as a response to changes in water quality. Malabar Coast, South Eastern Arabian Sea is a place where four rivers that carry anthropogenic effluents, not only from agriculture and human settlements, but also from industrial activities, drain. This study aims to assess the diversity of harmful bloom-causing dinoflagellates in response to water quality and climate change. Dinoflagellates were sampled from April 2023 to May 2024 at five locations, namely, Puthiyappa, Elathur, Kappad, Parapally, and Thikkodi, each with three replications. Results showed that five dinoflagellates categorized as harmful were recorded. The following order of dinoflagellates, based on abundance, was *Gymnodinium* sp. > *Ceratium* sp. >*Noctiluca* sp. > *Dinophysis* sp. > *Gonyaulax* sp. There were correlations between dinoflagellate abundance with water quality. This study shows Dinoflagellates, including both HAB taxa (for example, *Prorocentrum* sp.) and non-HAB taxa (for example, *Ceratium furca*), have declined in abundance compared to historical records in this area. Significant predictors differed between the subsets: HAB assemblages were explained by salinity, temperature, dissolved oxygen, and Total suspended matter; whereas, *Noctiluca* sp. assemblages were explained only by salinity and dissolved oxygen, and had greater variability. This study suggests that Malabar coastal waters should be monitored to investigate harmful species and to identify areas and seasons at higher risk.

Keywords: Dinoflagellate, Harmful bloom, Arabian Sea, Climate change



MBC-O3

ECOLOGICAL IMPACT OF FIDDLER CRAB BIOTURBATION ON NUTRIENT DYNAMICS IN THE VEMBANAD MANGROVE ECOSYSTEM

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Bioturbation, the stirring and reworking of sediment by burrowing and foraging benthic organisms such as fiddler crabs, plays a vital role in maintaining mangrove ecosystems. Fiddler crabs, particularly *Austruca annulipes*, act as ecosystem engineers by enhancing biogeochemical heterogeneity through their burrowing activities. This study evaluated the ecological function of bioturbation and nutrient dynamics in four stations within the Vembanad mangrove ecosystem. A spatiotemporal analysis of sediment, surface water, and porewater was conducted, measuring physical and chemical parameters, including temperature, pH, redox potential, and salinity. Particle size distribution and CHNS analysis (up to 25 cm depth) of crab burrow sediments were performed, alongside the quantification of dissolved inorganic nutrients (nitrate, phosphate, and silicate) in surface and porewater. While nutrient concentrations showed no significant spatial variation ($p>0.05$), they exhibited significant seasonal fluctuations ($p<0.05$) across pre-monsoon, monsoon, and post-monsoon periods. Higher CHNS ratios were observed at depths of 1–20 cm, where crab bioturbation activity was most intense. These findings suggest that fiddler crab burrowing facilitates nutrient exchange between burrow walls, porewater, and surface water, contributing to the overall nutrient enrichment of the mangrove ecosystem.

Keywords: Bioturbation, Fiddler crab, *Austruca annulipes*, Ecology, Nutrient Dynamics



MBC-O4

ASSESSMENT OF CORAL REEF CONNECTIVITY IN IMPROVED ORGANIC CARBON STORAGE OF SEAGRASS ECOSYSTEMS IN PALK BAY, INDIA

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The increase in climate-related extreme events and ecosystem degradation demands consistent and sustainable climate mitigation efforts. Seagrass plays a key role in nature-based carbon sequestration strategies. This study investigates the role of coral reef connectivity in blue carbon dynamics by comparing seagrass meadows with (SC areas) and without (SG areas) coral reef connectivity in Palk Bay, India. Sediment organic carbon was significantly higher in SC areas (90.26 ± 25.68 Mg org.C/ha) compared to SG areas (66.96 ± 12.6 Mg org.C/ha). The maximum above-ground biomass (AGB) was recorded in *Syringodium isoetifolium* (35.43 ± 8.50) in SC areas, while the minimum was in *Halophila ovalis* (7.59 ± 0.90) in SG areas. A similar trend was observed for below-ground biomass (BGB). These findings highlight the importance of coral reefs in enhancing the blue carbon potential of seagrass ecosystems. The study underscores the need for integrated conservation and restoration strategies for coral reefs and seagrasses to optimize carbon sequestration and ecosystem resilience.

Keywords: Ecosystem connectivity, Palk Bay, Coral reefs, Seagrass, Blue carbon



MBC-O5

DIVERSITY AND ECOLOGY OF GRAPSOIDEA CRABS IN TROPICAL MANGROVE ECOSYSTEMS, SOUTH-WEST COAST OF INDIA

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Mangrove crabs, particularly those from the dominant superfamily *Grapsoidea*, play a vital role in maintaining the structure and function of mangrove ecosystems. They are ecosystem engineers and have a significant role in nutrient recycling, detritus formation, and the dynamics of the ecosystem. The study aims to assess crab diversity and the pattern of their ecology for biodiversity documentation. The study was carried out in selected mangrove forests of Vembanad wetland, South-West coast of India, during the period 2019-2021. Physical and biological parameters were assessed using established methods. Crab sampling used a 100×100 cm quadrat per site, with abundance recorded through visual identification and counting in situ. Each sampling lasted one hour, and crabs for taxonomy were collected by hand-picking and burrow digging. A total of six brachyuran crab species from the superfamily *Grapsoidea* were identified in this region, belonging to two families: *Sesarmidae* (3 species) and *Grapsidae* (2 species): *Parasesarma plicatum*, *Psuedosesarma glabrum*, *Neosarmatium malabaricum*, *Clistocoeloma lanatum*, *Metapograpsus thukuhar*, and *Metapograpsus latifrons*. *Parasesarma plicatum*, *Psuedosesarma glabrum*, and *Neosarmatium malabaricum* showed maximum, whereas *Clistocoeloma lanatum*, *Metapograpsus thukuhar*, and *Metapograpsus latifrons* registered minimum abundance. The selection of the Vembanad wetland for this study is strategic, given its rich biodiversity and the environmental pressures it faces. Investigating the ecology and diversity of mangrove crabs in this estuary can offer valuable insights into the ecosystem's health.

Keywords: Brachyura, Grapsoidea, Sesarmidae, Grapsidae, Diversity and Ecology



ASSESSING THE ELASMOBRANCH DIVERSITY AND
CONSERVATION STATUS OF THE PENINSULAR STATE OF
INDIA (TAMIL NADU) AND IDENTIFYING
BIO-DIVERSIFIED HOTSPOTS TO IMPLEMENT *IN-SITU*
CONSERVATION

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Elasmobranchs are top oceanic predators that control the ocean ecosystem by top-down predation. Mostly K-selected species, they live longer, mature late, and are less in number. The rising demand for elasmobranch globally has resulted in unregulated fishing, depleting fish stocks. India has consistently ranked among the top three elasmobranch-producing nations, the state of Gujarat being the highest producer in the west, while Tamil Nadu ranks number one on the east coast of India. Elasmobranchs are mainly part of a non-targeted fishery in Tamil Nadu and are primarily composed of sharks, rays, and guitar fish. Despite having a high elasmobranch landing, an extensive coastline, high brackish water inflow from perennial rivers, and intertidal mangrove and coral reef ecosystems, chondrichthyan diversity in this state remains understudied. We tried to understand the present elasmobranch diversity, identifying pocket areas or quadrants (of high diversity) and estimating the current threat levels. We identified 41 species of elasmobranch (13 sharks, 19 rays, and six skates) with a Shannon index of 1.982 and Evenness of 0.59. Rays (57%) were the most dominantly landed group of elasmobranchs, with *Brevitrygon imbricata* being the highest caught species, followed by *M gerrardi*. Among sharks (26%), *Scoliodon laticaudus* was the most dominant species. Many species of elasmobranchs like *Brevitrygon imbricata*, *Narcine* sp, and *Rhinobatos annandalei* were treated as trash fish and discarded. The drier months (January, February, and March) were more productive compared to the post-monsoon period



(July, August, and September). Mechanized boats reported higher catches compared to other fishing methods. According to IUCN, 18% of species are listed as critically endangered (CE), 24% as Endangered (ED), and 36% as Vulnerable (VU). Quadrants B and E should receive serious attention to prevent the extinction of endemic species and enforce species-specific in-situ conservation to prevent regional extinction.

Keywords: Elasmobranch, Shannon Index, Quadrants, Indian Ocean, Conservation



MBC-O7

SEASONAL VARIATIONS OF MICROPLASTICS IN SURFACE
WATERS OF MANGROVE HABITATS IN VEMBANAD LAKE ON
THE SOUTHWEST COAST OF INDIA

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Mangrove ecosystems are important coastal habitats, performing crucial ecological services like coastal shoreline protection, biodiversity preservation, carbon sequestration, water filtration, and support to livelihood. In India, there is a need for more knowledge on the occurrence and distribution of MPs in mangrove forests under different seasons. The present study aimed to illustrate the seasonal pattern of microplastic distribution within the surface water in the mangrove ecosystems of Vembanad Lake, an ecologically significant Ramsar site and the largest estuary on the southwest coast of India. A significant difference was noted in the abundance of microplastics with seasons in mangrove waters, with the highest concentration in the dry season (66 ± 18.2 items/L) and the lowest in the wet season (42.7 ± 15.4 items/L). The highest abundance was recorded from S1, a highly tourist area and close to a mariculture area, while the lowest was found at S5 in a highly preserved area. Fragment emerged as the most abundant category, followed by film, fibre, and sphere in all the seasons. Microplastics of size 1-200 μm were dominant in all the seasons. Blue, red, transparent, and black were the major colours of MPs reported. The main MP polymer types identified were polyethylene, polypropylene, low-density polyethylene, and polyethylene-co-polypropylene. The results of the present study could be useful to prepare an effective management strategy to mitigate plastic pollution in similar habitats.

Keywords: Microplastics, Vembanad, Mangrove, Season, Ramsar site



MBC-O8

INTERTIDAL ASSEMBLAGE DYNAMICS: A LONG-TERM MONITORING PERSPECTIVE

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The intertidal zone is a vibrant ecosystem teeming with diverse marine life. This study reports on a decade-long monitoring effort to understand how intertidal communities change over time within a single intertidal belt of the south Saurashtra coastline of Gujarat, India. The rocky intertidal habitat of the selected coast was studied to track shifts in species composition, abundance, and diversity. A variety of statistical tools were used to analyze data, including traditional population ecology measures like density, abundance, and frequency of major animal groups (Porifera, Cnidaria, Platyhelminthes, Annelida, Arthropoda, Mollusca, and Echinodermata), Shannon diversity index, Simpson's diversity index, and Pielou's evenness. Bray-Curtis cluster analysis was also employed to further explore the relationships between different intertidal communities. Findings revealed that the types of organisms present were strongly influenced by the specific substrate and faunal assemblage pattern of the intertidal zone. Four different intertidal assemblages were identified on a single coastal belt with significant micro-spatial variation in their community structure. All species in this study showed high variation in patterns of abundance at the smallest spatial scales, between contiguous transects or between the areas that separated by less than 50 m of distance along a coastal belt. Species contribution in each assemblage was evaluated by SIMPER analysis after the confirmation of dissimilarity with ANOSIM. This research demonstrates that sustained monitoring is essential for understanding how these ecosystems change, their dependence on existing fauna and substrates, and the value of traditional ecological studies.

Keywords: Marine Biodiversity, Intertidal Zone, Assemblage Patterns, Community Structure, Long-Term Monitoring



ASSESSING MICROPLASTICS IN SURFACE WATER FROM THE ENNORE MANGROVES IN THE BAY OF BENGAL, INDIA

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Microplastics (MPs) pose the biggest threat to coastal ecosystems due to their extensive distribution. MP contamination in the surface water of Chennai's Ennore mangroves is documented in this study. Samples were taken during the Southwest monsoon in September 2021. Using Fourier Transform Infra-Red (FTIR) and Scanning Electron Microscopy (SEM), MP analysis uncovers the existence and characteristics of MPs influenced by chemical composition and morphological traits. MP levels were significantly higher in mangrove surface water (7 ± 1 particles/L) and lower in Ennore Creek (5 ± 2.6 particles/L). With sizes ranging from 0.5 to 1 mm, fibers (71%) and foam (11%) were prevalent to be the most MP types in surface water samples. The most prevalent FTIR-characterized polymers were diene, cellophane, polypropylene (PP), polyethylene (PE), and ethylene propylene (PEPP). The study concludes that these polymers were frequently connected at every sampling site. PE and PP were the most widely recognized polymers in water. Surface water contains a high percentage of polypropylene because of its low density (0.895 and 0.93). More bacterial contamination was discovered by SEM analysis, which proves MP degradation and cracks. During the monsoon season, when rainfall is prevalent and water flow is excessive, more discarded plastic waste is accumulated from streams, lakes, canals, and pipelines that transit through the river to the coast and its surrounding habitats. According to the interpretations, industrial discharge, untreated sewage, urban runoff, and intensive fishing are some of the leading causes of MP contamination. An abundance of MP along the coast and in the surrounding environment allows for serious health consequences for both humans and animals.

Keywords: Mangroves, Coast, Microplastics, Contamination, Polymers



MBC-O10

BIODIVERSITY OF SEAWEED-ASSOCIATED EPIPHYTIC DIATOMS ALONG THE SOUTHWEST COAST OF INDIA

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Seaweed, or the marine macroalgae, form a luxuriant and flourishing habitat for a wide variety of organisms, mainly diatoms and other microalgae, rectifying the limitation of space and food in the vast marine ecosystem. This study describes the biodiversity of epiphytic diatoms associated with red seaweed and *Gracilaria folifera* along the intertidal region of Thirumullavaram, on the Southwest coast of India. *Gracilaria* was sampled monthly for a period of four years, from February 2019 to January 2023, and physicochemical parameters were measured during the period. Seaweeds collected were washed thoroughly in a known volume of water and filtered through 20µm bolting silk, and the concentrates were preserved in 3% neutralized formaldehyde and analysed for epiphytic diatoms using standard keys. The highly branched thalli and articulated surface of *Gracilaria* supported a high abundance of epiphytic diatoms. A total of 134 diatom species were observed epiphytic on *Gracilaria* during the entire study period, which included 57 motile, 39 erect, and 38 adnate growth forms. The highest abundance and diversity of epiphytic diatoms were observed during 2019 ($N= 4.3 \times 10^5$ cells 100 g^{-1} , $H'= 5.33$), trailed by 2021 ($N= 7.7 \times 10^4$ cells 100 g^{-1} , $H'= 4.84$). This was followed by a higher abundance during 2023 ($N= 3.1 \times 10^4$ cells 100 g^{-1}) and a higher diversity in 2020 ($H'= 4.3$). Seasonally, pre-monsoon showed the maximum abundance ($N= 4.5 \times 10^5$ cells 100 g^{-1}) and diversity ($H'= 5.35$) of epiphytic diatoms, followed by post-monsoon and monsoon season. The abundance of diatom growth was positively influenced by physical parameters, and mainly influenced by the grazing of the macrofauna assemblage. The presence of epiphytic species may not cause economic loss, but their dense growth can impact seaweed production. Expanding the study of epiphytic growth to seaweed farming in our nation is necessary as it is one of the growing economies of the country and is at threat by multifarious diseases.

Keywords: *Gracilaria*, Epiphytes, Diatoms, Southwest coast



MBC-O11

MANGROVE ECOSYSTEMS IN THE MALDIVES: STATUS, THREATS, AND CONSERVATION PROSPECTS

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Mangrove forests, a critical component of the coastal ecosystems in the Maldives, provide significant ecological and economic services, including coastal protection, carbon sequestration, and support for biodiversity. This study investigates the distribution, species diversity, and conservation status of mangrove ecosystems across the Maldives archipelago. Utilizing a comprehensive approach that combines literature review, field surveys, and citizen science, we have identified 12 true mangrove species and mapped mangrove habitats on 160 islands. Our findings highlight the dominance of species such as *Bruguiera cylindrica* and *Lumnitzera racemosa*, with notable presence in Haa Alifu, Haa Dhaalu, Shaviyani, and Noonu Atolls. However, these ecosystems face significant threats from coastal development, climate change, and anthropogenic activities, leading to rapid degradation and loss. This abstract emphasizes the urgent need for targeted conservation and restoration efforts, including the designation of protected areas and the promotion of sustainable eco-tourism, to preserve the unique mangrove biodiversity of the Maldives.

Keywords: Mangroves, Islands, Maldives, Coastal ecosystems



MBC-O12

ANALYSIS OF HEAVY METAL BIOACCUMULATION IN THE MANGROVE CRAB *PARASESARMA PLICATUM* AS A BIOINDICATOR SPECIES

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Heavy metals pose a significant global concern due to their toxicity, persistence, and bioaccumulation in living organisms, leading to long-term ecological and health risks. In the mangrove ecosystems, heavy metal contamination has been exacerbated by anthropogenic activities such as sewage disposal, urban encroachment, and industrial runoff. This study investigates the bioaccumulation potential of the sesarmid crab *Parasesarma plicatum* as a bioindicator for heavy metal pollution in the mangrove ecosystems. The concentration of heavy metals such as Cu, Ni, Zn, Mn, Cr, Cd, As, Se, V and Pb were analysed in the water, sediment and various body parts of *P. plicatum* such as carapace, hepatopancreas, gills and muscle from Sambranikodi mangrove island, Kerala ($8^{\circ} 92' 90$ N, $76^{\circ} 56' 78$ E) during the pre-monsoon, monsoon and post-monsoon seasons. Bioaccumulation factors (BAFs), including the bio-water accumulation factor (BWAF) and bio-sediment accumulation factor (BSAF), were estimated to assess the bioaccumulation potential. Significant variations in heavy metal concentrations were observed across water, sediment, and crab tissues, with notable accumulations in specific tissues. Zn was the most abundant metal in water, while Mn was the most abundant metal in the sediment. Soft tissues of *P. plicatum* exhibited higher metal concentrations than hard parts. The hepatopancreas showed the highest concentrations of Ni and Cr, with BSAF values greater than one. The gills exhibited highest Pb concentration and the muscle tissue showed the highest Zn concentration, both with high BWAF values. The results show that the mangrove crab *P. plicatum* can be used as an effective bioindicator of these metals for evaluating the ecological health of mangrove environments.

Keywords: Sesarmid crab, Hepatopancreas, Chromium, Biomonitoring



MBC-O13

UNLOCKING BIODIVERSITY AND MOLECULAR TAXONOMY OF FISH LARVAL SPECIES IN SELECTED MANGROVE ECOSYSTEMS OF SOUTHWEST COAST OF INDIA

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Mangrove ecosystems along the southwest coast of India are crucial habitats supporting biodiversity, especially during the larval stages for fish species. Combined traditional and molecular taxonomy of these larval forms is essential for effective biodiversity conservation and management strategies of these species. This study aims to elucidate the diversity and molecular characterization of fish larvae inhabiting ten mangrove areas of Ernakulam district, the Southwest Coast of India. Molecular characterization through DNA barcoding revealed the identification of twenty-six species from nineteen families. The most abundant species recorded were *Ambassis dussumieri*, *Oryzia setnai*, *Terapon jarbua*, and *Planiliza macrolepis*. Among the identified species, eighteen are food fishes, five are ornamental aquarium fishes, and one serves as a model organism. Our findings provide valuable insights into the taxonomy, species composition, and distribution patterns of fish larvae in these mangrove habitats, contributing to the broader understanding of marine biodiversity in India's southwest coast.

Keywords: Fish larvae, Molecular Taxonomy, Biodiversity, Mangrove

Poster Presentations



MBC -P1

INCREASED NUTRIENT CONCENTRATIONS IN THE
ANTHROPOGENICALLY INFLUENCED MANDOVI ESTUARY
IN GOA PROMOTE PROLIFERATION OF *KARENIA MIKIMOTOI*
DURING LATE SUMMER

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Changes in phytoplankton communities can indicate shifts in ecosystem health and biodiversity. Therefore, phytoplankton abundance, their composition, and pertinent environmental parameters were analysed from the anthropogenically-influenced Mandovi and relatively-pristine Chapora estuaries in Goa, India. Surface water samples were collected from three sites along a salinity gradient from February to May 2024. A total of 74 and 92 species were recorded in the Mandovi and Chapora estuaries, respectively. The most diverse and abundant groups were diatoms (60%), followed by dinoflagellates (38%). In both estuaries, phytoplankton abundance increased from 10^4 cells L^{-1} in February to 10^6 cells L^{-1} in May. However, species diversity (H') in both systems declined. Dominance of *Karenia mikimotoi* (up to 10^6 cells L^{-1}) was observed at the mouth of the Mandovi in May. Spearman's rank correlation showed that dissolved oxygen related negatively to the abundance of *Karenia mikimotoi* ($r_s = -0.88$, $p < 0.05$), indicating increased oxygen consumption in organically-enriched regions. Canonical correspondence analysis (CCA) revealed a larger influence of pH, salinity, and phosphate levels on the abundance of *Karenia mikimotoi*. Warmer waters during late summer and nutrients generated via remineralization of organic matter derived from sewage discharge and tourism-related activities towards the mouth of the Mandovi could have triggered the increase in the abundance of *Karenia mikimotoi*. These findings highlight the impact of anthropogenic activities on estuarine ecosystems, emphasizing the need for better management strategies to mitigate nutrient enrichment and maintain ecological balance.

Keywords: Phytoplankton, Diversity, Environmental parameters, Estuary



MBC-P2

STUDY ON SOCIO-DEMOGRAPHIC STATUS OF FISHERFOLK ALONG THE COAST OF THE DUGONG CONSERVATION RESERVE IN PALK BAY, TAMILNADU

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India, one of the world's mega-diverse nations, supports marine and coastal ecosystems vital to coastal livelihoods. Palk Bay in Tamil Nadu is ecologically significant for its seagrass meadows, critical habitats for the vulnerable dugong (*Dugong dugon*). To enhance conservation, the Government of India established the Dugong Conservation Reserve, covering 448.34 km². This study provided an overview of the socio-demographic status of fisherfolk along this coast by analysing census data from villages within the reserve's boundary using statistical software and conducting a systematic review of literature, government reports, and official databases. The fisherfolk population comprised around 5,000 families and 22,000 individuals, with a gender ratio of 51 percent male and 49 percent female. Educational attainment showed that 51 percent had primary education, 31 percent reached higher secondary, 10 percent beyond higher secondary, and 8 percent were graduates or above. Housing conditions indicated that 71 percent resided in pucca houses, while 29 percent lived in kutch structures. Water sources primarily included other alternatives (97%), with 3 percent relying on wells and less than 1 percent on hand pumps. The majority of the fisherfolk were Hindus (72%), followed by Muslims (26%), and Christians (2%). Considering the occupational patterns, 73 percent were engaged in fishing, 26 percent participated in fishing-allied activities, and 1 percent worked outside the sector. Among allied activities, 28 percent were involved in fish marketing, 10 percent in net making and repairing, 3 percent in curing/processing, 3 percent in peeling, and 51 percent as labourers. Fishing crafts mainly comprised outboard vessels (63%), followed by mechanized (8%) and inboard (<1%) boats. The findings highlighted fisherfolk livelihood characteristics, emphasizing the need for targeted policy interventions to enhance their well-being.



and ensure social security. Understanding their socio-demographic landscape is crucial for developing conservation policies that balance ecological sustainability with community welfare.

Keywords: Fisherfolk demographics, Palk Bay, Dugong Conservation Reserve, Livelihood characteristics, Coastal communities



MBC-P3

COMPARATIVE ASSESSMENT OF MARINE BIODIVERSITY IN KERALA'S COASTAL HOTSPOTS: THIKKODI AND THIRUMULLAVARAM

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A comparative study conducted from December 2024 to February 2025 identified Thikkodi and Thirumullavaram as major coastal biodiversity hotspots along the Kerala coast, highlighting their unique ecological features, marine diversity, and anthropogenic challenges. Thirumullavaram Beach, located in the Kollam district, spans 423 meters in length and 16 meters in width, with a rocky substrate, neutral pH (7), lower TDS (714 ppm), and salinity of 30 ppt, supporting diverse hard corals, seaweeds and clear waters with minimal wave action and fishing activity. Its unique laterite-type reddish rocks, porous from wave action, create microhabitats for various organisms, while a slanting seawall and a short 20-meter sandy stretch used for temple rituals add to its ecological profile. In contrast, Thikkodi Beach in Kozhikode district, shorter at 180 meters and narrower at 10 meters, shares a rocky substrate and similar salinity (30 ppt) and temperature (32°C) but exhibits higher TDS (860 ppm) and slightly alkaline pH (7.2). Nearby Kodikkal Beach, part of the Thikkodi region, features a unique intertidal zone with sandy and rocky habitats, abundant seaweed, soft corals, and rocky pools hosting marine ornamental fishes. Kodikkal faces high fishing activity, plastic pollution, and tourism pressures, though it remains less disturbed than Thikkodi. Thirumullavaram, protected by a seawall and serving as a tourism and pilgrimage hub, shows higher biodiversity with unique purplish-pink pigmentation on rocks and corals, while Thikkodi struggles with greater anthropogenic pressures, including tourism, fishing, and plastic waste. Conservation strategies like waste management, community education, regulated fishing, and eco-friendly tourism are vital to protect coastal ecosystems and biodiversity for the future.

Keywords: Coastal biodiversity, Anthropogenic pressures, Ecological conservation, Plastic pollution



MBC- P4

A COMPARATIVE STUDY ON THE BIODIVERSITY OF KOVALAM AND VARKALA BEACHES

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This study compares the biodiversity of Kovalam and Varkala beaches, Kerala, India, through February 2025 field surveys. Kovalam's rocky-sandy substrate (charnockite rocks) sustains rare coral colonies (1–4 m depth), sponges, bivalves, reef fish, oysters, barnacles, and red/green seaweeds. However, coastal erosion, sedimentation (TDS: 962 ppm), fishing, and tourism activities (e.g., snorkelling) threaten its ecosystem. Varkala's sandy substrate and laterite cliffs (Varkala Formation) lack corals but host saline-adapted cliff vegetation, oyster shell remnants, and a freshwater spring. Its biodiversity is limited to sparse intertidal organisms, with anthropogenic pressures from pilgrimage rituals, resorts, and high-impact water sports (e.g., jet skiing). Morphologically, Kovalam (254 m length, 13 m width) is shorter and elevated (28 m) compared to Varkala's elongated stretch (424 m length, 10 m width, 24 m elevation). While both share salinity (30 ppt) and pH (7.3), Kovalam's rocky habitats enhance biodiversity through foundational species (corals, seaweeds), whereas Varkala's sandy substrate restricts ecological complexity. Kovalam faces reef fish overexploitation and pollution risks despite controlled tourism; Varkala contends with habitat degradation from intensive tourism. Conservation strategies must prioritise context-specific measures: coral protection, erosion control, and sustainable fishing in Kovalam; eco-tourism, cliff preservation, and pollution mitigation in Varkala. The findings underscore the urgency of balancing Kerala's socioeconomic activities with ecological preservation to strengthen coastal resilience against escalating anthropogenic pressures.

Keywords: Biodiversity, Coastal Ecosystems, Anthropogenic Pressures, Coral Reef Conservation, Sustainable Tourism



MBC- P5

JEWELS ON THE DOCKS: A PRELIMINARY STUDY ON THE BYCATCH OF MARINE ORNAMENTAL FISHES IN THE GULF OF MANNAR

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A preliminary study was undertaken from December 2024 to March 2025, at the Tuticorin Fisheries Harbour, Tamil Nadu, India, to assess the diversity of marine ornamental fishes taken as bycatch from shrimp and fish trawls operating in the Gulf of Mannar. A total of 35 species belonging to 19 families. Members of the family *Balistidae* and *Tetraodontidae* contributed to the highest diversity of species taken as bycatch. Three species, *Odonus niger*, *Halichoeres zeylanicus*, and *Fistularia petimba* were the three most dominant species. Of the 35 species, two species each are listed as threatened and Data Deficient on the IUCN Red List, while 30 species are assessed as Least Concern. One species could only be identified to the generic level. Family *Syngnathidae* was contributed by five species, all of which are listed in Schedule II of the Indian Wildlife (Protection) Act 1972. These species are marketed to the fishmeal and poultry feed industry in boxes of approximately 50kg with an average price of 10-50 Rs/10kg. During seasons of high catches (September to November), an average of 1500 boxes/day are transported from the harbour. The nature, intensity, and implications of marine ornamental fishes taken as bycatch is discussed, and options for sustainable management are presented.

Keywords: Bycatch, Marine ornamentals, *Syngnathidae*



MBC- P6

METAL ACCUMULATION IN BIVALVES AND FINE SEDIMENTS OF MALABAR COAST, SOUTH EASTERN ARABIAN SEA

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Aquatic ecosystems serve as vital sources of nutritious food; nonetheless, bivalves like clams, mussels, and oysters pose significant health threats to humans when contaminated with heavy metals. Accurate measurements of the concentrations of heavy metals in the environment and soft tissues are necessary. This process requires vigorous measurement of heavy metal levels in the soft tissues and the environment. The spatial distribution of metals was assessed in surface sediments and bivalves (*Saccostrea cucculata*, a suspension-feeding mollusc) within the Malabar coastal waters of the South Eastern Arabian Sea. *Saccostrea cucculata* from the coastal rocks were gathered on the same day and from various study locations, and the metal content in their tissue was analysed. The data revealed that As, Co, Fe, Mn, Ni, Pb, and V had low contamination, Hg showed moderate contamination, while Cd, Cu, and Zn exhibited very high contamination. The Se displayed significant contamination only in March 2024. The rocky shores might have contributed to the natural sources of heavy metal contamination in this study area. Furthermore, it is possible that the agricultural runoff from the Korappuzha River and the mini harbours had a significantly larger effect than the natural sources in the study area. Small-scale industries could also have played a role in the presence of these metals at all sampling locations, alongside the continuous contribution of pollutants from human activities. This research underscores the necessity of identifying sources and closely tracking the contamination from Cd, Cu, Zn, and Se on both seasonal and annual bases for practicing sustainable bivalve fisheries in the region.

Keywords: Bivalves, Metal, Arabian Sea



COMMUNITY STRUCTURE OF MICROPHYTOPLANKTON IN THE INTERTIDAL POOLS ALONG THE SOUTH-WEST COAST OF INDIA

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Intertidal pools represent a dynamic habitat characterized by high diversity and dense populations within confined spaces. Each species plays a crucial role in the ecological dynamics of these pools. Despite the predominance of sandy beaches along the southwest coast of India, research on these beaches and their intertidal pools is limited. Therefore, this study aimed to investigate the community structure of microphytoplankton in four distinct intertidal pools along the southwest coast of India through sampling and data collection carried out from October 2021 to June 2022, encompassing the monsoon, post-monsoon, and pre-monsoon seasons. The physicochemical characteristics revealed a surface water temperature ranging from 24°C to 33.5°C, with higher temperatures noted during the pre-monsoon season. Salinity exhibited an elevated mean value of 23.6 psu during the pre-monsoon season. Nutrient concentrations in the intertidal pools displayed considerable variation, occasionally reaching high levels. The monsoon season recorded the highest average values for phosphate ($40.6 \pm 28.7 \mu\text{mol/L}$), nitrate ($29.5 \pm 18 \mu\text{mol/L}$), and the maximum dissolved silicate concentration ($88.21 \mu\text{mol/L}$), coinciding with a notable microphytoplankton diversity. Principal Component Analysis (PCA) indicated elevated levels of chlorophyll a, Total Cells per Liter (TCL), and nitrate concentration during the post-monsoon season. Notably, nitrate significantly correlated with Total Cells per Liter throughout the study period. The peak surface chlorophyll a concentration was observed in the post-monsoon season, aligning with the highest microphytoplankton cell density ($179.2 \times 10^4 \text{ cells/L}$). Diatoms dominated in four stations, followed by dinoflagellates, cyanobacteria, green algae, silicoflagellates, and



Euglena. Noctiluca scintillans and *Gonyaulax polygramma* blooms were observed during the study. The k-dominance plot assessed the average phytoplankton composition in different seasons, demonstrating greater diversity during the monsoon and pre-monsoon periods compared to the post-monsoon season. This comprehensive assessment highlights the ecological significance of intertidal pools, providing insights into the dynamics of microphytoplankton across different seasons.

Keywords: Microphytoplankton, Dinoflagellates, Intertidal pools, South-west coast of India



BIOREMEDIATION: A SUSTAINABLE SOLUTION TO PLASTIC POLLUTION IN AQUATIC ECOSYSTEMS

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Microplastic pollution in marine environments has become a critical ecological concern, with millions of tons accumulating in oceans annually, affecting marine biodiversity and food chains. Bioremediation, utilizing bacteria, fungi, and microalgae, offers a promising and sustainable approach for microplastic degradation through biodeterioration, biofragmentation, assimilation, and mineralization. Studies indicate that marine microbial consortia can degrade up to 32% of microplastics within 60 days under optimized conditions. Notable degraders include *Pseudomonas* sp., *Bacillus* sp., *Aspergillus* sp., and *Chlorella* sp., which produce enzymes such as PETase and laccase to break down polymers. Environmental factors like salinity, UV radiation, oxygen availability, and nutrient levels significantly influence biodegradation rates, with optimal activity observed at salinities between 25–35 PSU and temperatures between 25–37°C. Analytical techniques such as Fourier-transform infrared spectroscopy (FTIR) and scanning electron microscopy (SEM) confirm structural and chemical modifications in degraded microplastics. Despite promising laboratory results, large-scale marine applications face challenges, including slow degradation rates, environmental stability of engineered microbes, and microplastic dispersion. Future research should focus on enhancing microbial efficiency through genetic engineering, improving enzyme activity, and integrating bioremediation with existing marine conservation strategies. Advancing marine-based bioremediation technologies could provide a long-term, eco-friendly solution to mitigate the global microplastic crisis in ocean ecosystems.

Keywords: Marine plastic pollution, Bioremediation, Plastic-degrading microbes



MBC- P9

DIVERSITY, DISTRIBUTION, AND ECOLOGICAL STATUS OF MARINE INTERTIDAL CRABS OF GUJARAT COAST, INDIA

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The marine intertidal zone along the Gujarat coast of India is home to a diverse assemblage of hermit crab species, which play a significant ecological role in maintaining the health and balance of these coastal ecosystems. This study investigates the diversity, distribution, and ecological status of hermit crabs in the intertidal zones of Gujarat, providing an in-depth analysis of their species composition and habitat preferences. Field surveys were conducted at several sites along the coastline, including rocky shores, sandy beaches, and mudflats, during different tidal phases. A total of fourteen species of hermit crabs were identified, belonging to multiple genera and families, with distinct spatial distribution patterns across the various intertidal habitats. The study highlights the ecological significance of hermit crabs in the intertidal zone, focusing on their role in nutrient cycling, sediment turnover, and as prey for higher trophic levels. Additionally, the research examines the impact of environmental stressors, such as pollution, habitat degradation, and climate change, on the populations and ecological status of hermit crabs. The findings provide valuable insights into the conservation and management of marine intertidal ecosystems in Gujarat, emphasizing the need for sustainable practices to protect these vital coastal habitats and their biodiversity.

Keywords: Diversity, Distribution, Ecological status, Hermit crabs, Intertidal zone, Gujarat



MBC- P10

THE EXCLUSIVE PRESENCE OF *CELLANA KARACHIENSIS* IN THE SAURASHTRA COASTLINE: A STUDY OF ITS HABITAT AND DISTRIBUTION

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Gujarat, with its unique coastal characteristics, is a biodiversity hotspot compared to other coastal states in India. The Saurashtra region, located between the two gulfs on the western coast, is known for its longest and most biodiversity-rich rocky-sandy coast. This study focuses on *Cellana karachiensis*, a common species of the rocky shore ecosystem in Gujarat, predominantly inhabiting the upper littoral zone. The species thrives in crevices, holes, and pools within rocky substrata but is absent from muddy and sandy shores. It was not observed in the middle or lower littoral zones and is restricted to the Saurashtra coastline, with no records from the remainder of the west coast or the entire east coast of India. Five sampling stations—Okha, Dwarka, Veraval, Sarkeshwar, and Naip (Mahuva)—were selected among 14 surveyed sites for this study. Temporal fluctuations in density were highest during the monsoon season, decreasing post-monsoon to winter. Spatially, the highest density was observed at Dwarka, while Okha exhibited the lowest. Abundance showed a contrasting trend, with higher values at Veraval and lower at Okha. The species' frequency was highest at Sarkeshwar and Dwarka. Vertical zonation patterns indicated that *C. karachiensis* was most abundant in the spray zone at rocky shores like Okha, Dwarka, and Veraval. At rocky-sandy or rocky-muddy shores like Sarkeshwar and Naip, it was more concentrated in the middle littoral zone. The species was absent in the lower littoral zone at Okha, Dwarka, and Veraval.

Keywords: *Cellana karachiensis*, Rocky shore, Gujarat coastlines, Abundance and density



MBC- P11

DECIPHERING DEEP-SEA FISH OTOLITHS: MORPHOLOGICAL AND MORPHOMETRIC APPROACHES FOR SPECIES IDENTIFICATION AND PREY SIZE ESTIMATION

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Deep-sea fish otoliths exhibit diverse morphological features and serve as valuable taxonomic tools for species identification. Additionally, numerical expressions derived from simple linear regressions of otolith morphometric measurements are used to back-calculate prey biomass. This study presents, for the first time, the diagnostic features of otolith morphology for 21 deep-sea scorpaenoid and dactylopterid species. Furthermore, it examines the relationships between fish size (total length and weight) and otolith size (length, width, area, perimeter, and weight) in 10 dominant species, using a total of 567 right sagittal otoliths. Morphological descriptions are based on otolith shape, outline, and sulcus acusticus features, as observed in SEM micrographs. Otolith morphometric measurements including width (OW), length (OL), perimeter (OP), and area (OA) were extracted from photographs using *ImageJ*. Significant positive correlations ($p < 0.05$, $r^2 > 0.9$) were observed, and numerical models were developed using linear regression. The r^2 values for the relationship between otolith variables and fish size ranged from 0.96 ($OL \times W$, *Neomerinthe erostris*) to 0.47 ($OW \times TL$, *Minous inermis*). Otolith length (OL) was the most effective predictor of fish length in five species: *Neomerinthe erostris*,



Setarches guentheri, *Dactyloptena orientalis*, *Snyderina guentheri*, and *Minous inermis*. In the remaining five species, otolith area (OA) provided more accurate predictions. For fish weight estimation, OA was the best predictor for six species via., *Satyrichthys laticeps*, *Snyderina guentheri*, *Pterygotrigla macrorhynchus*, *Pterygotrigla arabica*, *Minous inermis*, and *Dactyloptena papilio*. These findings enhance species identification and ontogenetic characterization, contributing to ichthyology by addressing taxonomic ambiguities within these groups. Moreover, the models provide novel insights into fish size prediction from otoliths, supporting future studies on prey biomass estimation for food-web dynamics. The representative otolith images included in this study offer valuable references for taxonomy, paleontology, and ecological research.

Keywords: Deep-sea fishes, Otolith morphology, Biometry, SEM, Diet studies



MBC- P12

SPECIES DIVERSITY AND COMMUNITY STRUCTURE OF
ICHTHYOFAUNA IN THE SEAGRASS ECOSYSTEM OF
MINICOY ATOLL, LAKSHADWEEP, INDIA

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The present study consists of the species diversity, abundance, and community structure of ichthyofauna in the seagrass meadow of Minicoy Atoll, Lakshadweep Islands. Two hundred and three species of fish were recorded during the study, from four stations in the Atoll. They belonged to 2 classes, 11 orders, 43 families, and 93 genera. Six species belonged to the class Chondrichthyes and 197 species to Osteichthyes. Family Pomacentridae showed maximum abundance of species (22%). Station I, having proximity to the coral reefs, observed the maximum number of families (37) and species (129), and the minimum number was in Station II (23 families and 52 species). The Bray-Curtis similarity plot showed a similarity range of 22 to 52%, seasonally. Station I showed the highest Shannon-Wiener diversity index ($H' \log_2$) (4.22) during August and the lowest (2.91) during June. Stations I and III showed comparatively higher abundance and diversity of fish. Variability in seagrass habitat structure and the interaction with coral reefs influenced the species composition and diversity of fishes in Minicoy Atoll. The findings of the present investigation can be used as baseline information for the fishery resource management of the region.

Keywords: Ichthyofauna, Seagrass, Species diversity, Minicoy Atoll, Lakshadweep



MBC- P13

ECOLOGICAL IMPLICATIONS OF SEA URCHIN DIVERSITY IN THE GULF OF MANNAR

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The Gulf of Mannar, a recognized marine biodiversity hotspot, supports diverse ecosystems, including significant sea urchin populations. This study assessed the diversity and distribution of sea urchin species across 13 islands from July 2023 to October 2024. A total of six species were identified, with Hare Island exhibiting the highest species richness, supporting five species (*Salmacis virgulata*, *Temnopleurus toreumaticus*, *Gymnechinus* sp., *Brissopsis alta*, and *Lovenia elongata*). The biodiversity indices reflect high species diversity and a relatively even species distribution. Notably, *Gymnechinus* sp. is recorded for the first time around Hare Island, marking a significant addition to the regional biodiversity. The Mandapam group exhibits higher species diversity, indicating a more ecologically stable and resilient marine community. The lower dominance index suggests that no single species is overwhelmingly prevalent, allowing for a more balanced species distribution. The higher Simpson's Diversity Index reflects greater species richness and evenness, signifying that the ecosystem supports multiple species without extreme population imbalances. The Mandapam Group has a seagrass-dominated ecosystem with 50% seagrass cover, followed by 20% coral cover, 20% macroalgal cover, and 10% sponges. The high seagrass presence supports diverse marine life, including herbivores and detritivores. Lower coral cover suggests environmental conditions favoring seagrass over coral growth. The presence of sponges adds to habitat complexity and biodiversity. Overall, this mixed substrate composition influences species distribution and ecosystem dynamics. Additionally, the higher Shannon-Wiener Index in the Mandapam group indicates a more complex and diverse ecosystem, where species are more evenly distributed. The species evenness index further supports this by showing that the relative abundances of different species are well-balanced. A higher Margalef's Index implies greater species richness, suggesting that the environmental conditions in this region favor biodiversity. These



results suggest that Mandapam's marine ecosystem is healthier and more diverse, likely due to favorable environmental factors such as moderate temperature, lower salinity, and the availability of food sources like macroalgae and coral-associated habitats. Environmental parameters such as sea surface temperature and salinity appear to influence biodiversity. The Mandapam group, with slightly higher temperature and lower salinity, supported greater species richness. In contrast, the Tuticorin group, with lower temperature and higher salinity, exhibited reduced biodiversity. These findings suggest that temperature and salinity are key drivers of sea urchin distribution in this region. Dissolved oxygen levels were comparable and did not negatively impact species diversity, indicating that other ecological factors, such as food availability, might play a more influential role. The study highlights the ecological significance of sea urchins in maintaining reef ecosystem stability.

Keywords: *Marine biodiversity, Sea urchins, Coral reef ecosystems, Gulf of Mannar, Keystone ecosystems*



MBC- P14

ECOLOGICAL ASSESSMENT OF ICHTHYOFaUNAL DIVERSITY
AND PHYSICO-CHEMICAL PARAMETERS OF MUNROE
ISLAND, KERALA

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Munroe Island is a traditional backwater village that is situated at the confluence of the Ashtamudi backwater and the Kallada River system. It is well known for its beautiful scenery and rich biodiversity. The objective of the study was to evaluate Munroe Island's fish diversity and water quality. 21 fish species from 16 families were found throughout the study, demonstrating the region's varied fish ecosystem. The comprehensive analysis of physico-chemical parameters of water quality highlighted various factors influencing ecosystem dynamics, including temperature fluctuations, pH levels, and dissolved oxygen concentrations. Despite its rich biodiversity, Munroe Island faces various anthropogenic pressures like pollution, habitat degradation, and the proliferation of invasive species, posing considerable threats to the indigenous fish diversity. Our findings highlight the critical need for integrated conservation strategies, habitat restoration efforts, and sustainable fisheries management to mitigate biodiversity loss and safeguard the ecological integrity of this vulnerable ecosystem.

Keywords: Fish diversity, Threats, Conservation measures



MBC- P15

RADIOMETRIC IN-VIVO SPECTRAL REFLECTANCE ANALYSIS OF HARD CORALS OF LAKSHADWEEP ISLANDS, INDIA

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In-situ spectral signature and spectroscopy data collection methods are significant for identifying, analysing, and distinguishing coral species at their taxonomic level. Researchers extensively use in situ radiometric surveys and techniques for various terrestrial and ocean applications; despite this, working in the marine environment has some limitations. The unprecedented climatic change disrupted the natural ecosystem for the suitable growth and survival of coral reefs worldwide. Massive coral bleaching events rapidly decline the live coral cover in the oceans by losing the equilibrium. This work showcases the in vivo spectral reflectance quantitative measurement techniques and analysis of hard-coral species of two islands, namely Andrott and Amini of Lakshadweep, and we also conduct comparative studies of corals in these two islands. The different coral species' spectral patterns and behavior were recorded using an Ocean Optics USB 4000 spectroradiometer, and photos were captured using a Canon EOS 750 D. Savitzky-Golay (SG) filtering methods are applied to reduce the signal-to-noise ratio (SNR) and smoothen the reflectance spectral curves for statistical computations. We used a step correction method to eliminate the thermal effects of the spectral data. In this study, we performed a T-test to check the significance level of the sample data of these islands. This study will also impact the corals' field-based radiometric data collection methods and preprocessing techniques that are essential in the research domain of coral ecology and coral bleaching studies.

Keywords: Radiometry, Spectral reflectance, Spectroradiometer, Lakshadweep Islands



MBC- P16

PHYTOPLANKTON COMMUNITY SHIFT BETWEEN THE LATE SOUTHWEST MONSOON AND FALL INTERMONSOON IN THE CENTRAL-EASTERN ARABIAN SEA (GOA)

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The present study investigates shifts in phytoplankton community structure, abundance, and diversity in the central-eastern Arabian Sea (Goa coastal waters) between the late southwest monsoon (LSWM; Sep. 2024) and fall inter-monsoon (FIM; Oct. 2024). It aims to understand how variations in hydrographical parameters such as temperature, salinity, nutrient concentration, water clarity, dissolved oxygen, and chlorophyll-a influence the diversity and composition of phytoplankton communities in this region. Water samples were collected from the surface, middle, and bottom layers at seven locations, including estuarine, coastal, and offshore waters, using a 5L Niskin sampler. Microscopic analysis was conducted to quantify phytoplankton community structure, abundance, and diversity. The results showed that phytoplankton were more abundant during FIM (avg. 78835 ± 46867 cells/L) than LSWM (avg. 52230 ± 47504 cells/L). In LSWM, phytoplankton abundance was higher in the coastal region and lower in the offshore region; whereas, in FIM, phytoplankton abundance was higher in the offshore region and lower in the coastal region. Phytoplankton diversity was high during LSWM (avg. 1.5 ± 0.6) compared to FIM (avg. 1.2 ± 0.3). Among the phytoplankton, centric diatoms were dominant (92.3%) during LSWM, primarily represented by *Chaetoceros* sp. and *Skeletonema* sp. For FIM, the centric diatom (70.8%) was lower than LSWM, primarily represented by *Leptocylindrus* sp., *Hemiaulus* sp., and *Skeletonema* sp. During LSWM and FIM, centric diatoms were dominant in the coastal (91.3% and 96.4%) region compared to the offshore (60 % and 86.8%) region.

Keywords: Phytoplankton, Centric diatoms, Pennate diatoms, Diversity, Central-Eastern



MBC- P17

MOLECULAR VS. MORPHOLOGICAL IDENTIFICATION:
RESOLVING TAXONOMIC CHALLENGES IN BIOERODING
SPONGE – A CASE STUDY OF *CLIONA* SP. FROM GUJARAT,
INDIA

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Bioeroding sponges play a crucial role in shaping marine ecosystems, particularly in coastal and coral reef environments, where they contribute to substrate erosion and reef degradation. Among them, species of the genus *Cliona* are known for their taxonomic complexity due to significant morphological plasticity, environmental influences on skeletal characteristics, and unresolved phylogenetic relationships. This study presents an integrative approach to the identification of a *Cliona* species from the intertidal zone of Gujarat, India, using both morphological examination and molecular analysis. Traditional taxonomic methods revealed similarities with *Cliona utricularis*, yet the absence of microscleres and the variability in tylostyle morphology raised challenges in definitive species confirmation. Molecular characterization, based on COI and 28S ribosomal DNA markers, showed high sequence similarity (99.42%) with *Cliona* sp. from Zanzibar and a moderate match (94.76%) with *Cliona mariae* from Costa Rica, highlighting potential cryptic diversity within the genus. Phylogenetic analysis further confirmed a close relationship with other *Cliona* species reported from geographically distant locations. The findings underscore the necessity of integrating molecular data with traditional taxonomy to accurately delineate species boundaries within *Cliona*. This study also marks the first record of this particular *Cliona* species from the Gujarat coast, contributing valuable insights into the biogeography of bioeroding sponges in the Indo-Pacific region. Given their ecological impact on reef structures, further studies on their distribution and bioerosion potential are essential for marine conservation and coastal management strategies.

Keywords: *Cliona*, Bioeroding sponges, Taxonomy, COI, 28S, Gujarat Coast, Molecular phylogeny



MBC- P18

FEEDING ECOLOGY OF ELASMOBRANCH SPECIES ALONG THE VISAKHAPATNAM COAST DURING THE MONSOON SEASON

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The feeding ecology of elasmobranchs provides insights into resource partitioning and food web dynamics in marine ecosystems, aiding their conservation and management. This study examined the feeding ecology of six elasmobranch species (*Acroteriobatus variegatus*, *Carcharhinus leucas*, *Gymnura poecilura*, *Iago omanensis*, *Maculabatis gerrardi*, and *Mobula mobular*) along the Visakhapatnam coast during the monsoon season (June–October 2024). Specimens were collected as bycatch using trawlers or gillnets. Stomach content analysis (SCA) and stable isotope analysis (SIA) were employed to examine: (i) the effect of habitat on diet and (ii) dietary differences among species. *I. omanensis*, *C. leucas*, and *G. poecilura* exhibited piscivorous diets, with *I. omanensis* showing greater prey diversity. In contrast, *M. gerrardi* and *A. variegatus* relied more on crustaceans, indicating lower dependence on teleosts. Consequently, benthic species (*G. poecilura*, *A. variegatus*, and *M. gerrardi*) showed distinct diet compositions from pelagic species (*C. leucas* and *I. omanensis*), minimizing niche overlap (PERMANOVA, $R^2 = 0.097$, $p < 0.05$). Similarly, SIA revealed pelagic species (*M. mobular* and *I. omanensis*) were depleted in ^{13}C , while benthic *G. poecilura* was enriched in ^{13}C , consistent with their feeding habitats (ANOVA, Tukey's HSD test, $p < 0.05$). *I. omanensis* exhibited a relatively larger isotopic niche, reflecting its diverse diet composition. Significant trophic level differences were highlighted by $\delta^{15}\text{N}$ values: *G. poecilura* had high $\delta^{15}\text{N}$ values, indicating its role as a top predator, while *M. mobular* had low $\delta^{15}\text{N}$ values, aligning with their planktivorous diet (ANOVA, Tukey's HSD test, $p < 0.05$). Thus, dietary differences among species and habitat-driven resource partitioning minimize niche overlap between elasmobranch species.

Keywords: Elasmobranchs, Diet composition, Stable isotope analysis



MBC- P19

EXPLORING THE INHABITANTS OF THE 'EIGHTH CONTINENT': ANALYSIS OF PLASTISPHERE BACTERIA ALONG THE COAST OF GOA

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While economic growth has brought advancements, it has also led to new forms of pollution, including 'white pollution,' commonly termed as plastic pollution. Plastics are omnipresent; they are reported in every niche, from the human gut to the Great Pacific Garbage Patch. This study examines the plastisphere communities on Plastic Marine Debris (PMD) from four Goan beaches: Vagator, Caranzalem, Colva, and Galgibaga. Aseptically collected plastic samples, stored in ice, were transported to the laboratory. One set was frozen (-20°C) for SEM. The other, washed with sterile seawater, was inoculated on ZMA agar (bacterial isolation) and Bushnell Haas Broth (enrichment). After two months of enrichment, bacteria were detected via spread plating onto Bushnell-Haas Agar and Mineral Salts Medium with LDPE as the sole carbon source. A total of 136 bacterial cultures were isolated (92 from isolation experiments; 44 from enrichment). Most isolates were from HDPE food wrapping (24), followed by nylon ropes (20), polypropylene labels (18), polyethylene plastic bags (11), and polypropylene-LDPE wrappers (11). Bacterial isolates were assessed for biofilm formation and lipase activity using the crystal violet assay and Tween 80 medium, respectively. Vagator had the most biofilm-forming and lipase-producing bacteria, followed by Caranzalem. SEM studies confirmed plastic-associated bacteria, but larger diatoms dominated most samples, likely overshadowing the bacteria. The influence of these bacterial cultures on the fate of PMD and their potential in plastic bioremediation warrants further study.

Keywords: Plastisphere, Plastic Marine Debris, Lipase Activity, Biofilm formation



MBC- P20

MANGROVE DISTRIBUTION AND EXTENT IN INDIA: A SATELLITE-BASED ASSESSMENT

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Mangroves play a crucial role in coastal protection, biodiversity conservation, and carbon sequestration. India's mangrove cover was recorded at 4,037.85 km² in 2020, constituting 31.01% of its 33,694 km coastline. However, between 1996 and 2020, the country witnessed a net loss of 73.34 km² in mangrove extent. This analysis, based on satellite imagery data from Global Mangrove Watch, has been instrumental in tracking these changes over time. The decline in mangrove cover is attributed to anthropogenic activities, coastal development, and climate-induced factors. From January 2019 to October 2024, a total of 7,059 mangrove disturbance alerts were issued, highlighting the vulnerability of these ecosystems. India is home to 37 species of mangroves, of which two species—*Sanataria griffithii* (Critically Endangered) and *Heritiera fomes* (Endangered)—are classified as threatened under the IUCN Red List. Conservation measures are essential to mitigate habitat loss and degradation. Satellite imagery, particularly data from Global Mangrove Watch, has been pivotal in assessing the health, distribution, and disturbances of mangroves. Remote sensing techniques have emerged as a valuable data source for policymakers and conservationists to implement targeted restoration efforts. Strengthening coastal resilience through mangrove conservation is imperative for sustaining biodiversity and protecting coastal communities from climate-induced hazards.

Keywords: Mangroves, India, Global Mangrove Watch, Satellite monitoring



MBC- P21

BACTERIAL DIVERSITY IN THE MANGROVE SEDIMENTS OF NORTHERN KERALA: A METAGENOMIC APPROACH

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Mangrove swamps are extremely productive marine ecosystems of considerable ecological significance; however, they are susceptible to human influences. The vitality of this ecosystem depends on the microbial communities within its sediments, highlighting the necessity to comprehend their functions and contributions. Taxonomic diversity and functional properties of bacterial species from eight mangrove areas in Northern Kerala were studied. Illumina HiSeq technology was used to sequence the V3–V4 region of the 16S rRNA gene. The metagenomic analysis revealed that the mangrove sediment in Northern Kerala comprises 64% bacteria, 35% unclassified groupings, and 1% archaea. The mangrove station at Edaat had the highest percentage of domain bacteria (79%). This was followed by Kasaragod (79%), Valappattanam (73%), Chettuva (69%), Ponnani (67%), Elathur (64%), Kadalandi (53%), and Pazhayangadi (45%). A total of 46 bacterial phyla were obtained, with Phylum Proteobacteria being the most predominant at 57%, followed by Bacteroidota, Actinobacteriota, and Firmicutes. The genera *Shewanella* and *Alcanivorax* were identified as the most abundant. The functional gene annotation identified genes responsible for the degradation of hydrocarbons, polysaccharides, and synthetic polymers, as well as the synthesis of lipids, nucleotides, amino acids, butanol, cobalamin, and secondary metabolites such as carotenoids and antibiotics in the mangrove sediment. This highlights the essential significance of the mangrove ecosystem in biogeochemical cycling and ecosystem functionality. The recent findings highlight a necessity for additional investigation of mangrove sediment bacteria, as numerous unnamed and uncultured fractions persist despite prior investigations.

Keywords: Mangrove sediment, Bacteria, Metagenomics, Diversity



MBC- P22

ECOLOGICAL SIGNIFICANCE OF MARINE ALGAE: EXPLORING SEAWEED DIVERSITY AND SYMBIOTIC INTERACTIONS IN DAKSHINA KANNADA AND UDUPI

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Marine algae play a vital role in coastal food webs, acting as primary producers that harness sunlight to generate food for animals. Similar to land plants, they form the foundation of marine ecosystems, supporting herbivores and offering shelter for young creatures seeking protection from predators, waves, or the sun. The diversity of marine algae, in terms of colours, shapes, sizes, and textures, creates rich underwater habitats. Seaweed beds, often referred to as underwater forests, serve multiple ecological functions, from providing food to herbivores to acting as a sheltering breakwater. In the coastal regions of Dakshina Kannada and Udupi district, the rich marine biodiversity presents an ideal setting for studying seaweed diversity and ecological interactions. A recent survey focused on intertidal zones along these coasts, examining seaweed distribution, abundance, and symbiotic relationships with organisms such as epiphytes and invertebrates. Preliminary findings revealed a diverse range of species, with seasonal variations in abundance. Notably, symbiotic interactions between seaweeds and associated organisms underscore their ecological roles in nutrient cycling and habitat formation. This study enriches our understanding of marine biodiversity in the region and paves the way for sustainable seaweed cultivation practices. Future research will explore the pharmacological properties of the species collected, potentially leading to the development of novel therapeutic agents.

Keywords- Seaweed, Biodiversity, Symbiotic relationships, Invertebrates



MBC- P23

EXPLORING THE EFFICACY OF PLANT-GROWTH-PROMOTING TRAITS OF MANGLICOLOUS YEASTS FOR MANGROVE CONSERVATION

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While bacteria and multicellular fungi have long been used for plant growth promotion, yeasts are emerging as new PGP agents. Mangroves, known for their unique and rich fungal diversity, offer a promising source. This study investigates the plant growth-promoting traits of manglicolous yeasts isolated from mangrove trees in Kumbalam and Puthuvype. A total of 215 isolates were screened for the following plant growth-promoting traits phosphate solubilization, production of phytohormone Indole Acetic Acid (IAA), siderophore, ammonia, catalase, nitrate, hydrogen cyanide, and different hydrolytic enzymes. The strain PV 23 produced a maximum IAA of $78.04 \pm 2.5 \mu\text{g ml}^{-1}$. The hydrolytic profile of the isolates revealed that 54% were proteolytic, 26.5% cellulolytic, 6.5% chitinolytic, 5.1% pectinolytic, and 17.7% ureolytic. The hydrolytic enzymes aid in plant nutrient acquisition. After screening PGP traits, three strains, P9 (*Candida tropicalis*), PV 23V (*Debaryomyces hansenii*), and KV35 (*Aureobasidium melanogenum*) were identified as the most potent candidates. P9 showed a significant antagonistic effect against *Sclerotium rolfsi* and *Rhizoctonia solani*. The strains P9 and KV 35 could tolerate drought stress. The potential of these strains in enhancing the growth performance of mangrove seedlings of *Rhizophora mucronata* was confirmed using the pot experiment. The results suggested that the consortium of three potent strains (P 9, PV 23, and KV 35) was more effective in increasing the number of shoot branches (89.2%), plant weight (87.5%), root length (83.3%), shoot height (57.9%) and total leaf area (35.1%) than that of control seedlings. This study highlights the potential of manglicolous yeasts in mangrove conservation through their diverse plant growth-promoting traits, supporting sustainable ecosystem management.

Keywords: Conservation, Mangroves, Plant growth promotion, *Rhizophora* sp.



A REVIEW ON THE PHYTOPLANKTON MORTALITY AND AN ASSESSMENT FROM THE CENTRAL WEST COAST OF INDIA (GOA)

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Aquatic, drifting, microscopic, and photosynthetic organisms are known as phytoplankton, which are essential primary producers and contribute to approximately half of Earth's oxygen supply. Phytoplankton mortality can be induced by various factors, such as rapid changes in temperature, salinity, light levels, and nutrient concentrations, as well as predation and diseases. Previous studies have reported sudden increases or declines in chlorophyll-a levels and the formation or disappearance of blooms due to environmental changes. However, limited research has been conducted to quantify or understand whether phytoplankton die during the decline phase of a bloom or under conditions of reduced chlorophyll-a levels. This study reviews the possible mechanisms and rates of phytoplankton mortality on a global scale and highlights the importance of such research, along with the need for improved methodologies. Experimental studies reveal that climate change-induced stressors, such as heat waves, are capable of causing mass mortality in phytoplankton (Baker and Geider, 2021). Furthermore, viral and fungal diseases, as well as high solar radiation, have also been reported to cause phytoplankton cell mortality. Fluorescent stains such as SYTOX Green, Fluorescein, and Propidium Iodide are more efficient in assessing cell viability and require fluorescence microscopy. Other stains, such as Neutral Red, Evans Blue, Trypan Blue, and Aniline Blue, have also been used for similar assessments with light microscopy. They are inexpensive but can also bind to debris, requiring careful attention. Neutral Red is a low-cost, low-toxicity substitute for fluorescent stains that is effective when used with light microscopy. Phytoplankton mortality was observed across the coastal waters of Goa, and the possible reasons are discussed.

Keywords: Phytoplankton, Viability, Mortality, Neutral red, Arabian Sea



MBC- P25

INTERACTIONS OF MICROPLASTICS WITH POLLUTANTS AND HEAVY METALS IN AQUATIC ENVIRONMENT

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Microplastics have become an emerging and persistent environmental pollutant, because their small size widely distributed across terrestrial, aquatic, and atmospheric ecosystems. Their presence is largely attributed to the rapid growth of plastic production and improper waste management, and it is difficult to remove through conventional remediation techniques and has been detected in various environmental matrices, including soil, water, air, and biological organisms. This review synthesizes recent search on sources, transportation, fate and environmental interactions of MPs, with a focus on their interaction with aquatic environment. MPs can absorb these pollutants due to their hydrophobic nature and large surface areas. These review highlights the negative impacts of MPs on organism and environmental health studied have reported that MPs can cause oxidative stress, cellular damage, DNA alterations and immune system disruptions in various organisms. MPs interact with these pollutants through surface absorption, altering their mobility and bioavailability. When digested by aquatic organisms, MPs and their associated contaminants can accumulate through trophic transfer, potentially affecting entire food chains and ultimately posing a risk to human health.

Keywords: Microplastics, Heavy metals, Bioaccumulation, Aquatic pollution, Environmental contaminants



MBC- P26

WATER QUALITY ANALYSIS OF VEMBANAD LAKE SYSTEM: A MULTIDISCIPLINARY APPROACH USING BIOLOGICAL INDICATORS, REMOTE SENSING, AND GEOSPATIAL ANALYSIS

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The Vembanad Lake system, one of the most important water bodies in Kerala, is facing increasing pollution due to human activities such as urbanisation, industrial discharge, agricultural runoff, and fisheries. This study observed the water quality at four locations, Udhayamperoor, Chellanam, Fort Kochi, and Panagad, using a multidisciplinary approach. The significant factors analysed were salinity, pH, chlorophyll-a (Chl-a), phosphate (PO_4^{3-}), nitrite (NO_2^-), and barnacle count, which was used as a biological indicator of pollution levels. The results showed significant differences in water quality across the locations. Fort Kochi recorded the highest salinity (30.45 ppt) and barnacle count (234), indicating high marine influence and pollution, while Udhayamperoor had the lowest salinity (24.70 ppt) and barnacle count (54), suggesting lower pollution levels. Panagad had the highest concentration of NO_2^- (2.423 $\mu\text{mol/L}$) and PO_4^{3-} (9.934 $\mu\text{mol/L}$), which pointed to excessive nutrient input and a higher risk of eutrophication. Chlorophyll-a levels, which indicate phytoplankton growth, were also highest at Panagad (4.225 mg/m³), while Udhayamperoor recorded the lowest Chl-a (0.221 mg/m³). Using Geospatial interpolation, pollution hotspots were identified at Fort Kochi, Chellanam, and Panagad, where nutrient levels and biological activity were highest. Barnacle counts proved to be a useful indicator of pollution and salinity variations. The present study highlights the importance of regular water quality monitoring to prevent further ecological threats. Implementing monitoring systems with a multidisciplinary approach can help in the timely detection of pollution load and ensure the sustainability of the Vembanad Lake ecosystem.

Keywords: Vembanadu Lake, Salinity, Barnacle, Pollution



MBC- P27

OFFSHORE AGGREGATING AREAS OF THRESHER SHARKS (ALOPIIDAE) ALONG THE WEST COAST OF INDIA FROM FISHER'S INTERACTION

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The family Alopiidae is made up of three known species of thresher sharks: the bigeye thresher (*Alopias superciliosus*), the pelagic thresher (*Alopias pelagicus*), and the common thresher (*Alopias vulpinus*). The most obvious characteristic that sets this group apart from other sharks is its extremely long upper caudal lobe, which is usually as long as the body. The quantification of spatial and temporal distribution patterns of sharks is important to understand their role in fishery dynamics. To assess the offshore distribution of family Alopiidae along the west coast of India based on Fisher's interview, we observed *A. superciliosus* and *A. pelagicus* landed at the Cochin fisheries harbour along the Kerala coast. We interviewed 150 fishers operating tuna longline based in Cochin fisheries harbour, Kerala, during December 2023 to March 2024 and gathered information on the catch locations of these sharks. The findings indicate that *A. superciliosus* (75%) dominated the catch over *A. pelagicus* (25%). During the study period, no records of *A. vulpinus* were found. The *A. pelagicus* was captured from 200 (Nautical Miles) NM±80NM at a depth of 100M±20M off the coast of Goa, and *A. superciliosus* was captured from 400NM±120NM at a depth of 100M±20M off the coast of Kerala (Lakshadweep). There was considerable spatial distinction, and the Northern Arabian Sea was used by *A. pelagicus*, and the Southern region was used by *A. superciliosus*, indicating that these are the aggregating areas of these sharks. Kernel density estimates (using QGIS) provided information regarding the distribution of *Alopias* species' core fishing area (50% kernel) and range outside the core area (95% kernel). Long-term landing monitoring and interaction with fishers can yield more insights to the spatial and temporal habitat use of these sharks.

Keywords: Distribution, Habitat use, GIS, Kernel density, Spatial partitioning



MBC- P28

INFLUENCE OF WATER PARAMETERS ON BIOLUMINESCENCE OF PLANKTONS IN THE POKKALI WETLANDS OF ERNAKULAM, KERALA

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The Pokkali wetlands are nutrient-rich, biodiverse ecosystems that lie under the Central Asian Flyway (CAF) and the Vembanad Ramsar site. An intensive study was carried out on the influence of water parameters on the bioluminescence of planktons in the Pokkali wetlands of Ernakulam, Kerala, from 01 June 2023 to 31 May 2024. Fortnightly samples were collected from three selected Pokkali wetlands of Ernakulam – Kumbalanghi, Chellanam, and Valiya Kadakkudy. During the study, a total of 20 species of phytoplankton were recorded. The water parameters, such as depth (cm), temperature (°C), pH, Total Dissolved Solids (ppm), Electrical Conductivity ($\mu\text{S}/\text{cm}$), Salinity (mg/L), Dissolved Oxygen (mg/L), were analysed and correlated with the bioluminescence activity of planktons in the study area. PAST software was used for statistical analysis. Bioluminescence by plankton is a remarkable adaptation that contributes to the diversity and beauty of marine ecosystems. The study provides valuable insights into the environmental influence on bioluminescence, biodiversity, and ecosystem health.

Keywords: Pokkali, CAF, Vembanad Ramsar site, Bioluminescence, Biodiversity



MBC- P29

DIVERSITY OF INTERTIDAL SABELLID AND SERPULID POLYCHAETES ALONG THE GUJARAT COAST, INDIA

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This study presents a quantitative survey of intertidal Sabellid and Serpulid polychaetes along the Gujarat coast, India, elucidating species diversity, distribution patterns and diversity indices. The 0.25 m² random quadrat method were used in monthly interval during lowest low tide of the selected sites of the Gujarat coast. Data analysis was performed in R ecological software. Ten Sabellid species, representing five genera (*Bispiria*, *Notaulax*, *Pseudobranchiomma*, *Branchiomma*, and *Pseudopotamilla*), were identified. *Bispiria porifera* exhibited a wide distribution, while site-specific occurrences were noted for various Notaulax species. The survey revealed twelve Serpulid species from six genera (*Vermilopsis*, *Spirobranchus*, *Marifugia*, *Hydroides*, *Filogranulla*, and *Laminatubus*), a significant expansion of known regional biodiversity. Distributional analyses indicated distinct species assemblages across Dwarka, Veraval, Okha, and Simar, suggesting habitat-specific preferences. Comparative morphological analysis of Serpulid tubes revealed intergeneric variations, highlighting taxonomic distinctions. This research establishes a comprehensive baseline for intertidal polychaete diversity in the Gujarat region, contributing to the understanding of their biogeographic distribution and ecological roles, and the application of biodiversity indices in assessing intertidal communities.

Keyword: Biodiversity, Polychaetes, Sabellidae, Serpulidae, Intertidal zone, Gujarat coast



MBC- P30

THE ROLE OF BLUE CARBON ECOSYSTEMS IN CLIMATE CHANGE MITIGATION AND COASTAL RESILIENCE: A REVIEW OF CURRENT UNDERSTANDING

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Blue carbon ecosystems, including mangroves, seagrasses, and tidal marshes, are now recognized as key contributors to the solution of global climate change and coastal protection. These ecosystems are highly efficient at capturing and storing atmospheric carbon, outperforming terrestrial forests. Their ability to store carbon in sediments for thousands of years makes them highly valuable in reducing increasing atmospheric CO₂ levels. In addition to carbon storage, these ecosystems offer essential coastal protection. Their complex structures absorb wave energy, actually minimizing erosion and reducing the effects of storm surges and sea-level rise. In addition, these ecosystems provide a myriad of ecological services, such as the provision of vital habitat, enhanced water quality through filtration, and the maintenance of rich marine biodiversity. Even though they are important, quantifying blue carbon stocks and fluxes remains challenging, and these ecosystems are exposed to significant threats from human activities like pollution and habitat loss. Conservation and restoration of mangroves, seagrasses, and tidal marshes, hence form a vital strategy towards achieving climate change mitigation goals and strengthening the resilience of coastal livelihoods. Embedding blue carbon principles into international and national policies is critical for ensuring the long-term sustainability and well-being of these important ecosystems.

Keywords: Blue carbon, Coastal resilience, Mangroves, Seagrasses, Carbon Sequestration



MBC- P31

CHARTING BIODIVERSITY IN ANTHROPOGENIC URBAN SEASCAPE – A CITIZEN-DRIVEN APPROACH

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The intertidal zone is a relatively poorly known wildlife habitat in India. Responsible utilisation and conservation of this space remain hindered partly by a dearth of data that can help evaluate its ecological significance. In 2017, we initiated a citizen-driven effort to collect biodiversity data from Mumbai's intertidal habitats. As part of this ongoing project, we use the iNaturalist platform as a database to document intertidal biodiversity, and have thus far documented 640 identified species, via 188 observers. The project has served to document previously unrecorded species and first records from the region, as well as species new to science; with iNaturalist's peer-reviewed identification system also serving to reliably identify some species misidentified in previously published literature. The data remains open-access in terms of use and has thus far seen significant use as a baseline source of biodiversity records in two third-party reports, two field guides, and one research paper. It was also used successfully in a legal case against an infrastructure project in the intertidal zone. The project continues to serve the broader purpose of engaging and educating diverse urban audiences of the existence and value of this habitat, and has served to enable some of our early participants to initiate their documentation efforts in different regions. We aim to expand this model to data-deficient intertidal regions outside our present geographies, whilst also utilising our public dataset to answer more specific ecological questions to aid better management of these areas.

Keywords: Citizen science, Intertidal ecology, Marine life, Open access, Outreach



MBC- P32

BIOLOGICAL MICROPLASTIC AND MACROPLASTIC CONTAMINATION IN BLUE CARBON ECOSYSTEMS: THREAT TO BIODIVERSITY AND CARBON SEQUESTRATION

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Plastic pollution has emerged as a critical threat to marine ecosystems, with microplastic and macroplastics impacting biodiversity, ecosystem health, and carbon sequestration processes. This study investigated the spatial distribution and ecological threats of plastic pollution across blue carbon ecosystems that include mangrove, seagrass meadows, seaweed beds, and coral reefs in the Gulf of Mannar (GoM), Palk Bay (PB), and the Lakshadweep. The core sampler and quadrant methods were employed for sample collection. To isolate the microplastic, the samples underwent wet peroxide oxidation treatment. Macro plastic pollution was highest in seagrass ecosystems (12 items/m² in PB) and seaweed ecosystems (10 items/m² in GoM). Microplastic distribution in sediments revealed higher retention in mangroves (0.47 particles/g in PB, 0.32 particles/g in GoM) due to their fine-grained structure. Depth-wise, microplastic accumulation was greater in subsurface sediments (Core B: 0.05 particles/cm in PB mangroves) due to biofouling and density-driven sinking. Water column analysis recorded the highest microplastic contamination in seaweed-dominated waters of GoM (0.053 particles/mL) and mangrove waters of PB (0.53 particles/mL). Shape categorisation resulted in fibres and filaments as dominant contributors, while size analysis revealed a prevalence of smaller microplastics (<500 µm). Biotic contamination was significant, with mangrove roots retaining the highest microplastics (28 particles/m² in PB, 12 particles/m² in GoM), followed by seaweed. Coral reefs exhibited higher microplastic in PB (0.46 particle/g) than in Lakshadweep. Plastic litter in coral reefs was more abundant in Lakshadweep (10 items/m²) compared to PB. Finally, soil carbon stock (SCS) analysis revealed that



mangrove sediments stored the highest carbon (23.4 Mg/C/ha in GoM) followed by seagrass and seaweed ecosystems. An inverse relationship between SCS and microplastic accumulation suggested that microplastics may alter carbon sequestration dynamics.

Keywords: Microplastics, Macroplastics, Blue carbon, Seaweed, Coral reefs
Mangrove, Seagrass,



MBC- P33

DIVERSITY AND POPULATION STATUS OF MARINE CRABS OF DIU ISLAND, INDIA

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A total of 33 marine crab species, representing 23 genera across 14 families, were recorded from the Diu coast, India. The highest crab diversity was observed on the Khukri coast, with 23 species from 17 genera in 11 families, followed by the Fudam coast (21 species from 15 genera in 9 families) and the Nagoa coast (20 species from 16 genera in 12 families). The Jalandhar coast exhibited the lowest diversity, with 17 species from 12 genera in 9 families. Each species was documented along with its habitat and distribution status. For the population ecological survey, four dominant crab species were selected based on their frequent occurrence: *Leptodius affinis*, *Epixanthus frontalis*, *Petrolisthes lamarckii*, and *Metopograpsus thukuhar*. Key population ecological parameters, including density and abundance, were analysed using standard ecological methods to assess species distribution and habitat preference.

Keywords: Marine crabs, Habitat distribution, Population status, Diu, India



MBC- P34

SPATIO-TEMPORAL VARIATION IN MEROPLANKTON COMMUNITY ALONG THE SOUTHWEST COAST OF INDIA

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Meroplankton are temporary plankton that represent the larval stage of nekton and benthos, which play essential ecological roles, including benthic-pelagic coupling and energy transfer to higher trophic levels. The distribution, metamorphosis, and settlement of meroplankton are influenced by several physico-chemical factors. To study the abundance and composition of meroplankton and its seasonal variation along the southwest coast of India, samples were collected using a working party net during the summer and winter monsoons. Summer monsoon samples were collected from five different transects (Mangalore, Beypore, Kochi, Alappuzha, and Kollam), while winter monsoon samples were collected from four transects (Mangalore, Kochi, Alappuzha, and Kollam). During both monsoons, the meroplankton community remained largely similar in composition, but notable variations were observed in their abundance and relative distribution. Meroplankton abundance was higher during the summer monsoon compared to the winter monsoon. Veligers were the most abundant meroplankton in the summer monsoon but among the least represented during the winter. Fish eggs and polychaete larvae were the other dominant meroplankton present in both seasons, with polychaete larvae found at most sampling stations. The seasonal variations in meroplankton abundance are driven by the distinct environmental conditions coupled with the recruitment window of benthic fauna. The upwelling during the summer monsoon enhances biological productivity, creating optimal conditions for larval survival and dispersal. Many benthic taxa synchronise their breeding cycles during the summer monsoon.

Keywords: Meroplankton, Southwest coast of India, Monsoon, Benthic fauna



MBC- P35

REPORT OF THE INVASIVE OCTA CORAL *CARIJOA RIISEI*
FROM THE ESTUARINE REGION OF DHARMADOM,
SWAMIKKUNNU

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Marine organisms have adapted to a multitude of environmental cycles, such as annual, seasonal, lunar/semilunar, daily, and tidal rhythms, and developed biological clocks entrained to these rhythms. However, molecular mechanisms of biological clocks that regulate the lunar- and tide-synchronised rhythms are still unknown. We have been researching molecular clockworks of the semilunar and tide-synchronised spawning rhythm of the grass puffer, *Takifugu alboplumbeus*, because it spawns several hours before high tide only during spring tide (new moon and full moon) in early summer. In the pineal gland, the expression of melatonin receptor genes exhibits ultradian variations with a period of 15 hours in the fish reared under constant darkness. To elucidate the molecular basis of the biological clock that makes this rhythm, a transcriptome analysis was conducted in the pineal gland. The pineal glands of mature male fish were sampled eight times every three hrs. Of approximately 20,000 expressed genes, about 1,100 genes were estimated to fluctuate in expression on 12–15-hour cycles, suggesting the presence of a circatidal clock of a 12.4-hour cycle. It has been revealed in the hypothalamus that there are many semilunar genes with peaks or troughs in the expression levels on the day of a new moon and full moon in a lunar month. These results suggest that the grass puffer may have circatidal and circadian clocks in the pineal gland, and they may regulate the semilunar gene expression in the hypothalamus because circatidal and circadian clocks only coincide once per semilunar month. Circatidal clock, a novel biological clock, as well as the circadian clock, may play important roles in the precisely-timed daily and semilunar spawning of the grass puffer.

Keywords: Corals, Dharmadom, Invasion



MBC- P36

THE IMPACT OF PREDATORY FISH SPAWNING AGGREGATIONS ON CORAL REEF SOUNDSCAPES

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Bioacoustics is a powerful tool for revealing spatial and temporal variations in ecosystems, but its correlation with ecological phenomena, especially in marine environments, is understudied. We examined the relationship between soundscapes and ecological factors during squaretail grouper (*Plectropomus areolatus*) spawning aggregation events in the Lakshadweep archipelago, India. By comparing audio recordings and visual fish community estimates at aggregation and non-aggregation sites, we assessed whether large predatory fish influence soundscape variation directly (via unique sounds produced by the groupers) or indirectly (via effects on other fish). We identified 13 distinct fish-related sounds that varied in temporal dynamics in relation to the presence or absence of spawning groupers. Aggregation sites did not feature any unique sounds, ruling out direct effects. However, they were dominated by percussive sounds at sunrise and sunset, likely from planktivorous fish, suggesting a signature of bottom-up facilitation during spawning events. Additionally, aggregation sites had fewer scraping sounds, suggesting top-down control on grazing behaviour by predators. Our findings show that ecological phenomena like apex predator aggregations, linked to lunar cycles (a commonly identified driver of biological soundscape variation), can significantly alter reef soundscapes. This demonstrates the role of species interactions in driving soundscape variability in marine ecosystems.

Keywords: Spawning aggregations, Bioacoustics, Ecological variability, Species interactions



MBC- P37

MICROPLASTIC POLLUTION IN ESTUARINE ENVIRONMENTS: A CASE STUDY FROM NORTHERN MALABAR COAST, INDIA

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An ecotone of freshwater and marine water ecosystems, estuaries play a significant role in harbouring a wide variety of living organisms, alongside acting as a sink for many environmental pollutants. The study focuses on the distribution of microplastics in two riverine estuaries, Bekal and Kumbla, along the Northern Malabar coast of Kerala, India. Water, sediment, and biota samples were analysed for the presence of microplastics. Sample preparation involved multiple sets of density separation, organic matter digestion, followed by membrane filtration. Identification and characterization carried out by optical microscopy and confocal Raman spectroscopy. An average microplastic abundance of 65 (IQR=28.33) par/kg and 130 (IQR=32.08) par/kg was found in sediments of Bekal and Kumbla estuaries, respectively. In biota samples, microplastic abundance was 1.88 to 3.43 MP/gram. The majority of microplastics were fibres, followed by fragments in colours blue, black, white, red, and green. Raman spectroscopic analysis revealed the predominance of polyethylene terephthalate and polyamides. Other major polymers include polyethylene, polystyrene, polypropylene, polyvinyl alcohol, and elastomers. The study underscores the widespread microplastic contamination of estuarine systems and its accumulation in sediments and the bodies of living organisms. Prominent sources of microplastic input in the river estuaries were fishing and aquaculture activities, wastewater discharge from local households, and improper solid waste disposal in and around the riverbanks. Microplastics in edible, commercially valuable aquatic organisms pose a serious threat to food security and can affect the health and well-being of the local population.

Keywords: Biota, Estuary, Microplastics, Raman Spectroscopy, Sediments



MBC- P38

STUDY ON GUT CONTENT OF *SCOLIODON SORRAKOWAH* (CUVIER) ALONG MUNAMBAM COAST, KERALA

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Fish gut content analysis provides valuable insights into feeding patterns. Direct observation of feeding habits in natural habitats is challenging, making gut content analysis a reliable alternative. *Scoliodon sorrakowah*, a demersal resource along the Kerala coast, was studied. India caught an average of 67,391 metric tonnes of sharks annually between 2007-2017. Methods of gut contents analysis include qualitative and quantitative approaches. Qualitative analysis involves identifying organisms in the gut, while quantitative analysis encompasses numerical, volumetric, and gravimetric methods (Chipp and Garvey, 2007). Stomach contents were collected from fresh fish, and weight, sex, and gonad maturity were recorded. The results show that shrimp have the highest frequency of occurrence in the gut (24%), followed by fish and polychaetes (19% each), and detritus (17%). Other components, including fish bones (7%), crustacean body parts (5%), copepods (3%), and ostracod and amphipod (2% each), were present in lower frequencies. Understanding the food and feeding habits of *S. sorrakowah* is crucial for evaluating its ecological role and position in the food web. This information informs aquatic management practices, including aquaculture and conservation.

Keywords: *Scoliodon sorrakowah*, Gut content analysis, Feeding patterns



MBC- P39

GLOMUS SPECIES AS A KEY TO SUSTAINABLE FARMING AND HABITAT RESTORATION

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This study explores the ecological significance of *Glomus* sp. in enhancing plant growth, nutrient uptake, and fruit yield, drawing parallels to its potential applications in marine ecosystems. While traditionally studied in terrestrial environments, the role of mycorrhizal fungi in nutrient cycling and plant-microbe interactions holds relevance for marine ecology, particularly in coastal and estuarine systems where plant-fungal symbiosis can influence ecosystem stability. A completely randomised design (CRD) was employed to assess the effects of *Glomus* inoculation on three Solanaceae crop varieties during the 2022–2023 autumn-winter season, with implications for broader ecological applications. The experiment involved seed pre-treatment and transplant inoculation with *Glomus* sp. Seeds were sown in trays containing a 1:1 potting mix of fungi and soil, and 20-day-old seedlings were immersed in the inoculum for 30 minutes before transplantation into pots. Morphological traits and yield parameters were recorded at 30, 60, 90, and 120 days for both inoculated and control plants. Results demonstrated that *Glomus* inoculation significantly enhanced yield and morphological traits by improving nutrient absorption and plant vigour compared to control varieties. These findings highlight the crucial ecological role of *Glomus* sp. in promoting sustainable agriculture by enhancing soil fertility, improving nutrient cycling, and reducing reliance on synthetic fertilizers. Translating this knowledge to marine ecology, the symbiotic potential of mycorrhizal-like associations in seagrasses, mangroves, and salt marshes could contribute to coastal ecosystem resilience, carbon sequestration, and habitat restoration. This study underscores the potential of vesicular-arbuscular mycorrhiza (VAM) as an eco-friendly bio-fertilizer with broader applications in supporting biodiversity and ecosystem stability in both terrestrial and marine environments.

Keywords: *Glomus*, Fruit yield, Carbon sequestration, Sustainable crop production



MBC- P40

PREVALENCE OF MICROPLASTICS IN THE OPEN OCEAN: INSIGHTS FROM THE CENTRAL INDIAN OCEAN

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Microplastics have emerged as a significant contaminant in marine environments, posing serious threats to aquatic ecosystems. This study investigates microplastic contamination in surface water samples from the Indian Ocean, collected during the ORV Sagar Nidhi cruise (SN/189). Sampling was conducted at two stations: S1 ($20^{\circ}45.632'S$, $80^{\circ}46.448'E$) and S2 ($4^{\circ}11.583'S$, $80^{\circ}46.448'E$). Surface water samples (5 L each) were collected using a Conductivity-Temperature-Depth (CTD) device and filtered through Whatman filter paper (1.2 μm pore size) using a vacuum filtration unit. The dried samples were examined under a Nikon SMZ 1500 stereo microscope for microplastic quantification. Results revealed a higher concentration of microplastics at station S2 compared to station S1. At S2, 29 fibres and 1 fragment were recorded, whereas S1 contained only 7 fibres. The microplastic fibres exhibited various colors, with black being the most dominant, followed by blue, red, and transparent. At both stations, fibres were the predominant form of microplastic contamination. The selected stations fall within the southern part of the central Indian Ocean, far from the mainland. Nevertheless, the presence of significant microplastic contamination even in these remote open ocean waters highlights the pervasive nature of plastic pollution in the Indian Ocean, warranting urgent measures to mitigate microplastic pollution and protect marine ecosystems.

Keywords: Central Indian Ocean, Microplastics, Fibre, CTD



MYCOSPORINE-LIKE AMINO ACIDS IN SCLERACTINIAN CORALS FROM THE LAKSHADWEEP ARCHIPELAGO: SPECIES AND DEPTH-DEPENDENT VARIATIONS

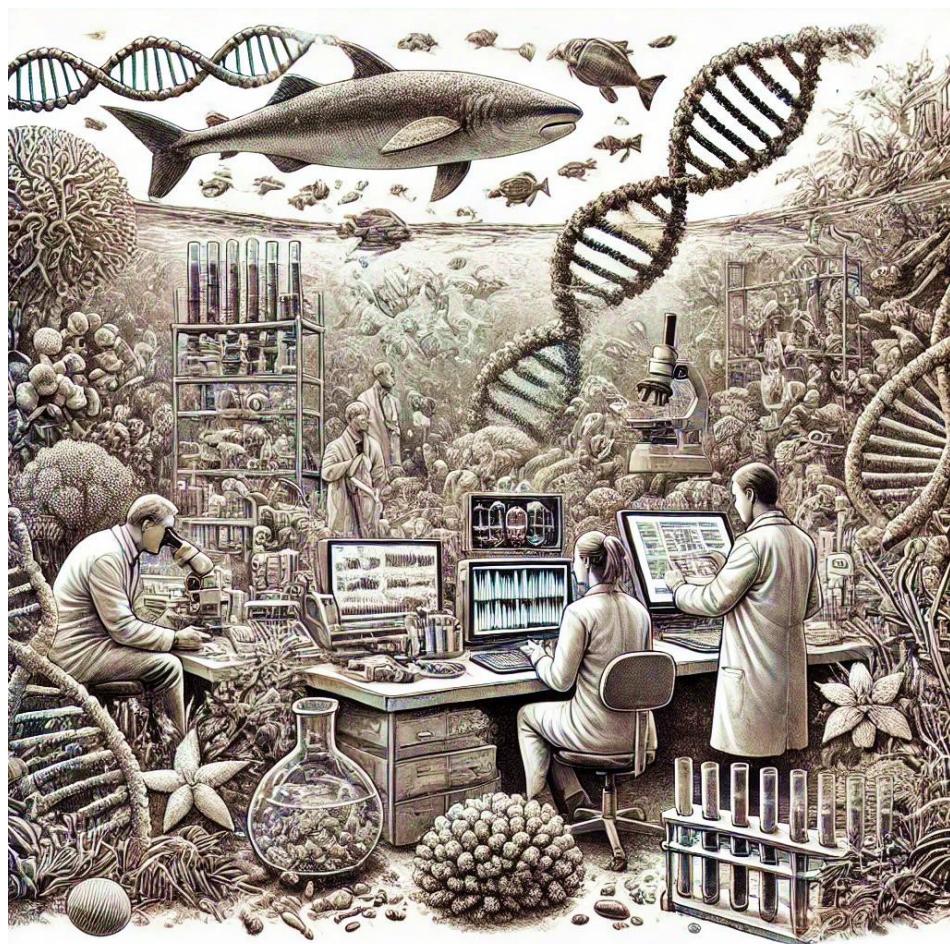
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Corals and other marine organisms are protected from harmful UV radiation through photoprotective processes, including the production of UV-absorbing compounds like mycosporine-like amino acids (MAAs). MAAs are water-soluble, low molecular weight compounds with absorption maxima between 309 and 360 nm. This study aimed to identify MAAs in corals and associated dinoflagellates, assess MAA diversity, and investigate bathymetric variations in MAA concentrations. Scleractinian corals from the Lakshadweep Islands were sampled at three depths: lagoon (0–5 m), 12 m, and 20 m from the Kavaratti, Kadmat, Agatti, and Andrott islands. Coral nubbins (1–2cm) were collected, sonicated in methanol to disrupt cells, and analyzed spectrophotometrically. Observations revealed that corals in shallow regions, particularly the lagoon, exhibited higher UV absorption maxima, indicating elevated MAA concentrations. The highest UV absorption maxima (310–362 nm) were found in corals from Kavaratti and Kadmat. Branching corals, such as *Acropora* and *Pocillopora*, which are more prone to bleaching, exhibited greater MAA diversity. Bathymetric analysis showed that MAA concentrations decreased with depth, with deeper samples containing MAAs in precursor forms. These results suggest that MAA production is stimulated by solar radiation and serves as a biochemical defense mechanism against UV damage. The study highlights the significant role of MAAs in coral photoprotection, particularly in shallow, high-radiation environments. Understanding MAA diversity and depth-related variations contributes to broader insights into coral adaptation to changing environmental conditions.

Keywords: Mycosporine-like Amino Acids, Scleractinian corals, UV radiation, Photoprotection, Bathymetry



Marine Biotechnology and Genomics

Invited Talks



MBG-IT 1

GENOMICS AND METABARCODING TOOLS FOR EXPLORING AND PRESERVING BIODIVERSITY

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Reference genomes are crucial for biodiversity research and conservation, providing detailed genetic maps that help us understand species diversity, evolutionary history, and population dynamics. This information is essential for developing conservation strategies and for exploring the potential of environmental species. Microbial natural products are important for the understanding of microbial interactions, chemical defense, and communication, and have also served as an inspirational source for numerous pharmaceutical drugs. Tropical marine cyanobacteria have been highlighted as a great source of new natural products; however, few reports have appeared wherein a multi-omics approach has been used to study their natural products. We collected from several sites around the world and sequenced the genomes of 24 tropical filamentous marine cyanobacteria. Our results highlight highly interesting biosynthetic gene clusters for genome mining among these cyanobacterial samples. Hence, to further explore this potential, we developed a machine learning classifier to connect mass spectrometry fragmentation data to biosynthetic gene clusters. Our new pattern-based genome mining pipeline links biosynthetic genes to metabolites that they encode for, as detected via mass spectrometry from bacterial cultures or environmental microbiomes. The rapid expansion of Next-Generation Sequencing data has driven the development of user-friendly tools for DNA metabarcoding analysis, increasing accessibility. However, many existing tools, despite their robustness, offer limited database customization,



restricting flexibility in taxonomic assignments. To address this, our group previously developed PIMBA, a pipeline for Metabarcoding Analysis. Nevertheless, PIMBA was originally implemented in Bash, which posed limitations in structure and processing speed. To enhance usability, reproducibility, and scalability, we developed a Snakemake-based version of PIMBA. This new Snakemake-based pipeline (PIMBA 3.0) optimizes metabarcoding analyses, offering a powerful tool for biodiversity research, ecological monitoring, and health sciences applications. Benchmarking analyses comparing versions 3.0 and 2.0 showed a significant reduction in execution time. Additionally, we introduced PIMBA Place, a new module designed for phylogenetic placement of OTUs/ASVs into a reference tree, providing evolutionary insights into unclassified sequences. Overall, PIMBA 3.0 significantly enhances the original pipeline, making it a valuable addition to the metabarcoding toolbox.

Keywords: Marine cyanobacteria, Reference genomes, DNA metabarcoding, PIMBA



MBG- IT 2
THE GENOMICS OF TISSUE REGENERATION: LESSONS FROM
ZEBRAFISH AND MICE

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Epimorphic tissue regeneration is bliss among lower vertebrates such as fish and frogs. However, mammalian regeneration, including humans, is restricted to simpler tissues such as skin, nails, hair, etc, with a compensatory regeneration seen with the liver. Genomics analysis reveals 70% genomic similarity that zebrafish exhibit to that of humans. Unlike mammals, upon injury, adult zebrafish retinas rely on their ability to reprogram resident. Retina regeneration remains incomplete in mammals despite extensive efforts to emulate zebrafish regenerative conditions. Several regeneration studies reveal that different gene expression events are triggered soon after an organ injury in mice and zebrafish. Still, gene expressions persist only in zebrafish to complete the task of regeneration. Here, we show that the long non-coding RNA (lncRNA) *malat1*, crucial for many biological functions, plays essential roles during retina regeneration. We explored the governing factors that affect the regulation of lncRNA *malat1*, which is differentially regulated after retinal injury in zebrafish and mice retina. We demonstrate that *malat1* functions through an Egr-dependent axis, modulated by Wnt, Notch, and TGF- β signaling pathways, and is necessary for effective retina regeneration. We performed RNA immunoprecipitation to establish the association of *malat1* with epigenome modifiers such as Ezh2 and Hdac1 in the regenerating retina. Moreover, we uncover that the antisense lncRNA *talam1*, which regulates *malat1* stability and bio-availability, is differentially regulated in zebrafish and mice, highlighting species-specific gene regulatory mechanisms after retinal injury. Cells with active TGF- β signaling stabilize Malat1 in mice while the same signaling destabilizes *malat1* in zebrafish. Taken together, our work uncovers a new role for the *malat1*/Egr1 axis in necessitating retina regeneration, which may have critical causative implications for differential gene expression dynamics and tissue regenerative ability among vertebrates.

Keywords: Tissue regeneration, lncRNA *talam1*, lncRNA *malat1*, Zebrafish

Oral Presentations



MBG -O1

EXPLORING THE HIDDEN DEEP-SEA VIROME: FIRST METAGENOMIC INSIGHTS FROM THE INDIAN WATERS

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The virosphere plays a crucial role in biogeochemical cycling, microbial mortality, horizontal gene transfer, and evolutionary dynamics in deep-sea environments. Despite their ecological significance, deep-sea viruses remain poorly characterized due to challenges associated with in situ sampling and cultivation. A significant portion of the deep-sea virome remains largely unexplored, particularly in the Indian waters. The present study reports the first-ever deep-sea virome from the east coast of India, specifically from a depth of 3,740 meters. Briefly, deep-sea sediments were subjected to a combination of centrifugation, filtration, and flocculation to purify and concentrate viral particles. This was followed by high-throughput metagenomic sequencing and bioinformatics analysis to investigate the biodiversity of deep-sea viral communities. The analysis revealed a dominance of Caudoviricetes (tailed bacteriophages), along with uncultivated marine viruses and unclassified dsDNA viruses, indicating the presence of both known and novel viral groups. The detection of *Vibriophages*, *Synechococcus* phage Mediterranean, and *Bellamyvirus bellamy* suggests potential ecological roles in host regulation and biogeochemical processes. This study highlights the vast genetic reservoir of deep-sea viruses and underscores the need for further exploration to elucidate their functional roles in marine ecosystems. Our findings expand current knowledge on deep-sea viromes and provide a foundation for future bioprospecting efforts targeting novel enzymes and bioactive compounds.

Keywords: Deep-sea virome, Indian Ocean virome, Marine viruses, Metagenomics, Viral diversity



MBG -O2

METHANOGENESIS IN TROPICAL COASTAL SEDIMENTS INFERRRED FROM 16S METABARCODING DATA

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The microbial production of methane or methanogenesis is an important biogeochemical process occurring in coastal sediments. In this study, methanogenesis pathways are investigated in nearshore sediments from a tropical coastal lagoon (Pulicat lagoon, India) using a combination of benthic flux measurements and 16S metabarcoding microbial data. Methanogenesis is indicated by *mcrA/B* (predicted using PICRUSt2), marker genes for the process. Additionally, benthic flux measurements indicate that the sediments are a perennial source of methane to the water column. This has implications for methane supersaturation in the surface waters and coastal emissions of methane to the atmosphere. Linkages between methane (*mcr genes*), nitrogen (*nif, nir, nos, nor, nrf genes*), and sulfur (*dsr genes*) metabolisms, and relationships with environmental conditions, are explored using network analysis. Salinity and sediment organic carbon concentrations are found to be crucial controls of methanogenesis in these sediments. The results are compared with other studies on benthic methane fluxes from coastal ecosystems and earlier reports on methane fluxes from Pulicat lagoon. Thus, the potential use of metabarcoding data in tracking ecosystem services (such as greenhouse gas sequestration) is revealed.

Keywords: Methanogenesis, 16S metabarcoding, Nearshore sediments, *mcr genes*



GENOMIC PROFILING OF *STREPTOCOCCUS AGALACTIAE* GEOGRAPHICAL ISOLATES TO DEVELOP A UNIVERSAL VACCINE

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Tilapia (*Oreochromis* sp.) is a large-scale farmed fish species worldwide due to its rapid growth and resistance to several diseases. The most infecting pathogen of tilapia in Asia is *Streptococcus agalactiae*, commonly referred to as Group B *Streptococcus* (GBS). The present study aims to investigate the genomic profiling of *S. agalactiae* isolates from India and Taiwan and the cross-protectivity of a formalin-killed vaccine in *Oreochromis niloticus*. Genotypic distribution by Pulsed-field Gel Electrophoresis (PFGE) was clustered utilizing SmaI and ApaI restriction enzymes. Also, ERIC PCR was performed to check the genetic differences among the geographical isolates. Furthermore, the *S. agalactiae* inactivated vaccine of 3×10^7 CFU.fish⁻¹ with sonicated β -glucan and alkoxyglycerol (AKG) was administered intraperitoneally in Nile tilapia. Fish blood was sampled weekly to measure immunochemical parameters like sodium oxide dismutase (SOD), myeloperoxidase (MPO), and lysozyme activity following bactericidal activity. PFGE results showed similar clusters between the Indian and Taiwan *S. agalactiae* isolates. The similarities among the isolates in PFGE are likely to showcase that *S. agalactiae* isolates can produce cross-protectivity against infection. Following immunization, on the 14th and 28th days post-vaccination, fish serum IgM titre values and immune genes MHC II β , IgM, TCR- β , IL-1 β , IL-6, and IL8 expressions were elevated ($p < 0.05$). The study highlights that the distribution of



similar *S. agalactiae* clusters has the potential for commercial vaccine production which can generate cross-protectivity against the pathogen.

Keywords: *Streptococcus agalactiae*, Genotyping, Universal vaccine, AMR



BIOACTIVITY SCREENING AND GENOME ANALYSIS OF SEAWEED ASSOCIATED BACTERIA FOR ANTIMICROBIAL METABOLITES

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Seaweed is known for several bioactive compounds, which are used in traditional medicines and provide health benefits and nutrition. The microorganisms of epiphytic and endophytic nature inhabiting seaweed also play a role in mineral recycling and chemical defense system which in turn has promising biotechnological applications. In this study, 305 seaweed-associated bacterial isolates from the South East coast of India were screened for antimicrobial activity against eleven clinically relevant pathogens. A total of 21 isolates showed antimicrobial activity against at least one of the tested pathogens. *Bacillus* species forms the dominant flora, constituting 81% of the share. Among these 21 isolates, one active isolate showing broad-spectrum antimicrobial activity was chosen and taxonomically assigned to the Genus *Vibrio* via biochemical and genomic methods. The ethyl acetate extract showed broad-spectrum antimicrobial activity against *E. coli*, *V. cholerae*, *V. parahaemolyticus*, *Enterococcus faecalis*, *Bacillus subtilis*, *Aeromonas hydrophila*, *Salmonella enterica*, and *Pseudomonas aerogenosa*. The most potent inhibitory zone measured was 28 mm, while the minimum zone was 16 mm. Bacterial extract also showed potent antioxidant activity. The presence of plant growth-promoting factors such as nitrite reduction, ammonia, and indole acetic acid (IAA) production confirms the symbiotic association between the bacteria and seaweed. Genome mining revealed the presence of antimicrobial and antioxidant compounds in the bacterial extract. The findings in this study highlight the potential of seaweed-associated bacteria as a source of several secondary metabolites with potential applications in the biotechnological field.

Keywords: Seaweed, *Vibrio* sp., Genome taxonomy, Secondary metabolites



MBG -O5

TRANSCRIPTOMIC PROFILING IN BRINE SHRIMP *ARTEMIA FRANCISCANA*

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The brine shrimp *Artemia franciscana* is a model organism for studying stress tolerance, developmental biology, and aquaculture applications. It plays a vital role in the aquatic food chain, serving as a primary nutritional source for fish larvae in culture systems. However, its omics resources remain limited, necessitating transcriptome-level insights. Here, we present a de novo transcriptome assembly of *A. franciscana* to establish a comprehensive molecular resource for functional and evolutionary studies. Given the emerging relevance of genotoxicity, transcriptomic profiling of *A. franciscana* was performed using next-generation sequencing. The sequencing results yielded a substantial dataset comprising 383,589 transcripts with an N50 value of 2,069. The completeness of the genome assembly was evaluated using BUSCO, which identified 95% conserved genes, ensuring high assembly quality. Functional annotation was conducted using multiple tools, including BLAST and EggNOG, while Gene Ontology (GO) annotation was assigned through GO analysis using blast2GO. Pathway annotation was performed using the Reactome and KEGG databases. This study provides a comprehensive reference dataset, reinforcing *A. franciscana* as a valuable model organism for future research.

Keywords: Transcriptome assembly, Functional annotation, *Artemia franciscana*



CHROMOSOME-LEVEL GENOME ASSEMBLY AND GENOME-WIDE CHARACTERIZATION OF FOX GENE FAMILY IN THE ASIAN GREEN MUSSEL (*PERNA VIRIDIS*): INSIGHTS INTO EVOLUTION AND AQUACULTURE GENOMICS

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The Asian green mussel, *Perna viridis*, is an ecologically and economically significant bivalve species in aquaculture. We build a high-quality chromosome-level genome assembly of *P. viridis*, generated using PacBio SMRT sequencing, Illumina short-read sequencing, Hi-C scaffolding, and Bionano optical mapping. The final assembly spans 723.49 Mb with a scaffold N50 of 49.74 Mb, anchoring 99% of the genome into 15 chromosomes. A total of 49,654 protein-coding genes were identified. Using this genomic resource, we performed a comprehensive genome-wide characterisation of the Forkhead box (FOX) gene family, which plays a pivotal role in cellular regulation, development, and environmental adaptation. We identified 28 *PvFox* genes classified into 12 subfamilies, with lineage-specific losses of *FoxI* and *FoxQ1*. Gene duplication in *FoxL1*, *FoxB1*, *FoxH1*, and *FoxD2* suggests adaptive diversification in response to marine stressors. Structural analysis revealed exon-intron variations, with some *PvFox* genes exhibiting intron loss, potentially facilitating regulatory plasticity. Phylogenetic analysis confirmed evolutionary conservation, while selection pressure analysis indicated strong purifying selection. GO enrichment highlighted FOX involvement in apoptosis, oxidative stress, and immune responses, reinforcing their functional significance in stress tolerance and disease resistance. This study provides the first FOX gene landscape in *P. viridis*, advancing our understanding of its adaptive success and offering insights into the evolutionary dynamics of key regulatory genes in marine bivalves.

Keywords: Genome assembly, Forkhead box genes, *Perna viridis*, Evolutionary adaptation



MBG -O7

HEPCIDIN GENE EXPRESSION IN GENETICALLY IMPROVED FARMED TILAPIA (*OREOCHROMIS NILOTICUS*): A MOLECULAR PERSPECTIVE ON GRAM-NEGATIVE AND GRAM-POSITIVE BACTERIAL INFECTIONS

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Hepcidins are a family of highly conserved cysteine-rich peptides found in several tissues, with the liver being the major production site. Gram-positive *Streptococcus iniae* and Gram-negative *Vibrio vulnificus* bacterial strains are a major threat to aquaculture, which calls for implementing remedial measures ensuring product biosecurity. Antimicrobial peptides (AMPs), with their immune-modulating capacity, are a promising biological alternative to antibiotics, which, on application, could improve the disease resistance of culture species. In vivo expression profiling of antimicrobial peptides generates real, high-throughput data, representing its expression dynamics under natural physiological conditions. The real-time quantitative PCR (RT-qPCR) was employed to quantify the expression dynamics of the gene under consideration, and the relative gene expression was calculated by the $2\Delta\Delta cT$ method. The hepcidin peptide discovered from genetically improved farmed tilapia (GIFT- *Oreochromis niloticus*) is a 90aa pre-propeptide with a 26aa mature peptide. The peptide on molecular analysis revealed the presence of an iron regulatory motif QSHLSL and a bactericidal stretch at S57-R89 in the mature peptide region, which classifies it as a dual-function peptide. The experimental challenge by *Vibrio vulnificus* and *Streptococcus iniae* induced a temporal expression pattern of hepcidin, which is pathogen-specific, indicating its targeted host defense role. The data offers crucial insights for AMP-based disease management strategies and drug discovery in aquaculture.

Keywords: *Vibrio vulnificus*, *Streptococcus iniae*, Gene expression profiling, Hepcidin, Genetically improved farmed tilapia



MBG -O8

dsRNA-MEDIATED SILENCING OF P53 GENE IN PRIMARY LYMPHOID CELL CULTURE OF *PENAEUS MONODON* FOR THE DEVELOPMENT OF A NOVEL CELL LINE

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Shrimp farming contributes to the major share of shrimp available in the market. Shrimp diseases, especially viral outbreaks including white spot virus (WSV), cause a financial loss of US\$4 billion annually. A major impediment to the extensive study of shrimp viruses and the development of effective therapeutic measures is the absence of a shrimp cell line. Despite several attempts over the years since 1986, none of the efforts led to the development of a shrimp cell line or even any other invertebrate cell line, except a hybrid cell line of shrimp and insect. The objective of the present study is to silence the p53 gene in the primary lymphoid culture of *Penaeus monodon* by the application of dsRNA. RNA was isolated from the lymphoid organ of *P. monodon*, cDNA was generated, and a partial sequence of the p53 gene was amplified, cloned, and sequenced. dsRNA of p53 was synthesized by in-vitro transcription method by adding T7 promoter sequence to p53 gene and using T7 RNA polymerase. To the primary culture of lymphoid organ, p53-dsRNA was added directly and also with lipofection. Significant ($p<0.05$) downregulation of the p53 gene was proved by qPCR in ds-RNA treated cells with and without lipofection. P53 gene silencing could pave the way for cell regulation as an initial step towards the development of a shrimp cell line.

Keywords: Shrimp cell culture, p53, White spot virus, ds RNA



MBG -O9

OMICS-DRIVEN INVASIVE SPECIES DETECTION IN BALLAST AND HARBOUR WATER: AN INNOVATIVE APPROACH TO PROTECT THE NATIVE BIODIVERSITY

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Human activities have accelerated the spread of species outside their natural habitats, often disrupting ecosystem dynamics and threatening native biodiversity, with ballast water discharge being a major factor in ecological disruption. This study uses metabarcoding of the 18S rRNA V7 region to analyze eukaryotic communities in ballast water samples collected from two ships and a harbour in the Gulf of Mannar. Ballast water samples were taken from ships originating in the Maldives and Durban, while a harbour sample represented the native aquatic environment. The analysis revealed 2,025 unique Operational Taxonomic Units (OTUs), showing significant variations in species composition based on geographic origin. The Maldives sample had high species diversity, with a predominance of phyla such as Arthropoda and Bacillariophyta. In contrast, the Durban sample had a more diverse composition, including Chordata, Ascomycota, and other taxa. The harbour water, though having the highest OTU count, showed a less-even distribution of species. Notable non-native species identified include *Limaria pellucida*, *Calanus finmarchicus*, and *Siokunichthys nigrolineatus*, highlighting the potential ecological risks posed by ballast water discharge in new environments. This study demonstrates the value of metabarcoding as a powerful tool for early detection of non-native species, aiding biosecurity efforts and the management of aquatic ecosystems. The differences observed in community structures are influenced by environmental and geographic factors, underscoring the importance of continuous monitoring to prevent the spread of invasive species.

Keywords: Invasive species, Gulf of Mannar, Next-generation sequencing, 18S rRNA, Metabarcoding



MBG -O10

ISOLATION AND IN VITRO PROPAGATION OF
THRAUSTOCHYTRID FROM BIVALVES IN INVERTEBRATE
CELL CULTURE MEDIA FOR BIOMANUFACTURING
DHA AND EPA

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Thraustochytrids are large-celled marine heterokonts recognized for their production of docosahexaenoic acid (DHA) and eicosapentaenoic acid (EPA), classifying them as oleaginous microorganisms. In this study, we compared two different invertebrate cell culture media, L-15 and DMEM Ham's F12, for isolation and in vitro propagation of Thraustochytrids from the gill tissue of *Villorita cyprinoides* and *Perna viridis*. The identity of Thraustochytrids was confirmed through 18S rDNA sequence analysis. The isolates were successfully cultured in vitro, maintaining proliferation for over two months. Subsequently, the cells were cryopreserved and later revived, demonstrating the viability of the long-term preservation method. There is an emerging demand of microbial DHA and EPA in human health, supported by numerous clinical studies. In this context, the isolated strain of Thraustochytrid MCCP-101 can serve as the candidate species for biomanufacturing DHA and EPA commercially.

Keywords: Thraustochytrids, In vitro propagation, Invertebrate cell culture medium



MBG-O11

IMMUNOGENOMICS APPROACH TO EVALUATE THE
EFFICACY OF *STREPTOCOCCUS INIAE* VACCINE IN NILE
TILAPIA (*OREOCHROMIS NILOTICUS*)

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Nile tilapia is an essential source of high-quality protein and is economically important in low- and middle-income countries. Incidence of disease outbreaks causes severe economic losses, leading to frequent use of antibiotics, which often pose a threat to antimicrobial resistance. Vaccination is a promising preventive measure, but a clear understanding of the immune response is needed, requiring an immunogenomics approach. The emerging pathogen *Streptococcus iniae* causes high mortality in aquaculture. The synthesized biomaterials were biophysically characterized with scanning electron microscopy (SEM). Vaccination and challenge studies were conducted in four groups (negative control, positive control, adjuvant, and vaccine with adjuvant), with samples collected at 14, 28, 42, 56, and 78 days post-vaccination. Comprehensive serological analyses to evaluate non-specific immune response, including lysozyme activity, superoxide dismutase (SOD) activity, bactericidal activity, and myeloperoxidase activity, were performed. Antibody titre assessments for IgM were conducted by ELISA. Immune genes (IgM, IL-1, IL-8, IL-6, MHC-1, and TCR-β) were studied in the spleen and head kidney. Elevated IgM levels were found in the Chitosan/alginate + Vaccine + lectin group. Specific antibody (IgM) against the antigen was significantly higher after booster vaccination. Cell-mediated immune response showed upregulated gene expression in the scaffold-encapsulated vaccine feed group. Survival rates were higher with the scaffold-encapsulated vaccine with lectin. Histological changes in organs showed notable effectiveness in orally vaccinated fish. This study suggests oral vaccine delivery as a promising approach for aquaculture and drug applications

Keywords: Nile tilapia, *Streptococcus iniae*, Chitosan, Alginate, Lectin, Vaccine

Poster Presentations



MBG-P1

RECENT ADVANCEMENTS IN MARKER-ASSISTED SELECTION
AND HORMONAL REGULATION FOR IMPROVING *P.*
MONODON BROOD STOCK DEVELOPMENT AND STRAIN
PERFORMANCE: A REVIEW

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Penaeus monodon (black tiger shrimp) represents one of the most economically valuable species in global aquaculture, yet production faces challenges from disease outbreaks and reproductive limitations. This review synthesizes findings from studies published between 2010 and 2024 on the application of genetic tools, reproductive physiology, and hormonal manipulation in the breeding and development of *P. monodon* strains. Developing superior strains and healthy brood stocks is essential for improving production efficiency and sustainability. Genetic diversity, which is critical for disease resistance and adaptive capacity. Marker-assisted selection (MAS) has emerged as a powerful tool for identifying and selecting beneficial traits, such as growth rate, disease resistance, and reproductive performance. With recent studies there has been 15-30% improvements in growth rates and also up to 40% enhanced survival rate against WSSV and EMS. Research on reproductive hormones, particularly GnRH-like peptides and methyl farnesoate, has shown enhancement in spawning frequency and larval quality without affecting broodstock health. The combination of marker-assisted selection and hormonal regulation provides a powerful strategy for improving *P. monodon* brood stock development and strain performance. However, challenges persist in maintaining genetic diversity and standard protocols across different farming environments. Future research should develop region-specific genetic markers, improve hormone delivery methods, and investigate environmental influences on trait expression.

Keywords: Genetic Diversity, Marker Assisted Selection, Hormonal regulation



MBG-P2

OBSERVATION OF GENETIC VARIATION IN THREE CERITHIINAE SPECIES USING COI GENE SEQUENCE

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The Cerithiinae subfamily (Gastropoda: Cerithiidae) encompasses a diverse group of marine snails that play crucial ecological roles in coastal and estuarine ecosystems. Despite their ecological importance, the taxonomy of many cerithiid species remains unresolved due to reliance on traditional morphological characters, which often fail to capture cryptic diversity. This study examines the molecular relationships among three cerithiid species—*Clypeomorus bifasciata*, *Clypeomorus subbrevicula*, and *Rhinoclavis sinensis*—from Indian coastal waters. Based on COI gene sequence data, the highest (G+C) content was observed in *Rhinoclavis sinensis* (43.9%), while the lowest was in *Clypeomorus bifasciata* (41.2%). Conversely, the highest (A+T) content was found in *Clypeomorus bifasciata* (58.8%), whereas *Rhinoclavis sinensis* exhibited the lowest (56.1%). The highest K2P distance (1.152) was observed between *Clypeomorus bifasciata* and *Rhinoclavis sinensis*, indicating they are the most genetically distinct. Whereas the lowest K2P distance (0.466) was observed between *Clypeomorus subbrevicula* and *Clypeomorus bifasciata*. However, the maximum K2P distance within the genus was found in *Clypeomorus subbrevicula*, and the minimum was found in *Rhinoclavis sinensis* (0.002). The low intra-species genetic distance for *Rhinoclavis sinensis* (0.002) suggests strong genetic homogeneity. The highest interspecific distance (1.152) between *Clypeomorus bifasciata* and *Rhinoclavis sinensis* indicates significant evolutionary divergence. The genetic distance analysis revealed that *Clypeomorus subbrevicula* and *Clypeomorus bifasciata* are more closely related, whereas *Rhinoclavis sinensis* exhibited the highest divergence from both species. Further research is needed to find the genetic variation among all species belonging to the subfamily Cerithiinae from Indian coastal waters.

Keywords: Cerithiinae, Indian marine fauna, Molecular phylogeny, COI gene



COMPARATIVE METAGENOMIC ANALYSIS OF DEPTH-STRATIFIED BACTERIAL COMMUNITIES IN ARABIAN SEA SEDIMENTS

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Marine bacteria are a vital component of the marine ecosystem, playing key roles in biogeochemical cycling, nutrient transformation, the microbial loop, organic matter decomposition, and symbiotic associations. The advent of metagenomics has revolutionized culture-independent analysis of bacterial diversity. The present study investigates depth-stratified microbial diversity employing 16S rRNA metagenomic sequencing of sediment samples collected from the Arabian Sea at depths of 10 m, 20 m, 200 m, and 400 m, hereinafter referred to as AS10, AS20, AS200, and AS400, respectively. Briefly, samples were processed using a combination of filtration and centrifugation, followed by DNA extraction according to Zhou et al. (1996) and high-throughput sequencing. Comparative microbial community analysis revealed the lowest Shannon diversity index in AS10 and the highest in AS400, indicating a progressive increase in bacterial richness with depth. Taxonomic composition analysis identified Proteobacteria, Firmicutes, Bacteroidota, and Actinobacteria as the most abundant phyla across all depths, with significant shifts in community structure. AS10 was dominated by heterotrophic bacteria (*Lentimicrobiaceae*, *Flavobacteriaceae*, and *Prevotellaceae*) involved in organic matter decomposition under oxygenated conditions. AS20 contained abundant sulfate-reducing bacteria, indicating a transition zone associated with carbon and nitrogen cycling. In AS200, anaerobic fermentative bacteria (*Anaerolineaceae* and *Planctomycetaceae*) were predominant, suggesting adaptation to deeper, low-oxygen sediments. AS400 exhibited the highest microbial diversity, enriched with extremophilic bacteria (*Pectostreptococcaceae* and *Comamonadaceae*) adapted to deep-sea environments. These findings provide insights into depth-stratified bacterial diversity in the Arabian Sea, highlighting microbial functional adaptations, sediment microbiome dynamics, and their implications for ocean nutrient cycling and deep-sea biogeochemistry.

Keywords: 16S rRNA sequencing, Arabian Sea, Marine microbiome, microbiota



MBG-P4

INTEGRATED TAXONOMIC APPROACH FOR THE
IDENTIFICATION OF SEA FANS AND SEA WHIPS FROM
LAKSHADWEEP ARCHIPELAGO

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Gorgonians are Cnidarians that mainly comprise of sea fans, sea whips, and sea pens, which produce a flexible skeleton made up of gorgonin protein and calcium-rich aggregates called sclerites. The present study is aimed at identifying gorgonians from Lakshadweep using morpho-taxonomy, and to conduct phylogenetic interpretation of sea fan and sea whip families. Here, four sea fan species, *Acanthogorgia spinosa*, *Menella rigida*, *Anthopleaura dimorpha*, and *Melithea* sp., are analysed and identified using an integrated taxonomic approach. The amplified *msh1* mitochondrial gene is sequenced for analysis and the phylogenetic trees were constructed. The evolutionary relationship and ancestry of the collected species were investigated using phylogenetic analysis. The structure of the sclerites which has been historically used for taxonomic classification of gorgonians, are also analysed to identify confirm the Genera and species. The evolutionary relationship of four gorgonian families – *Astrogorgiidae*, *Paramuriceidae*, *Ellisellidae* and *Melithaeidae* is also examined. *Ellisellidae* is the family of sea whips comprising of the genera *Juncella*, *Viminella*, *Verrucella* and *Dichotella*. The characteristics of colonies and their sclerites provided insights into the identification and study of the species. Specific forms of sclerites are present on the gorgonians and diversities in the natural structure of sclerites help analyse the variations and evolutions that have occurred within the species. The work is thus a combination of phylogenetic and morphological analysis of gorgonians. These species play a vital role in the marine ecosystem, and the initiatives for the conservation of gorgonians are guided by phylogenetic data. Identifying this unique species and their lineages will help to protect this vital and vulnerable gorgonian species in their ecosystem.

Keywords: *Gorgia*, Sea fans, hips, Sclerite morphology, Integrated taxonomy



MBG-P5

16S rDNA-BASED BACTERIAL DIVERSITY ANALYSIS OF SOUTH ANDAMAN MARINE SEDIMENTS

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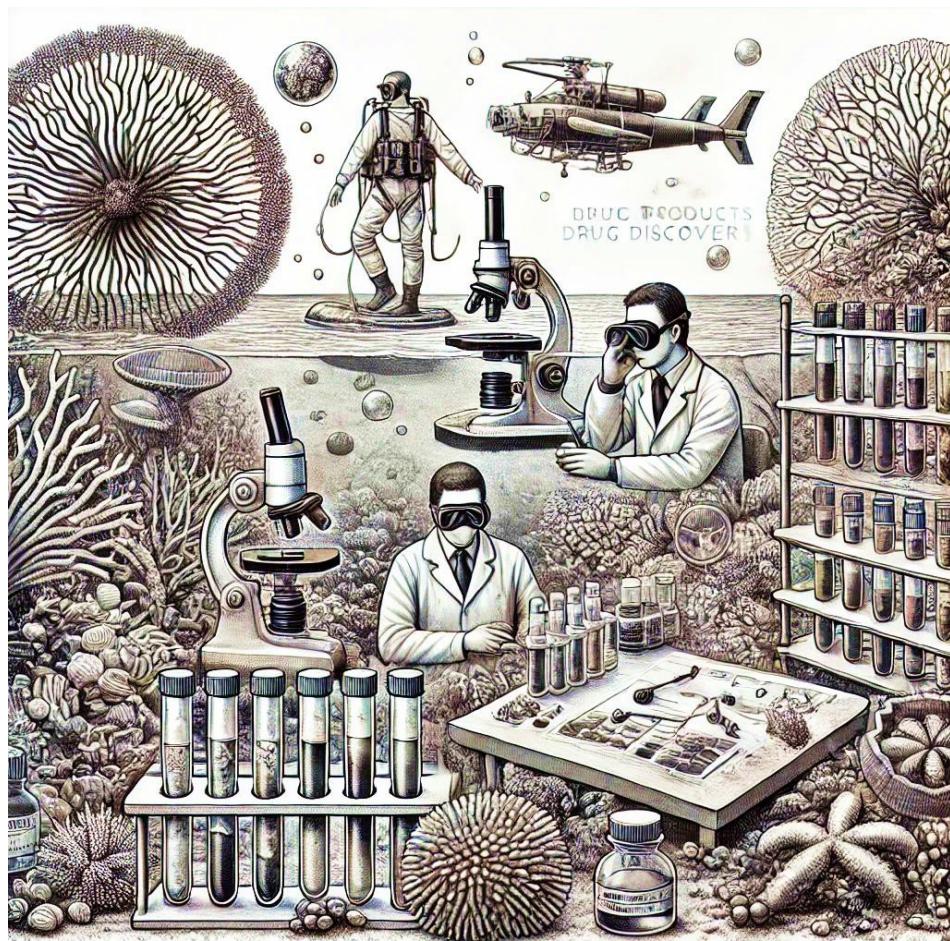
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The Andaman Islands are characterized by their isolated and distinct ecosystem, consisting of diverse bacterial communities involved in various ecological processes. Metagenomics, a culture-independent approach combined with next-generation sequencing, helps unveil the bacterial composition of environmental samples, thus providing deeper insights into ecosystem dynamics. The present study involves the 16S metagenome analysis of sediment samples collected from six different intertidal regions of South Andaman. DNA was extracted, and the V3–V4 region of the 16S rRNA gene was sequenced using the Illumina NextSeq 2000 platform. The raw FASTQ files thus obtained were analyzed using QIIME2. The top 20 genera of each station, the Alpha-diversity (Shannon-Wiener and Simpson's index), and Beta-diversity (Bray-Curtis NMDS) was visualized using the DADA2 pipeline. Based on the data obtained, some stations exhibit the dominance of a single genus, such as *Oceanisphaera* at Carbyn Beach and *Vibrio* at Bunker Beach. Collinpur was dominated by *Photobacterium*, followed by *Malaciobacter*. Burmanallah has an even distribution among multiple genera of *Alteromonas*, *Vibrio*, and *Catenococcus*. In Wandoor and Chidiyatapu the bacterial composition was more diverse, and there was no single dominant genus. The genus *Vibrio* was present in most of the stations. Collinpur had the highest Shannon and Simpson indices, indicating high bacterial diversity, whereas Burmanallah had the lowest bacterial diversity. Bray-Curtis NMDS showed similarity between Bunker Beach and Chidiyatapu, with Carbyn Beach having the most distinct bacterial microbiome. Bacterial composition was influenced mainly by the physicochemical factors and sediment texture.

Keywords: Metagenomics, Genus, Microbiome, Andaman



Marine Natural Products and Drug Discovery

Invited Talks



MND- IT 1

DEVELOPMENT OF PHARMACEUTICALS FROM THE MANGROVES, MARINE ORGANISMS, AND MICROORGANISMS

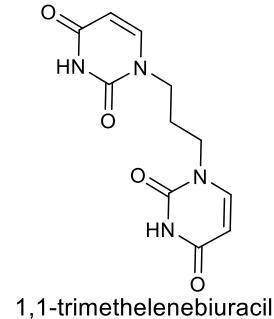
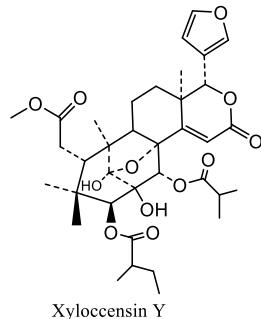
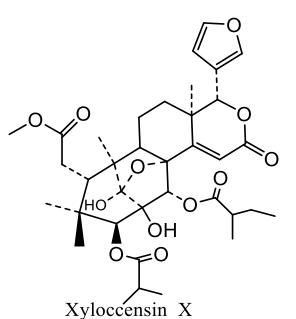
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Mangroves and marine organisms, including microorganisms are reservoirs of valuable compounds of pharmaceutical importance. As a part of our drug discovery program, we identified few promising bioactive compounds from the marine mangroves, marine organisms and microorganisms. The recent developments on isolation, characterization of bioactive compounds and the challenges involved in the drug development from marine sources will be discussed in detail.



Keywords: Bioactive compounds, Mangroves, Drug development



MND-IT 2

MARINE NATURAL PRODUCTS: FROM SEABED TO BEDSIDE AND BEYOND

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The triple-negative breast cancer (TNBC) is an aggressive, strongly chemo-resistant breast malignancy. The prevalence of triple-negative breast cancer (TNBC) poses significant challenges in effective treatment, primarily due to its associated drug resistance. In this study, we explore the potential of marine natural products as innovative therapeutic agents against cancerous growths, focusing on TNBC. We will discuss the role of the pro-inflammatory cytokine LIF in promoting drug resistance, highlighting how it complicates treatment strategies. In response to this pressing issue, we introduce Streptopyrrole, a novel marine-derived bacterial metabolite, which shows promise in overcoming the resistance mechanisms employed by TNBC cells. Streptopyrrole showed a cytotoxic effect in a concentration-dependent manner with an IC₅₀ value of 50 μM on metastatic murine 4T1 TNBC cells. Streptopyrrole induced apoptotic cell death, reduced mitochondrial potential, G2/M cell cycle arrest, and blockade of the migration in 4T1 cells. Transcriptomic analysis revealed that Streptopyrrole treatment (50μM for 12 and 24 h) resulted in the reduction of LIF, and MCL-1 at the mRNA level. These results indicated that Streptopyrrole reduced the drug resistance and stemcellness under in vitro studies.

Keywords: Apoptotic, Streptopyrrole, Mitochondrial potential, Cytokine

Oral Presentations



MND-O1

EXPLORING ANTICANCER ACTIVITY OF MARINE HALOTOLERANT BACTERIAL-DERIVED SECONDARY METABOLITES

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Marine microorganisms constitute a promising source of metabolites with therapeutic potential for drug screening and development. In recent years, bacteria associated with marine organisms have become the prime focus of marine research for their potential to generate novel anticancer compounds. The work aims to identify the anticancer activity of seaweed-associated bacterial metabolites. In this study, seaweed samples were collected from intertidal regions of Kovalam and Mandapam (East Coast Chennai), and marine halotolerant bacteria were isolated and identified using 16S rDNA sequence analysis. The secondary metabolites were extracted using the solvent extraction method and purified by HPLC. The structural elucidation of the purified compounds was performed using NMR spectroscopy. The anticancer activity of the compound was determined using the SRB assay. The compound S1 showed dose-dependent cytotoxic effects on cancer cell lines A549 (lung), AW1356 (oral), SK-OV-3 (ovarian), MDA-MB-231(breast), and Hep-G2 (liver) at all the concentrations starting from (10 µg/ml- 80 µg/ml). Further, compound S1 demonstrated anti-cancer activity against A549 and MDA-MB-231 cells by induction of necrosis and apoptosis in a dose-dependent manner as compared to untreated cells. In A549 cells, S1 induced necrosis and late apoptosis at concentration 5 and 10 µg/mL whereas in case of MDA-MB-231 cells, it has induced 49% early apoptosis at concentration 5µg/mL. The marine bacteria-derived compound S1 has a higher cytotoxic effect and could be explored as an anticancer agent in cancer therapeutics.

Keywords: Seaweed, Marine bacteria, Metabolite, Anticancer activity rhythm



MND-O2

A MARINE CRUSTACEAN-DERIVED *CHRYSEOMICROBIUM AMYLOLYTICUM* TYPE II L ASPARAGINASE: BIOPROCESS DEVELOPMENT, CHARACTERIZATION AND EVALUATION FOR BLOOD CANCER THERAPY

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L-asparaginase (EC 3.5.1.1) is a pivotal antineoplastic drug. Currently used therapeutic L-asparaginase formulations from *E. coli* and *Erwinia chrysanthemi* have multiple side effects, captivating researchers to explore novel candidates. The study optimised the production process, evaluated the clinically desirable features and anti-oncogenic efficacy of a novel *Chryseomicrombium amylolyticum* type-II L-asparaginase from the marine crab hemolymph, *Scylla serrata*. Statistical optimization using Plackett and Burman and central composite designs increased the production to 155.44 and 281.6, respectively, from 115.69 IU/mL. The purified enzyme with a molecular weight of ~142 kDa displayed high specificity towards its natural substrate L-asparagine, with the *Km*, *Vmax*, and *Kcat* were 6.364 μM, 909.09 μM/min, and 222.82/sec. *In vitro* trypsin and serum half-life were ~39 h and ~27 min. The study enlisted various ions, protein-modifying agents, and surfactants influencing its activity. The study also generated the complete functional gene sequence of the enzyme and demonstrated low identity with the commercial variants. A homotetrameric model of the enzyme was developed using AlphaFold. Molecular docking revealed a higher binding affinity for L-asparagine than L-glutamine and urea, supporting its substrate specificity. The *IC₅₀* values against MCF7 and MOLT4 cell lines were 0.043 and 0.041 IU/ml, respectively. Flow cytometry demonstrated 81.4% apoptotic cells in the MOLT-4 cells at *IC₅₀*, signifying the potent anticancer activity. The enzyme did not affect normal human fibroblast cells and was non-haemolytic.

Keywords: Antineoplastic, Statistical optimization, Clinical safety



MND-O3

**ARMENIASPIROL-C ISOLATED FROM A MARINE
STREPTOMYCES SP. MMCC42 INHIBITS NCI-H460 HUMAN
LUNG CANCER CELLS**

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Cancer has emerged as a major threat to human health, and among different types, lung cancer is reported to be the major cause of cancer deaths worldwide. Several natural product-derived drugs are in use today and the search for new therapeutics is an important field of research. In this regard, Actinomycetes isolated and stored in the Marine Microbial Culture Collection at CUSAT, Kerala were screened for anti-cancer activity. The strains were cultured in broth media for 14 days, secondary metabolites extracted using ethyl acetate and the solvent vaporized under vacuum to yield the crude extract. A strain designated MMCC42 showed complete inhibition of NCI-H460 lung cancer cells in MTT assay. It was mass cultured and the crude extract was prepared. Fractionation of crude extract was carried out using Flash Chromatography and the cytotoxicity of the fractions were evaluated. Further HPLC-based purification of active fractions followed by High Resolution Mass Spectrometry (HRMS) and Nuclear Magnetic Resonance (NMR) spectroscopy analysis yielded Armeniaspirol-C, a bioactive benzofuran compound. IC₅₀ of Armeniaspirol-C against NCI-H460 lung cancer cell was found to be 19.71µg/ml. Annexin-V/Propidium Iodide staining carried out at 0th, 6th, 12th, 24th and 48th hour post-treatment showed apoptotic cell death being induced in the cells whereas the scratch wound healing assay showed that Armeniaspirol-C inhibited cell migration. In summary, the findings of the present study provide evidence that Armeniaspirol-C is a potent inhibitor of NCI-H460 lung cancer cells. Insights into the mode of action of this potent molecule should be gained to evaluate its prospect as a candidate for *in vivo* studies.

Keywords: Streptomyces, Bioactive compounds, Lung cancer



MND-O4

FIGHTING SUPERBUGS NATURALLY: *ULVA LACTUCA* AS AN ANTIBACTERIAL AGENT AGAINST MDR *PSEUDOMONAS* *AERUGINOSA*

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MDR *Pseudomonas aeruginosa* represents a frequent and challenging nosocomial pathogen with high rates of persistent infections and associated deaths. Green seaweed, *Ulva lactuca*, classified under the marine macroalgae, offers various potential bioactive compounds with therapeutic applications. In our previous study on activity of ulvan extract against various human and fish pathogens, it was found that ulvan extract is a promising antibacterial agent against *P. aeruginosa* (ATCC® 10145™), with MIC and MBC values of 128 mg/l and 256 mg/l respectively. In this study, 70 seafood and water samples were screened for environmental strains of *P. aeruginosa* and the prevalence was 45.7%. A total of 32 isolates of *P. aeruginosa* were subjected to antibiotic susceptibility testing with disc diffusion method against 16 antibiotics belonging to different classes. It is found that 65.6% of *P. aeruginosa* isolates were resistant to different antibiotics, and 43.75% were classified as MDR. All the isolates were then subjected to a well diffusion assay with ulvan extract, and the average zone of inhibition was found to be 29 ±2 mm. This study demonstrates that *Ulva lactuca* is a promising source of antibacterial agents against MDR *P. aeruginosa* and offers a sustainable avenue for future drug development.

Keywords: Seaweed, Marine bacteria, Metabolite, Anticancer activity rhythm



MND-O5

WOUND HEALING POTENTIAL OF IODINE GRAFTED CHITOSAN GEL IN FEMALE WISTAR RATS

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Wound healing is a complex process essential for restoring the skin's barrier function following trauma from accidents or medical procedures. Prompt care is crucial to minimize the risk of infection and to facilitate appropriate healing while reducing scarring. Traditional medicine has made use of shellfish powders for wound treatment; however, there is a limited understanding of their chemical properties and molecular mechanisms. Chitosan-based hydrogels have been demonstrated to support healing at various stages and to address factors that hinder recovery, such as inflammation and chronic infections. Among the antimicrobial agents available, iodophore-based formulations like povidone-iodine are favoured for their effectiveness and tolerability in wound care. The method has been standardized for synthesis of iodine grafted chitosan. In the current study, we investigated the wound healing potential of iodine-grafted chitosan gel in female Wistar rats. The experimental animals, subjected to wound incisions, were divided into five groups for treatment as follows: Group I - Control; Group II - Chitosan gel; Group III - Iodine; Group IV - Chitosan-Iodine; Group V - Betadine. The wound healing process was closely monitored over a period of 30 days. Results indicated that the rate of wound healing in Group IV (chitosan-iodine treated rats) was significantly higher compared to the other groups. Furthermore, the wound healing activity of the chitosan-iodine gel proved to be comparable to that of the standard drug administered to Group V animals. This enhanced wound healing activity is likely due to the improved tissue regeneration capabilities of chitosan combined with the antimicrobial properties of iodine.

Keywords: Chitosan, Iodine, Wound healing



MND-O6

EXPLORING THE IMMUNE FUNCTIONS OF THYMOSEN AND ALF ANTIMICROBIAL PEPTIDE IN *FENNEROPENAEUS* *INDICUS* POST WSSV INFECTION

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Antimicrobial peptides (AMPs) are essential components of the innate immune system, known for their antimicrobial and immunomodulatory functions. In invertebrates like shrimp, AMPs play a crucial role in defending against viral infections, including White Spot Syndrome Virus (WSSV), by modulating the host immune response and interfering with viral replication. In this study, we performed a transcriptomic analysis of two major AMPs—thymosin and ALF—in *Fenneropenaeus indicus* to investigate whether these peptides exhibit any expressional variation between WSSV-infected and healthy shrimp. Our findings reveal significant differences in the expression levels of these peptides, suggesting their involvement in the immune response to WSSV infection. These results provide insights into the potential role of thymosin and ALF in immune regulation, advancing our understanding of their contribution to antiviral defense mechanisms in shrimp. Furthermore, the study lays the groundwork for future investigations into the therapeutic potential of these AMPs in combating viral infections in aquaculture.

Keywords: Antimicrobial peptides, Aquaculture, Shrimp, Thymosin, ALF



MND-O7

BIOPROSPECTING OF ACTINOMYCETES FROM MANGROVES OF NORTH KERALA COAST FOR ANTICANCER COMPOUNDS

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Actinomycetes are well known for producing diverse secondary metabolites with promising chemotherapeutic value and unique chemical structures. This study explores Actinomycetes isolated from the mangroves of northern Kerala, a highly productive yet largely unexplored ecosystem with rich microbial diversity. Sediment samples were collected from various locations and subjected to pretreatment before spread plating on Actinomycetes Isolation Agar (AIA) and Zobell Marine Agar (ZMA). A total of 152 strains were isolated from 8 mangrove sites across two districts, with 95 strains from AIA and 57 from ZMA. From these, 61 pure isolates were cultured on a large scale in fermentation media, and crude extracts were prepared for screening. The anticancer potential of these extracts was evaluated against the NCI-H460 non-small cell lung cancer (NSCLC) cell line using the MTT assay at a concentration of 50 µg/mL. 11 isolates exhibited significant cytotoxic activity (>50%), with MSM 47 demonstrating complete (100%) inhibition. 16S rRNA gene sequencing of five potent isolates identified four belonging to the *Streptomyces* genus and one to *Micromonospora*. These findings highlight the untapped potential of mangrove-derived Actinomycetes as a promising source of novel anticancer compounds. Furthermore, molecular identification of isolates, purification, and structural elucidation of lead compounds are in the pipeline.

Keywords: Mangroves, North Kerala, Actinomycetes, Anticancer, Cytotoxicity



MND-O8

BIOPROSPECTING OF MACRO-ALGAE FOR INSECTICIDAL POTENTIAL AGAINST STORED PRODUCT INSECT PESTS

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Postharvest grain losses due to insect pests account for 25–33% of global production, threatening food security. Seaweed (macroalgae) is a good source of secondary metabolites and is reported for antibacterial, antifungal, and larvicidal activities. This study explores a red seaweed, *Gracilaria edulis*, for its insecticidal potential against stored product insect pests. Different solvent extracts of *G. edulis* were analysed for phytochemical composition, antioxidant activity, and pesticidal efficacy (repellent and contact toxicity assay). Qualitative analysis confirmed the presence of alkaloids, terpenoids, and phenols in all extract. Ethanol extracts showed a higher phenolic content and significant DPPH radical scavenging activity (>60% at 300 µg/mL), followed by other extracts. Major bioactive compounds such as gallic acid, chlorogenic acid, 4-aminobenzoic acid, palmitic acid, oleic acid, and linoleic acid, which are well known for larvicidal and insecticidal properties was analysed via HPLC and GC-MS. Repellency assays against the adult insects of *Tribolium castaneum* showed the highest repellency (93.33% at 3.15 mg/cm² after 9-12 H), while *Callosobruchus chinensis* and *C. maculatus* exhibited moderate repellency at higher concentrations (peaking at 3–9 H). *Rhyzopertha dominica* showed minimal repellency, even at high doses. Contact bioassay against pulse beetle revealed that higher concentrations and prolonged exposure increased the mortality. Future studies will expand this research to evaluate the efficacy of *G. edulis* extracts in protecting products in postharvest, while optimizing application methods.

Keywords: Red seaweed, Biopesticides, Stored grain pests, *Gracilaria edulis*, Phytochemicals, Food security



MND-O9

**ANTIPARASITIC ACTIVITY OF MARINE ACTINOMYCETE
NOCARDIOPSIS SP. MMCC 15 AGAINST MALARIAL PARASITE
*PLASMODIUM FALCIPARUM***

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Marine Actinomycetes have always proved their worth in the field of drug discovery from producing antibiotics, anticancer agents and other metabolites of pharmaceutical importance. Malaria remains a significant challenge for drug development, as researchers strive to create effective treatments to combat the parasite's resistance to existing medications. The following study aims at exploring potential antimalarial compounds from marine actinomycete designated as DM 15 isolated from an arctic fjord region. Molecular identification of the isolate showed 99% similarity with the *Nocardiopsis synnemataformans* strain LPB0126 (accession number KX078080.1). Mass production of the actinomycete was done in A1BFe + C medium, and a resin-based extraction of secondary metabolites was carried out using Amberlite XAD 7 beads. The crude extract prepared in methanol was taken forward for antimalarial drug susceptibility assays. Two strains of the malarial parasite *Plasmodium falciparum* - 3D7 and MRA 1236 were used in the study. The crude extract was tested at 14 varied concentrations in two-fold serial dilutions ranging from 1ug/ul. The antiparasitic agent Chloroquine was used as positive control and *Plasmodium* infected RBCs served as negative control. Upon 72h treatment, the crude extract showed significant inhibition in the growth of both parasitic strains. The extract exhibited antiplasmoidal activity with 1C₅₀ values of 0.02ug/ul against 3D7 and 0.6ug/ul against MRA1236 strain. These results indicates that the strain *Nocardiopsis* sp MMCC 15 is a promising candidate with significant antiplasmoidal activity and can be taken forward for further studies aiming to develop a potent drug lead against malaria.

Keywords: *Nocardiopsis*, *Actinomycetes*, *Plasmodium falciparum*, Antimalarial



MND-O10

SEED PRIMING WITH MARINE CYANOBACTERIAL CARBON QUANTUM DOTS: A NOVEL APPROACH FOR ENHANCING PLANT GROWTH AND RESILIENCE FOR SUSTAINABLE AGRICULTURE

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Carbon quantum dots (CQDs) derived from marine cyanobacterial biomass of *Leptolyngbya* sp. nov. KMBMA-1 were assessed for seed priming efficacy in *Vigna radiata*. The findings indicate that CQD priming significantly improves seed germination, shoot and root growth, and photosynthetic performance by acting as a carbon source. CQD-treated seeds exhibited superior germination rates relative to the control group. Within 48 hours, the seed coats of CQD-primed seeds had opened more rapidly than those of water-primed controls. Enhanced germination and sprouting rates were recorded in experimental pots compared to control pots, attributed to CQDs' facilitation of water uptake through altered seed coat permeability. The experimental design involved priming pea seeds using CQD solution, while control seeds were primed solely with water. The CQD uptake resulted in a distinct colour change in the seeds, confirming their role in promoting water absorption and enzymatic activation. Throughout all growth stages, experimental pots revealed significantly improved seed germination rates and expedited seedling emergence. Seeds primed with CQDs in experimental pots (E1, E2, E3) displayed robust growth and accelerated development of root, shoot, and stem. Notably, roots in experimental pots were characterized by increased length and thickness, reflecting a more effective root system for enhanced water and nutrient uptake. The shoot length in these pots exceeded that of the control group, with the plants exhibiting more robust and healthier stem. Combining CQD priming with other techniques, such as hydro- and nano-priming, could further enhance



agricultural productivity. Future studies shall focus on optimisation of CQD concentration and explore alternative biomass sources to develop cost-effective and environment-friendly priming methods. This study highlights cyanobacterial CQDs as a potential tool for sustainable agriculture, contributing to food security and crop resilience.

Keywords: Nanomaterials, Carbon quantum dots, Cyanobacteria, Nanoprimeing, Seed priming, Nano agriculture



MND-O11

**NERITIC AND BATHYPELAGIC SHRIMP SHELLS AS SOURCES
OF ASTAXANTHIN: COMPARATIVE YIELD ANALYSIS,
STABILITY, AND IN-VITRO BIOLOGICAL ACTIVITIES**

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Astaxanthin (AST), a xanthophyll carotenoid, exhibits exceptional antioxidant potency, exceeding that of other carotenoids and α -tocopherol by tenfold and hundredfold, respectively. This potent antioxidant activity, coupled with diverse biological properties including antibacterial, anticancer, and neuroprotective effects, has driven significant research interest into this compound. This study explored AST extraction from neritic (*Penaeus monodon*, *Metapenaeus dobsoni*) and bathypelagic (*Solenocera hextii*, *Aristeus alcocki*) shrimp shells, employing organic solvent extraction. *Aristeus alcocki* yielded the highest AST concentration (80 $\mu\text{g/g}$), subsequently utilized for biological activity assessments. Thermal stability of the crude extract was evaluated via Differential Scanning Calorimetry (DSC), while Thin Layer Chromatography (TLC) confirmed the presence of AST, revealing three distinct bands indicative of potential AST isomers (free, monoester, diester). The crude extract demonstrated significant antioxidant activity via DPPH assay, alongside antibacterial and anticancer effects assessed by MTT assay. High-Performance Liquid Chromatography (HPLC) facilitated the separation and identification of the three observed AST forms. Supercritical Fluid Extraction (SFE), a green extraction method, was employed to enhance yield and efficiency. Further studies focusing on detailed characterization of each HPLC-separated compound, including structural elucidation and comprehensive comparative analysis of their respective biological activities, to determine the relative potency of free astaxanthin, astaxanthin monoesters, and astaxanthin diesters. Such results will provide critical insights into the optimal utilization of astaxanthin from crustacean sources for therapeutic applications.

Keywords: Astaxanthin, Neritic, Bathypelagic



MND-O12

BIOACTIVE POTENTIAL OF MANGROVE DERIVED ACTINOMYCETES FROM CENTRAL KERALA: INSIGHTS INTO ANTI-MICROBIAL AND ANTI-CANCER COMPOUNDS

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The mangrove ecosystem serves as a promising reservoir of actinobacteria with diverse beneficial bioactive secondary metabolites, capable of mitigating existing antimicrobial resistance. The study aimed to explore the bioactivity of actinomycete isolated from five different mangrove ecosystems of central Kerala. Primary (cross streak) and Secondary (Kirby-Bauer disc diffusion) screening methods were employed to assess the antimicrobial activity of all the 154 isolates against various gram-positive and gram-negative human pathogens. Primary screening identified 31 actinomycete isolates with anti-microbial activity. Subsequent screening via well diffusion method using raw supernatant confirmed 4 isolates with significant antimicrobial potential. Isolate CH4A selected for its prominent antimicrobial activity was confirmed through secondary screening and further assessed for its anticancer activity using MTT assay. The ethyl acetate crude extract exhibited remarkable antimicrobial activity against *Staphylococcus aureus* (MTCC3061), *Bacillus cereus* (MTCC 1272), *Vibrio cholera* (MTCC 3906), and *Escherichia coli* (MTCC1610) and anticancer activity against human lung cancer cell line (NCI-H-460). Molecular identification through 16S rRNA gene sequencing revealed that the isolate CH4A belongs to *Streptomyces* sp. These findings highlight the scope of mangrove associated Actinomycetes in natural product discovery.

Keywords: Mangrove Actinomycetes, Anti-microbial, Human pathogens, Anti-cancer, Bioactive metabolites, Streptomyces



MND-O13

METAL SENSING AND TUNABLE BIOIMAGING APPLICATIONS OF SEAWEED-DERIVED CARBON NANODOTS

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Nanomaterials, particularly fluorescent ones like carbon nanodots (CNDs), hold immense promise across numerous fields such as medicine, biosensing, energy, and catalysis, owing to their unique properties. CNDs, with their low toxicity, high biocompatibility, and easy surface modification, are particularly attractive. Utilizing a green synthesis approach, this study focuses on synthesizing and purifying CNDs from three different types of seaweeds with commercial and pharmaceutical importance. The research aims to analyze the Bacterial staining, Metal quenching, Dye degradation and Antioxidant properties of the synthesized CNDs. Synthesis involves Hydrothermal and microwave assisted synthesis, followed by purification using filtration, dialysis, and centrifugation. Optical properties are investigated through UV-visible and fluorescence spectra, while characterization is carried out via TEM and FTIR analysis. The obtained carbon dot with particle size around 4.5 nm, shows an excitation around 280 nm and emission around 450nm. They show good and tunable fluorescence properties with metal specific quenching and dye degradation activity. Future investigations include antibacterial and wound healing properties of the synthesized CND, paving the way for more potential biomedical applications.

Keywords: Carbon nanodot, Seaweed, Fluorescence, Metal sensing

Poster Presentations



MND-P1

BIOSURFACTANT FROM MANGROVE YEAST *GEOTRICHUM CANDIDUM* PV37: PRODUCTION, OPTIMIZATION, AND APPLICATIONS

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Biosurfactants are surface-active compounds produced by microorganisms, offering eco-friendly and biodegradable alternatives to synthetic surfactants. They have diverse applications in industries such as detergents, bioremediation, pharmaceuticals, and food processing. The present study explored the biosurfactant-producing potential of *Geotrichum candidum* PV37, a yeast strain isolated from mangrove ecosystems. As a Generally Recognized As Safe (GRAS) organism, *G. candidum* PV37 demonstrated significant biosurfactant production. Optimization of production conditions was achieved using Response Surface Methodology (RSM), a statistical approach that enhances process efficiency by evaluating multiple variables like pH, salinity, and sunflower oil simultaneously. Sunflower oil was identified as a key factor influencing biosurfactant synthesis. Optimized conditions suggested by the model was pH 5.75, salinity 5%, and sunflower oil concentration of 3.66 %, the solution suggested was validated, and the experimental value is very close to the predicted value in terms of OST on Day 7. The surfactant was extracted from the production medium, and the yield obtained was 0.530g/l. Chemical characterization confirmed its glycolipid nature, highlighting its potential for diverse industrial applications. Notably, the biosurfactant exhibited excellent grease stain removal efficiency, underscoring its applicability in detergent formulations. The study's findings pave the way for scaling up production and commercial exploitation, contributing to the development of sustainable, bio-based cleaning solutions.

Keywords: Mangrove Yeast, Biosurfactant, Glycolipid, RSM, Bioremediation



MND-P2

POTENTIAL OF MANGLICOLOUS YEASTS IN ENHANCING RICE GROWTH UNDER SALINITY STRESS

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In Kerala, agricultural productivity is being greatly impacted by climate change; with saltwater intrusion adversely impacts rice, a major staple crop. Nowadays sustainable, eco-friendly approaches are being explored using plant growth-promoting microbes (PGPM) and mangroves are one of the promising sources. This study aims to explore the largely untapped potential of manglicolous yeasts as PGPM to improve salinity tolerance in rice. Yeast strains from mangrove ecosystems were screened for plant growth promoting (PGP) traits under varying salinity conditions. The strains K17, KV17, KV35, P9, and PV23 were selected based on the expression of PGP traits. Further K17, KV35, and two consortia (CO1: K17 + KV17; CO2: P9 + PV23 + KV35) were tested on rice variety Jyothi during germination and seedling phases under salinity stress. Among these, CO1 (K17 + KV35) notably enhanced seed germination and seedling growth by increasing shoot and root length in saline conditions (0- 15ppt). Re-isolation of the yeast strains from soil confirmed their establishment, with K17 identified as *Candida tropicalis* and KV35 as *Aureobasidium melanogenum*. Interaction studies with nitrogen-fixing and phosphate-solubilizing microbes showed a rise in phosphate solubilizers and a reduction in nitrogen fixers under high salinity. This study highlights mangrove-derived yeast strains as effective agents for promoting rice growth under salinity stress, though further research is needed for large-scale agricultural applications.

Keywords: Manglicolous Yeast, Plant Growth Promoting traits (PGP), Salinity stress, Rice



MND-P3

EXPLORING THE β -DEFENSIN FROM SILVER POMPANO (*TRACHINOTUS BLOCHII*): MOLECULAR FEATURES AND ANTIMICROBIAL PROSPECTS

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The present study highlights the first-ever report of β -defensin (TbBD) from the fish silver pompano, *Trachinotus blochii*. This species is widely favoured for mariculture due to its taste, adaptability to various cultural conditions, compatibility with formulated diets, excellent meat quality, and strong demand in international markets. Gene sequence analysis revealed an open reading frame of 189 nucleotides, encoding a peptide consisting of 63 amino acids. Phylogenetic analysis indicated a close association of TbBD with β -defensin from *Trachinotus ovatus*. *In silico* molecular characterization of the peptide sequence revealed a molecular mass of 7.2 kDa, a net charge of +4.5, and two predicted bactericidal segments—one spanning T²⁹ to Q⁴³ and the other spanning V⁴⁷ to R⁶². Additionally, *in silico* analysis predicted cell-penetrating and anticancer motifs. Further scientific investigations into the antimicrobial efficacy of TbBD, either as a synthetic or recombinant peptide, could reveal its potential as a viable therapeutic agent in aquaculture and medicine.

Keywords: Antimicrobial peptides, Defensin, Silver Pompano, *Trachinotus blochii*



MND-P4

**IN VITRO EVALUATION OF ANTIOXIDANT, ANTIBACTERIAL,
AND ANTIBIOFILM ACTIVITY OF CARRAGEENAN FROM
KAPPAPHYCUS ALVAREZII AGAINST AQUATIC PATHOGENS**

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Aquaculture is a highly important and expanding industry in Southeast Asia (SEA). An upcoming problem is the emergence of antibiotic-resistant pathogens due to the unrestricted use of antibiotics and human clinical practices. However, in aquatic animals, the fastest growing food animal sector globally AMR trends are seldom documented, particularly in Asia, which contributes two-thirds of global food fish production. The misuse of synthetic antibiotics is one of the leading causes of the emergence of antibiotic-resistant microorganisms that have become the primary health concern. To overcome this resistance and counteract all the side effects of synthetic drugs, attention was diverted towards natural resources for developing antimicrobial substances. Carrageenan is a high molecular weight sulphated polysaccharide used to induce experimental inflammation in mammals. In addition, it possesses a wide variety of properties that have not yet been studied in fish. This study evaluated the antioxidant, antibacterial and antibiofilm activities of Carrageenan. Carrageenan was extracted from *K. alvarezii* using alkaline extraction method and characterized by the FTIR and GC-MS analysis. The antibacterial activity was tested against the aquatic pathogenic bacteria like *Staphylococcus iniae*, *Aeromonas veronii*, *Edwardsiella tarda*, and *Streptococcus agalactiae*. The antibacterial property of Carrageenan was tested using the minimum inhibitory concentration and the bacterial cell growth rate. At the highest concentration (100 µg/ml), the strongest reduction of biofilm formation was observed in the presence of carrageenan against the *Staphylococcus iniae*, *Aeromonas veronii*, *Edwardsiella tarda*, and *Streptococcus agalactiae*. The biofilm morphology was also investigated by fluorescence microscopy. Our results suggest that the antibiofilm activity of



carrageenan is related to the inhibition of the early bacterial adhesion. Consequently, these non-toxic and biodegradable polysaccharides, with surfactant and antiadhesive properties, could be proposed to prevent biofilms in aquaculture. The study suggests that Carrageenan has potential applications in aquaculture and aquatic pharmaceutical industries as an antibacterial and antibiofilm agent.

Keywords: Carrageenan, Aquaculture, Aquatic pathogens, *Kappaphycus alvarezii*, Antibiofilm



MND-P5

POTENTIAL BIOACTIVE COMPOUND FROM DEEP-SEA SEDIMENT ASSOCIATED MICROORGANISMS

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Deep-sea ecosystems are one of the most unexplored and unique habitats on Earth, harbouring a diverse array of microorganisms that are adapted to extreme environmental conditions to produce a broad range of bioactive compounds with significant pharmaceutical potential. Actinomycetes represent the most economically and biotechnologically valuable microorganisms, and they are excellent producers of extremely unique secondary metabolites. The present study attempts to discover unique microbial metabolites as anticancer and antimicrobial compounds from Actinomycetes isolated from deep-sea sediments. For this, the sediment samples collected from the Bay of Bengal employing a gravity corer at a depth of 3747m during a cruise on the Sagar Nidhi Research vessel and spread on three different media such as Actinomycete isolation agar (AIA), Zobell marine agar (ZMA), and Nutrient agar (NA). Later, six Actinomycete strains were isolated and purified. The purified strains were cultured in fermentation media (A1BFe+C), and crude extracts were prepared for preliminary bioactive screening. The anticancer activity was assessed using the MTT assay against the NCIH 460 lung cancer cell line. Among these six Actinomycetes, five isolates exhibited significant cytotoxicity with more than 98% activity. Antimicrobial assays were done for all six Actinomycete isolates against selected pathogens such as *Salmonella typhi*, *Staphylococcus aureus*, *Escherichia coli*, *Vibrio cholerae*, and *Mycobacterium smegmatis*. Among these, DSS ACT-1 showed a zone of inhibition against *Vibrio cholerae*. Molecular identification of these isolates, which showed promising anticancer activity, was performed. Phylogenetic tree analysis revealed that these isolates were closely related to *Streptomycetes* sp. In addition to this, mass production of potent DSS ACT-1 strain followed by bioassay-



guided fractionation using automatic flash chromatography was done. The potent flash fraction (Fraction 7) was subjected to further purification using HPLC. Cytotoxic activity of HPLC subfraction 7.2 was tested on the NCIH 460 cell line and was found promising. This study warrants the strain DSS ACT-1 to be a promising candidate for further research, to be developed as a potent pharmacotherapeutic agent.

Keywords: Deep sea, Actinomycetes, Cytotoxicity, Anticancer assay, Antimicrobial assay



MND-P6

L-ASPARAGINASE FROM MARINE ACTINOMYCETES: A POTENTIAL SOURCE FOR MEDICAL AND INDUSTRIAL APPLICATIONS

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L-asparaginase (EC 3.5.1.1), a chemotherapeutic agent that catalyzes the hydrolysis of L-asparagine to L-aspartic acid and ammonia. This enzyme gained significant attention for treating various malignancies, particularly acute lymphoblastic leukemia. Despite its clinical efficacy, L-asparaginase derived from conventional bacterial sources such as *Escherichia coli* and *Erwinia chrysanthemi* raises challenges, including hypersensitivity reactions, glutaminase contamination, and short half-life. This review focuses on marine Actinomycetes as alternative sources for L-asparaginase production. The marine environment is still an under-discovered reservoir with novel organisms. Marine Actinomycetes with unique morphology and metabolic capabilities, able to synthesize novel secondary metabolites with significant pharmaceutical potential. Marine Actinomycetes, particularly *Streptomyces* species, have developed unique physiological adaptations to thrive in extreme environmental conditions, leading to the production of variants of L-asparaginase with novel properties and reduced immunogenicity. Various *Streptomyces* strains, including *S. ginsengisoli*, *S. gulbargensis*, and *S. noursei*, have shown promising L-asparaginase activity. Apart from the oncological applications, L-asparaginase from Actinomycetes has potential utilization in the food industry for curtailing acrylamide formation in processed foods. This review synthesizes current knowledge on marine Actinomycete-derived L-asparaginase and highlights future research directions for optimizing the production, characterization, and application of this enzyme.

Keywords: *L-asparaginase, Streptomyces, Anticancer agents, Acute lymphoblastic leukemia*



MND-P7

GROWTH DYNAMICS AND STRESS-INDUCED β -CAROTENE ACCUMULATION IN *DUNALIELLA SALINA*

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Marine microalgae are a valuable source of bioactive compounds with significant pharmaceutical and industrial applications. *Dunaliella salina*, a halotolerant alga, is particularly prized for its high natural β -carotene content and essential antioxidants and vitamins. Natural β -carotene from *D. salina* serves as a potent antioxidant and provitamin A source, primarily synthesized under stress conditions such as high salinity, nutrient limitation, and UV exposure, making it highly desirable for nutraceutical and therapeutic applications. Given the growing interest in marine-derived natural products, *D. salina* remains a key organism for biotechnological advancements in drug discovery and health sciences. Previous studies have demonstrated that stress conditions can induce or enhance β -carotene accumulation in *Dunaliella* species, though the magnitude of these effects is often strain-specific. In this study, we assess the β -carotene production dynamics and growth patterns of *D. salina* over a 35-day growth period under controlled stress conditions, including nitrate limitation, UV irradiation, elevated salinity, supplemental carbon sources, increased temperature, and oxidative stress, based on insights from existing literature. By monitoring growth alongside β -carotene accumulation, this study provides a comprehensive understanding of the physiological responses of *D. salina* to environmental stressors, contributing to the optimization of cultivation strategies for enhanced metabolite production.

Keywords: *Dunaliella salina*, Beta-carotene, Pharmaceutical, Nutraceutical, Oxidative stress.



MND-P8

PROTEIN CHARACTERIZATION OF MUCUS IN *MYTELLA STRIGATA*

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The characterization of mucus proteins is highly significant, as these proteins play a crucial role in immune defence, disease pathogenesis, and mucosal protection. This study discusses the characterization of mucus proteins from *Mytella strigata* in terms of physiological function, environmental significance, and potential biomedical application. Mucus secretion in bivalves plays a critical role in immune defence, adhesion, and environmental acclimation. Proteins were precipitated with acetone and analysed by the Bradford assay, which confirmed a high protein concentration (27.23 µg/mL). SDS-PAGE showed specific protein bands in the range of 65–100 kDa, suggesting the presence of structural, immune, and enzyme proteins. UniProtKB protein characterization indicated the presence of heat shock proteins (HSPs), metabolic enzymes, and adhesins, which reflect their functional diversity in stress response and cellular homeostasis. The presence of antimicrobial peptides and glycoproteins suggests potential application in wound healing and antimicrobial therapeutics. The findings highlighted the ecological adaptation of *Mytella strigata* and further support the future potential of its protein sources in the area of biotechnology and environmental monitoring. Molecular interaction, protein modification, and large-scale protein extraction methods should be the focus of future research to realize their full application potential.

Keywords: *Mytella strigata*, Mucus, Extraction, Protein, Characterisation



MND-P9

BIOACTIVE LIPIDS FROM MARINE SEAWEEDS: ANTIBACTERIAL PROPERTIES AND *IN SILICO* ANTICANCER POTENTIAL

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Marine macroalgae are a promising source of bioactive compounds with potential applications in drug development, particularly in combating antibiotic-resistant bacterial infections and tumour progression. Seaweed-derived lipids may also possess antibacterial and anticancer properties, as has been demonstrated by several studies. This study investigates the antibacterial and anticancer activity of the non-saponifiable fraction of total lipids extracted from three different seaweed species—*Portieria hornemannii*, *Turbinaria conoides*, and *Hypnea cervicornis* against a panel of Gram-positive and Gram-negative bacterial pathogens. The lipid extracts were obtained via liquid-liquid extraction to isolate the non-saponified constituents. Antibacterial activity was evaluated through disc diffusion and microbroth dilution assay. With differing levels of inhibition seen in the three species, the results showed strong antibacterial potential, especially against *Staphylococcus aureus* and *Escherichia coli*. Fatty acids, sterols, and other hydrophobic metabolites with antimicrobial qualities were detected by GC-MS analysis of the bioactive fractions. To assess anticancer potential, major identified compounds were docked *in silico* against cancer-related proteins. The results highlight seaweed-derived lipids as promising antibacterial and anticancer agents, warranting further research into their mechanisms and biomedical applications. Future studies should include *in vitro* cytotoxicity assays and *in vivo* models to validate their therapeutic potential.

Keywords: Anti-bacterial, Seaweed, Non-saponifiable fraction, Microbroth dilution assay, *in-silico*



MND-P10

PATENTS IN MARINE NATURAL PRODUCTS AND DRUG DISCOVERY

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Natural remedies for human illnesses have been derived from plants, animals, microorganisms, and minerals. The marine environment is a unique resource with potential for groundbreaking treatments. As more chemicals from marine sources enter clinical trials, their influence on the pharmaceutical industry grows. Marine natural products (MNPs) are a significant source for new drug discovery due to their unique chemical variety and bioactivity. Patents are essential to safeguard these inventions, ensure commercialization, and encourage further research. This study examines the use of patents in the drug development process for marine natural products, examining case studies, international agreements, and patent laws. A search of patent databases for patterns in the patenting of marine products, a legal analysis of current patent laws, and an assessment of successful case studies involving drugs derived from marine sources are all part of the process. Academic research on the relationship between intellectual property rights and the utilization of marine resources is also conducted in order to investigate ethical issues through a doctrinal study. The success of medications produced from marine sources has been largely attributed to patents, according to the results; nonetheless, issues with guaranteeing fair access and safeguarding indigenous knowledge still exist. Although the legislative frameworks frequently fall short in addressing ethical considerations, the data indicates a increasing interest in marine natural product patents. To conclude, patents are still essential for innovation, but in order to strike a balance between commercialization and morally sound, sustainable marine bioprospecting methods, there is a need for better international collaboration and legislation.

Keywords: Marine Natural Products (MNPs), Patents, Drug discovery, Ethical considerations



MND-P11

**QIPENGYUANIA PELAGII: A CORAL-ASSOCIATED BACTERIA
THAT SHOWS ALGICIDAL ACTIVITIES WITH POTENTIAL
APPLICATIONS IN THE MANAGEMENT OF HARMFUL ALgal
BLOOMS**

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Harmful algal blooms (HABs) have seen an increase in both frequency and extent over the years, posing significant threats to marine organisms, fisheries, tourism, and human health. The traditional control methods for these blooms typically involve physical and chemical techniques, which can carry substantial risks, including the potential for secondary pollution. Moreover, these methods tend to be time-consuming, costly, and labour-intensive. Therefore, there is a pressing need for the development of environmentally friendly approaches to manage algal blooms. In this context, utilizing microorganisms to control algal blooms has proven to be highly effective. Among them, algicidal bacteria have demonstrated the most significant impact. A variety of algicidal bacteria have been isolated worldwide. The current study investigates the algicidal activities of a coral-associated bacterium, *Qipengyuania pelagii*, along with its mode of action. This bacterium exhibited the production of cellulase and amylase activities. Our results indicated that *Q. pelagii* could reduce the chlorophyll concentration of Chlorella species by 88% within three days of incubation. These findings were consistent with the cell count measurements conducted using microscopy and flow cytometry techniques. Additionally, the supernatant collected from a three-day-old culture of *Q. pelagii* exhibited similar algicidal activity against Chlorella. Ongoing research aims to further evaluate the algicidal effects of *Q. pelagii* on environmental samples of algal blooms. The findings from this study may have potential applications in aquaculture, tourism, fisheries, and desalination systems, where harmful algal blooms pose considerable threats.

Keywords: Harmful algal blooms, Algicidal, One health



MND-P12

STEROID BIOTRANSFORMATION AND TESTOSTERONE
SYNTHESIS BY CORAL ASSOCIATED BACTERIA
PAENIGLUTAMICIBACTER QUISQUILLARUM AND
VREELANDELLA PIEZOTOLERANS

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Steroids are chemical analogues of hormones that hold significant market value within the pharmaceutical industry. Recent research indicates that microorganisms can effectively substitute traditional chemical synthesis routes for the biotransformation of steroids. In this study, we evaluated the efficiency of approximately 250 coral-associated bacteria in the biotransformation of androstenedione (AD) into androstanediene (ADD) and testosterone. Testosterone has emerged as a potential treatment for alleviating depression, particularly in older men with diminished testosterone levels. Our results revealed that ten isolates were capable of converting androstenedione to testosterone, with two isolates, *Paeniglutamicibacter quisquiliarum* (MMRF 2662) and *Vreelandella piezotolerans* (MMRF 2062), demonstrating conversion rates of 56% and 20%, respectively. Other coral-associated bacteria with biotransformation abilities were identified as *Psychrobacter* sp., *Brachybacterium* sp., *Shewanella* sp. This study concentrates on the 17-beta reduction pathway in bacteria exhibiting steroid conversion, with the goal of identifying the most efficient method for testosterone production. Furthermore, our findings offer insights into the immune response of corals associated with steroid conversion, as some studies suggest that testosterone production by these bacteria may play a role in coral immunity.

Keywords: Testosterone, Steroid, Biotransformation, Marine bacteria



MND-P13

ASSESSMENT OF THE VOLATILE AND NON-VOLATILE SECONDARY
PRODUCT IN PLANT-DERIVED EXTRACT USING A
QUALITATIVE APPROACH WITH CONSIDERATION FOR
CHEMICAL ECOLOGY

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The major sources of secondary metabolites are plants (80% of secondary metabolites), bacteria, fungi, and a variety of marine creatures, including snails, tunicates, corals, and sponges. Plants produce a wide range of secondary metabolites that play vital roles in their primary functions, such as growth, defence, adaptations or reproduction. Humans use a variety of secondary metabolite secretions to increase agricultural productivity (pesticides, insecticides, effectors of ecological competition and symbiosis, and pheromones), expand the pyramid of healthy nutrition (pigments and nutraceuticals), improve human health (antibiotics, enzyme inhibitors, immunomodulators, antitumor agents, and growth promoters of animals and plants), and ultimately have a positive economic impact on our society. The selected plant leaves are green with a minty fragrance when crushed. Aromatic plants are a good source of compounds with a positive impact on human health, such as phenolic compounds, flavonoids and terpenes. Based on the qualitative analysis of the plant extract, the secondary metabolites found in the plant leaves in this study include alkaloids, phenols, flavonoids, terpenoids, glycosides, quinones, and steroids. According to GC-MS analysis, 42% of the pinene compound has been identified in their leaves. According to preliminary research, TLC and GC-MS analysis, the main chemical found in Brazilian snapdragon leaves is terpenoids. Terpenoids, are a large group of plant secondary metabolites, with significant properties in the context of chemical ecology. The literature claims that pinene, a monoterpane, is essential to plant ecology because it influences plant communication, serves as a defensive mechanism against pests and herbivores, and enhances the scent and aroma of plants. Therefore, more phytochemical research on this plant identifies its potential use in the future.

Keywords: Secondary metabolite, GC-MS, TLC, Terpenoids



MND-P14

EXTRACTION, CHARACTERIZATION AND POTENTIAL APPLICATIONS OF ACROMITUS FLAGELLATUS DERIVED COLLAGEN

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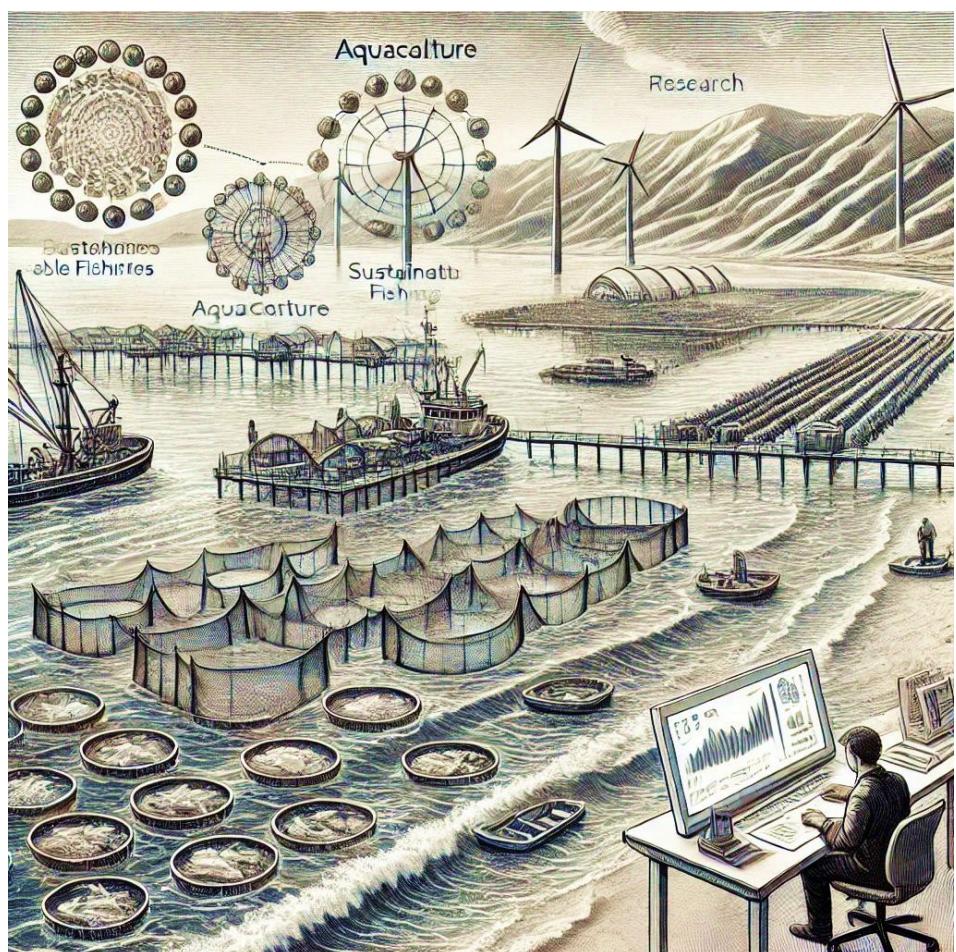
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Jellyfish are a rich source of bioactive compounds, including collagen, which has potential applications in biomedical, cosmetic, and food industries. This study focused on the extraction and characterization of collagen from the jellyfish *Acromitus flagellatus* and evaluated its structural and functional properties. The extraction process showed a reduction in sample weight, confirming the successful isolation of collagen with a yield percentage ranging between 96.9% and 97.3%. SDS-PAGE analysis identified a distinct protein band at ~180 kDa, revealing the presence of high molecular weight collagen. Further, Uniprot analysis revealed the extracted protein identity as heavy chain fibrillar collagen. The structural analysis confirmed its stability under acidic conditions and its high glycine and proline content. The study also compared the extracted collagen with related marine species, which showed high sequence similarity with *Aurelia aurita* and *Chrysaora quinquecirrha*. Overall, this study highlights the potential of jellyfish-derived collagen as a natural biomaterial, with further research needed to enhance extraction efficiency and reveal its functional applications.

Keywords: Jellyfish, Collagen, SDS-PAGE, Glycine, Proline



Sustainable Fisheries, Aquaculture and Blue Economy

Invited Talks



SAB- IT 1

GLOBAL GOALS AND MARINE BIODIVERSITY CONSERVATION IN INDIA: STATUS, CHALLENGES AND OPPORTUNITIES

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India now harbours close to 18% of humanity, with a population density of close to 500 people/km². Approximately six percent of this population resides in and around the coastal zones of the country, resulting in high levels of habitat alterations and resource use. These anthropogenic impacts have caused significant damage to the functioning and health of critical coastal as well as marine ecosystems, as well as the loss of biodiversity. There is hence an urgent need for global, regional and local efforts to effectively manage these ecosystems and conserve their unique and threatened taxa, so as to halt further deterioration and loss. At the center of such an ambitious goal is the ‘Kunming-Montreal Global Biodiversity Framework’ (KMGBF) a landmark agreement and crucial roadmap for safeguarding the planet’s biodiversity, and guiding global action on nature through to the year 2030. Comprising four overarching goals (and 23 specific targets), the KMGBF and the associated National Biodiversity Strategies and Action Plans (NBSAP) has an overarching aim to halt and reverse nature loss in the next five years. While its predecessor, the ‘Aichi 2020 Targets’ did not achieve much success, there is strong concern and apprehension whether KMGBF will be able to at least partially achieve its intended goals. Of the 23 global targets for urgent action towards 2030, many explicitly concern marine ecosystems, their biodiversity, sustainable use, and conservation. These include, among others the restoration of degraded ecosystems, effective protection of critical areas, and ensuring zero extinction of threatened and conservation-concern species. Achieving the targets of KMGBF in India will require effective implementation of its national targets envisaged in the NBSAP through an inclusive and collaborative approach. This presentation provides a synopsis of the various guiding questions for achieving national targets in India, and reviews the status, challenges and opportunities for effectively endorsing and implementing them.

Keywords: Biodiversity Conservation, KMGBF, NBSAP



SAB-IT 2

MARINE BIODIVERSITY AND FISHERY: CHALLENGES AND SOLUTIONS FOR A SUSTAINABLE FUTURE

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India's long coastline and vast Exclusive Economic Zone (EEZ) support rich biodiversity and are vital for the country's food security and livelihoods, particularly through fisheries. However, the escalating impacts of climate change and other anthropogenic activities pose unprecedented challenges to marine ecosystems and the sustainability of oceanic resources. Researchers are closely monitoring Sea Surface Temperature (SST), ocean acidification, and other climate-related variables to understand and predict changes in community structure, phenological changes, and shifts in fish distribution. In the face of global warming and its profound impact on marine ecosystems, the concept of sustainability has emerged as a critical strategy for a healthy ocean and human well-being. Implementing measures such as size and catch limits, gear modifications, seasonal closures, etc. helps to reduce overfishing and mitigate the impacts of climate change on vulnerable species. Sustainable fisheries management goes hand in hand with the protection of critical habitats, such as coral reefs, seagrass, and mangroves, which act as breeding and nursery grounds for many commercially important species. Community engagement and stakeholder involvement are also essential components of successful sustainable fisheries initiatives. By using ocean resources responsibly and by protecting our marine ecosystems, we can ensure a healthy planet for generations to come.

Keywords: Exclusive Economic Zone, climate change, Sustainable fisheries management

Oral Presentations



SAB- O1

UNVEILING THE POTENTIAL OF MULTI-GENERIC ALGAL DIETS IN NEUTRALIZING THE OXIDATIVE STRESS MARKERS OF ARTEMIA FRANCISCANA METANAUPLII

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Artemia franciscana represents an age-long, popular live food applied in hatcheries. Being a non-natural diet for aquatic larvae, *Artemia nauplii* exhibits an inferior nutritional profile. Enrichment using mixed-algal diets will improve the prey quality in terms of nutritional and antioxidant profile. The present study evaluates the dietary impact of selected di-algal combos in improving the antioxidant-to-prooxidant ratio in *Artemia metanauplii*. Batches of *Artemia nauplii* were fed using three enrichers- *Nannochloropsis salina* + *Isochrysis galbana* (I), *Chaetoceros calcitrans* + *Isochrysis galbana* (II), *Nannochloropsis salina* + *Chaetoceros calcitrans* (III) for 12 hours duration. The control batch was starved for 12 hours by incubating in sterile saline (Salinity- 30‰). The subsamples drawn from treated and control batches were macerated in PBE buffer (pH-7.4) and centrifuged to yield crude extract for the analysis of total antioxidant capacity (TAC), H₂O₂ content, lipid peroxidation index (LPx), catalase and SOD. The obtained data were statistically analyzed by applying two-way ANOVA. The estimates of TAC, LPx, SOD, and catalase had a significant hike. The estimates of TAC, LPx, SOD, and catalase had a significant hike ($p < 0.05$) in starved Artemia. The metanauplii enriched on Diet-III combo ($p < 0.05$) showed a reduction in the contents of the aforementioned indices. On the contrary, H₂O₂ concentration increased in the batch fed on the Diet-III combo. In conclusion, enrichment using selected combinations of microalgae would reduce the biomarkers of oxidative stress in live food organisms.

Keywords: *Artemia franciscana*, *Nannochloropsis salina*, *Chaetoceros calcitrans*, *Isochrysis galbana*



SAB-O2

GENOMICS AND GUT MICROBIOTA EVALUATION OF
CHITOSAN AND SODIUM ALGINATE SCAFFOLD DELIVERED
ORAL VACCINE AGAINST *EDWARDSIELLA Tarda* IN
OREOCHROMIS NILOTICUS

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Edwardsiella tarda is a re-emerging pathogen affecting the productivity of the cultivated fish species of both marine and freshwater, causing Edwardsiellosis disease. Vaccines are an excellent tool and seem to be an effective way to overcome the re-emerging disease in aquaculture. Our study aims to investigate an alternative vaccination strategy using a biomaterial-based scaffold with an α -ketoglutarate (AKG) adjuvant for the oral vaccine against *E. tarda* in Nile tilapia. The gut microbiome plays a significant role in regulating the fish's immune system. Understanding how oral vaccines interact with the gut microbiota can help optimize vaccine formulations to enhance immune responses. The scaffold was prepared using chitosan and alginate and characterized by SEM and FTIR analysis. Fish were separated into four experimental groups, including a control (basal diet), a positive control (formalin-inactivated vaccine-coated feed), a scaffold alone (scaffold-coated feed with AKG), and scaffold encapsulated vaccine (scaffold-encapsulated vaccine with AKG-coated feed). Fish were immunized for 7 days, followed by a booster vaccine given during the third week of the experiment. On days 7, 14, 21, and 28 post-vaccination, serum samples were collected. Fish were challenged with *E. tarda* on the 35th day post-vaccination, and the relative percentage of survival was calculated on day 15 post-challenge. Significantly elevated levels of estimated lysozyme, myeloperoxidase, catalase, and superoxide dismutase were noted in the



vaccinated group compared with the control group ($P < 0.005$). Specific antibody (IgM) against the antigen was upregulated, and a significant difference was observed between the prime and booster vaccinated fish. Gut microbiome analysis revealed alterations in the microbial community composition, with the vaccinated fish showing a more balanced and diverse microbiota compared to the control group. The vaccinated fish showed a high rate of survival in the treatment group fed with the scaffold-encapsulated vaccine with AKG. Our study presents a novel approach for vaccine delivery in aquaculture through the oral route, where the same approach can be utilized for different vaccines and drug delivery in aquaculture.

Keywords: *Edwardsiella tarda, α-Ketoglutarate, Scaffold, Nile tilapia, Gut microbiome*



SAB-O3

PROBIOTIC POTENTIAL OF ACTINOMYCETES IN AQUACULTURE

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Actinomycetes are filamentous, Gram-positive bacteria that bear a resemblance to fungi. They are found in a variety of natural environments, such as soil, sediment, mangrove areas, and marine ecosystems. They are recognized for producing secondary metabolites, which account for about 30% of all microbial metabolites. Various research studies suggest that Actinomycetes have great potential as probiotics for aquaculture. This research aimed to assess the probiotic potential of Actinomycetes obtained from sediment samples from the Andaman Islands. A total of 75 isolates exhibiting unique colony morphologies and pigment colors were extracted from sediment samples gathered from different sites in the Andaman Islands. The chosen isolates were evaluated for essential probiotic characteristics, such as resistance to acidic conditions and bile salts, as well as their antimicrobial properties against pathogenic bacteria. Antimicrobial tests were conducted on several test organisms, including *Staphylococcus aureus*, *Escherichia coli*, *Bacillus cereus*, *Vibrio harveyi*, and *Edwardsiella tarda*, using the disk diffusion technique. The evaluation of probiotic potential involved tests for salt tolerance and resistance to acidic pH. These isolates displayed enzyme production, especially in the hydrolysis of starch and lipase. The majority of the isolates show encouraging potential and may be utilized as probiotics within the aquaculture industry. Their adaptability, antimicrobial properties, and enzymatic activities indicate their ability to enhance disease resistance and improve nutrient absorption in aquaculture systems. Further investigations, including in vivo studies, are needed to confirm their efficacy and safety for aquaculture use.

Keywords: *Actinomycetes, Probiotics, Antimicrobial, Andaman Islands*



SAB-O4

EARLY DETECTION AND NEUTRALIZATION OF WHITE SPOT SYNDROME VIRUS IN SHRIMP USING CHICKEN EGG YOLK IMMUNOGLOBULIN (IgY) AGAINST RECOMBINANT VP28 PROTEIN

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White spot syndrome virus (WSSV) is a major pathogen in shrimp farming that causes significant economic losses in aquaculture. VP28 envelope protein mediates the initial stage of systemic WSSV infection in shrimp. Traditionally, mammalian-derived antibodies have been used for diagnostic tests. However, the high production costs, animal welfare concerns, and technical limitations have led to the search for alternative strategies. This study aimed to produce specific immunoglobulin Y (IgY) by immunizing laying hens with the VP28 envelope protein, offering a cost-effective alternative for WSSV detection and control. Anti VP28-IgY antibody titres were quantified, specificity evaluated using ELISA and western blotting, and performance compared with anti VP28-IgG rabbit antibody. The stability was determined by exposure to pH (6–8) and salinity (0–25ppt). A time-course infectivity experiment analyzed infection progression using western blotting, providing information about virus spread within the host over time. The results showed that WSSV infection appeared at 6 h post-infection (h p.i.) in the hemolymph and eyestalk. By 12 h p.i., the gills, head soft tissue, and appendages had also tested positive. Shrimp mortality was observed at 36 h post-infection. Western blot findings were consistent with those of anti-VP28 IgG rabbit antibodies, demonstrating that IgY is a suitable alternative. IgY may be used as an innovative biological recognition component to diagnose WSSV as early as 6 h post-infection. A preliminary neutralization technique was used to test the efficacy of the anti-VP28 IgY antibody against WSSV. Anti-VP28 IgY completely neutralized 1×10^5 copies of WSSV at a concentration of 5 µg. For early WSSV detection, this technique provides a more ethical, practical, and economical option that can enhance disease management and control in aquaculture.

Keywords: WSSV, VP28 envelop protein, Diagnosis and Neutralization.



SAB-O5

INTEGRATING SEAWEED FOR GREENER SHRIMP FARMING:
THE ROLE OF SEAWEED IN ENHANCED PRODUCTIVITY,
NUTRIENT REMEDIATION AND STRESS REDUCTION

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Shrimp aquaculture intensification enhances yield through increased stocking densities and efficient management, but it also increases the chance of disease outbreaks, eutrophication, and ecosystem stress, underscoring the need for sustainable techniques. Sustainable incorporation of seaweeds in shrimp farming systems can provide economically useful seaweed biomass, enhance water quality by nutrient bioremediation, and potentially reduce the environmental effects of shrimp aquaculture. The initial experiment was carried out to sort the seaweeds that were available locally along the Maharashtra coast in accordance with their yield and efficiency of nutrient uptake. Then the selected seaweed at constant stocking density was cultured in a co-culture unit with different stocking densities of *Penaeus vannamei*. The co-culture of *P. vannamei* and seaweed showed improved growth compared to their monocultures. The co-cultured seaweed plays a crucial role in water quality enhancement by reducing Total Ammoniacal Nitrogen, Nitrite, Nitrate, and Phosphate compared to monoculture. Additionally, it reduced the stress in the culture system by lowering the antioxidant enzyme activity like Superoxide Dismutase (SOD) and Catalase in the liver and gills, as well as serum glucose levels. Compared to shrimp monoculture, histological alterations in the hepatopancreas were determined to be normal under co-culture treatments. By acting as a natural nutrient utilized, seaweed helps mitigate pollution in intensive shrimp aquaculture, supporting eco-friendly farming practices while enhancing productivity from both species and reducing the environmental impact of high-intensity aquaculture systems.

Keywords: Seaweed, *P. vannamei*, Bioremediation, Physiology



SAB-O6

COMPARATIVE ANALYSIS OF GENDER-SPECIFIC GROWTH
PATTERNS AND BIOMETRIC INDICES IN *SCYLLA SERRATA*
AND *SCYLLA OLIVACEA* FROM THE COCHIN ESTUARY,
SOUTHWEST COAST OF INDIA

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This study investigates the biometric indices and gender-specific growth patterns of *Scylla serrata* and *Scylla olivacea*, both commercially important crab species, from the Cochin Estuary, southwest coast of India. A total of 4022 *S. serrata* (2048 males and 1974 females) and 4138 *S. olivacea* (2157 males and 1981 females) specimens were systematically collected and analysed from June 2020 to May 2023. Morphometric data, including carapace width (CW), carapace length (CL), chelar propodus length (ChL) and width (ChW), abdominal width (AW) and length (AL), and weight (W), were gathered and evaluated. Biometric indices, such as length frequency distribution (LFDs), carapace width-weight relationships (CW-WRs), and condition factors (Allometric condition factor (Ka), Fulton's condition factor (K), and relative condition factor (Kn)), are crucial in assessing the biological changes in crabs. Statistical analyses using the R program (ver. 4.4.0) were employed to derive the CW-WRs and different condition factors for both male and female crabs and pooled data. Statistical analyses revealed significant correlations between carapace length and weight for both species while exhibiting sex-specific variations in growth patterns. For *S. serrata*, the length-weight relationship was expressed as $W=0.0000447*CW^{3.268}$ for males and $W=0.0000281*CW^{2.86}$ for females, for *S. olivacea*, the CW-WR equations were $W=0.0000716*CW^{3.212}$ for males and $W=0.000276*CW^{2.875}$ for females. The key aspects reveal that males of both *S. serrata* and *S. olivacea* exhibit positive allometric growth, with weight increasing more rapidly than carapace width. In contrast, females show negative allometric growth, suggesting proportional weight increase with carapace width across the overall population. These findings are



essential for precise biomass estimation and effective fisheries management strategies. In *S. olivacea*, males have higher ranges and mean for Fulton's condition factor (K) and the relative condition factor (Kn) compared to females. Similarly, in *S. serrata*, males display higher mean values for Fulton's condition factor (K) and the relative condition factor (Kn) than females. However, females of both species show higher values for the allometric condition factor (Ka), indicating differences in growth and condition patterns. These gender-specific variations highlight the importance of tailored approaches in biometric analysis and fisheries management for *S. olivacea* and *S. serrata*.

Keywords: *Scylla serrata*, *Scylla olivacea*, Biometric indices, Carapace width-weight relationships, Allometric growth



SAB-O7

EFFECTS OF DIFFERENT LEVELS OF MARINE ALGAL OIL SUPPLEMENTATION ON GROWTH AND MATURATION PERFORMANCE OF *CLARIAS MAGUR* UNDER CAPTIVE CONDITIONS

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Seed and feed are crucial components of the aquaculture domain. *Clarias magur* is a commercial and potential candidate for freshwater catfish species for aquaculture diversification in India. However, seed production is stuck by the scarcity of mature male brood fish and its scarification during breeding. This study investigates the effects of marine algal oil supplementation on the gonadosomatic index (GSI), hepatosomatic index (HSI), sperm quantity, and associated histological changes in *C. magur*. The experiment included four treatment groups, including a control, with commercial feed (Growel, containing 6% crude fat and 40% protein) used as the base diet. In the control group, 3% cod liver oil was supplemented, while the experimental groups received marine algal oil at different levels 3% (T_1), 4% (T_2), and 5% (T_3). *C. magur* weighing 98-102g were stocked at a density of 5 fish/m³ and reared for 90 days, feeding a diet at 3% of their body weight. At the final sampling, the highest GSI was observed in the group supplemented with 5% marine algal oil, followed by T_2 and T_1 , and HSI had no significant variation. Sperm count varied significantly ($p < 0.05$) among all treatments. Histological observation also showed an increased number of sperm cells in T_3 . These findings suggest that supplementing with 4 to 5% marine algal oil, rather than fish oil, could be a beneficial strategy for farmers to enhance the maturation performance of *C. magur* under captive conditions.

Keywords: *Clarias magur* male, Marine algal oil, Gonadosomatic index, Gonad histology



SAB-O8

ACUTE SALINITY CHALLENGE IN *PIARACTUS BRACHYPOMUS* (CUVIER, 1818): ESTABLISHING LETHAL LIMITS AND LC50 FOR 96 HOURS

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Salinity plays a crucial role in the survival, growth, and physiological functions of freshwater fish species, particularly in the context of species diversification and adaptability to changing environmental conditions. The ability of fish to tolerate varying salinity levels determines their potential for expansion into different salinity regimes, which can enhance production in regions with limited freshwater availability. However, its salinity tolerance must be assessed to determine its culture potential in saline environments and establish suitable rearing conditions. This study evaluated the acute salinity tolerance of *P. brachypomus* through a 96-hour exposure experiment. A range-finding test was conducted at (T1) 10, (T2) 15, and (T3) 20 ppt salinity levels (along with a control) in triplicate to determine the lowest lethal salinity. Results indicated that all fish died within 12 hours at T3, while complete mortality occurred at T2 within 60 hours. No mortality was observed at T1 throughout the 96-hour exposure, establishing 15 ppt as the lowest lethal salinity. A subsequent acute salinity tolerance experiment with treatments of (T1) 11, (T2) 12, (T3) 13, (T4) 14, and (T5) 15 ppt (along with a control) in triplicate determined the 96-hour LC50 as 12.5 ppt using probit analysis. These preliminary findings suggest that *P. brachypomus* can tolerate low-salinity environments up to 10 ppt, making it a viable option for brackish water as well as Inland saline Aquaculture. *Piaractus brachypomus* is a promising candidate species in freshwater due to its fast growth and herbivorous feeding habits. However, regular salinity monitoring with stable salinity levels and gradual acclimatization strategies can help optimize survival rates and productivity in farming operations of *Piaractus brachypomus* in low-salinity environments.

Keywords: Salinity, *P. brachypomus*, LC50, Species Diversification



SAB-O9

TAURINE AS A DIETARY INTERVENTION FOR *CHANNA STRIATA*: IMPLICATIONS FOR SUSTAINABLE AQUACULTURE IN SALINE ENVIRONMENTS

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The salinization of groundwater and soil is a major environmental concern, affecting extensive land areas worldwide. Aquaculture presents a sustainable solution for utilizing inland saline groundwater (ISGW), with finfish farming emerging as a viable alternative to shrimp aquaculture due to its lower environmental impact. This study evaluated the effects of dietary taurine (Tau) supplementation on the growth, histopathological, and toxicological responses of *Channa striata* cultured in ISGW at 12 and 14 ppt salinity. Juveniles were acclimated and fed diets containing 0, 5, 10, and 15 g Tau/kg for an experimental period of 150 days. Growth performance, survival, genotoxicity, mutagenicity, and histopathology were assessed. The highest growth and survival rates were recorded at 10 g Tau/kg diet in 12 ppt salinity. Genotoxic and mutagenic assays revealed significant DNA damage and nuclear abnormalities in fish reared at higher salinities without taurine supplementation. Tau inclusion mitigated genotoxicity at a 10 g Tau/kg in 12 ppt salinity. Histopathological analysis indicated severe tissue alterations in unsupplemented fish, whereas Tau supplementation at a 10 g Tau/kg diet in 12 ppt salinity improved the tissue integrity. These findings highlight taurine's role in enhancing salinity tolerance, reducing oxidative stress, and supporting the sustainable cultivation of *C. striata* in ISGW. This research provides insights into dietary interventions for optimizing aquaculture productivity in saline environments while ensuring environmental sustainability.

Keywords: Sustainable aquaculture, Mutagenicity, Genotoxicity, Histopathology, Supplementation



SAB-O10

UNLOCKING CARBON STORAGE POTENTIAL THROUGH NOVEL SEAWEED FARMING TECHNOLOGIES ALONG KUTCH REGION, GUJARAT: CONTRIBUTING TOWARDS SDGS

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Seaweeds are marine macrophytes that play a crucial role in ecosystems by providing habitat, oxygen, and facilitating carbon sequestration. As a part of the blue carbon ecosystem, seaweeds capture and store organic carbon in oceans and coastal areas. Although most seaweed cultivation is for processing, offering only short-term carbon sequestration, it can still offset emissions by replacing more carbon-intensive products. Additionally, seaweed farming supports the livelihoods of remote coastal communities and contributes to achieving Sustainable Development Goals (SDGs) through climate change mitigation, maintaining healthy marine ecosystems, and promoting responsible consumption. Our study focused on culture of commercially important red seaweed species *Kappaphycus alvarezii* at five sites along the Gulf of Kutch: Kori, Padala, Juna Bandar, Luni, and Jarpara. A total of nearly one hundred customized HDPE rafts were deployed, each with an area of nine square meters, equipped with net tubes and monolines. The culture periods varied, with the longest at Kori and Juna Bandar and the shortest at Padala. A total of approximately 3,000 kg of seaweed is stocked, yielding over 24.5 metric tons across all locations. Carbon storage, assessed using the dry weight method, revealed that 688 kg of carbon was stored across all sites, with the highest storage observed at Juna Bandar and the lowest at Kori. This carbon storage has significant implications for future evaluations of the Net Zero concept, carbon sequestration, and climate change mitigation.

Keywords: Blue carbon, SDGs, Seaweed farming, Coastal livelihood, Climate change mitigation



SAB-O11

BEYOND ECONOMIC GROWTH: INTEGRATING GENDER ANALYSIS INTO MARINE SPATIAL PLANNING FOR EQUITABLE COASTAL RESOURCE MANAGEMENT

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Marine Spatial Planning (MSP), when integrated with coastal resource management, provides a strategic framework for sustainable marine resource use. However, despite the growing recognition of gender studies in equitable development, their intersection with coastal management remains underexplored. This study examines the necessity of incorporating gender analysis into marine resource governance, analyzing how spatial planning affects livelihoods, resource access, decision-making autonomy, and power structures. Focusing on Malpe Fisheries Harbor, India, a key marine fisheries hub, this research explores women's roles in post-harvest activities and their economic contributions to the fisheries value chain. Despite their involvement, women face systemic barriers, including restricted access to marine resources, exclusion from decision-making, and socio-economic marginalization. Using a mixed-methods approach combining qualitative in-depth interviews, field observations, and policy analysis, the study identifies persistent gender disparities in labor division and governance representation. Findings reveal a gendered hierarchy where men dominate frontline roles, while women remain in lower-tier positions, balancing productive and reproductive responsibilities with limited economic agency. The study highlights the gender-blind nature of coastal management and calls for integrating gender responsive policies within MSP. By embedding gender analysis into MSP, this research contributes to discussions on equitable and sustainable fisheries management, advocating for gender-inclusive blue economies and resilient coastal communities.

Keywords: Marine Spatial Planning, Coastal governance, Post-harvest sector



SAB-O12

EFFECT OF 2,4-D HERBICIDE ON HAEMATOLOGICAL PARAMETERS OF TILAPIA

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The widespread use of 2,4-Dichlorophenoxyacetic acid (2,4-D) as an agricultural herbicide has raised concerns about its impact on aquatic life. This study examines the effects of 2,4-D exposure on haematological parameters of Tilapia (*Oreochromis mossambicus*), an ecologically and commercially significant freshwater fish. Tilapia specimens (60–80 g, 10–12 cm) were exposed to three sub-lethal concentrations of 2,4-D (39.2 mg/L, 56.02 mg/L, and 78.4 mg/L), derived from the 96-hour LC50 value (392.17 mg/L), for 100, 200, and 300 hours. A control group was maintained under identical conditions without 2,4-D exposure. Blood samples were collected via cardiac puncture and analyzed for red blood cell (RBC) count, white blood cell (WBC) count, and haemoglobin (Hb) concentration. The results revealed a dose-dependent decline in RBC count and Hb concentration, with the highest 2,4-D concentration (78.4 mg/L) leading to a 17.6% reduction in RBC count and a 9.4% decrease in Hb concentration after 300 hours. In contrast, WBC count increased by 13.3%, indicating immune stress and physiological disruption. These alterations suggest that 2,4-D exposure induces anaemia, hypoxia, and haematological stress in Tilapia, which may have broader implications for fish health, aquatic biodiversity, and ecosystem stability. The study underscores the need for stricter regulations on herbicide runoff to protect freshwater ecosystems and sustain healthy fish populations.

Keywords: 2,4-D, Haematology, Tilapia, Herbicide toxicity, Freshwater pollution

Poster Presentations



SAB-P1

EVALUATION OF ANTIBIOTIC-RESISTANT PATHOGENS IN SHRIMPS COLLECTED FROM THE MARKETS AROUND COCHIN – KERALA

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The overuse and inappropriate use of antibiotics in animals and humans is the major cause for the selection of antibiotic-resistant (AMR) bacteria, which is posing an increasing risk to public health worldwide. Shrimp farming might contribute to the spread of AMR worldwide as the antibiotics are often used to control diseases in culture systems. In this study, we analyzed the prevalence of antibiotic resistance among the bacterial isolates from shrimps collected from the local markets. The samples were collected in January 2024. A total of 15 morphologically distinct bacterial colonies were isolated using the standard plate count method. Gram staining and biochemical tests were conducted on the isolated colony from Eosin Methylene Blue agar to confirm the presence of *E. coli*. The presence of *Vibrio* species in the samples were tested using Thiosulfate–citrate–bile salts–sucrose agar. All the isolates were tested by the Kirby-Bauer method to determine the prevalence of resistance against 5 antibiotics. Results revealed that the following percentage of isolates were resistant to various antibiotics: Cephalothin 93.33%, Ceftizoxime 80%, Streptomycin 80%, Amoxicillin 73.33%, and Cefotaxime 40%. The present study highlights the prevalence of a high degree of antibiotic resistance among the bacteria from shrimp samples. The knowledge acquired from this study is useful to shed light on the spread and transmission of antibiotic resistance in shrimp farming. To mitigate the issues associated with rising AMR, a coordinated strategy including professionals from both the private and public sectors in the fields of aquaculture, medicine, the environmental and social disciplines would be needed.

Keywords: Aquaculture, Shrimps, Antibiotic resistance, *Vibrio*, *E. coli*



EVALUATION OF THE PROBIOTIC POTENTIAL OF GUT ASSOCIATED BACTERIA OF POPULAR INDIGENOUS FISHES OF KERALA

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Probiotics are live microbial adjuncts that can result in increased systemic immunity, improved enzymatic digestion of food, better gut microbial balance, and inhibition of pathogenic bacteria in freshwater fish. In the present study, we have focused on the isolation, characterization, and primary screening of probiotic-producing bacteria from common fish species of Kerala, the southwest coast of India. The fish samples were collected from the fresh and brackish water sources near the Edavanakkad region in January 2025. A total of 34 bacteria isolated from the gastrointestinal tract of fishes namely Orange chromide (*Pseudetroplus maculatus*), Silver biddy (*Gerres oyena*), *Etroplus* (*Etroplus suratensis*), Glassy perchlet (*Chanda nama*) and Guppy (*Poecilia reticulata*) were used for the study. The antagonistic activity against pathogenic bacteria (*S. aureus*, *V. vulnificus*, *E. tarda*, *B. cereus*, *E. coli*, *A. hydrophila*) was conducted using the agar well diffusion assay. Most of the isolates exhibited antagonistic activity against fish pathogens such as *Aeromonas hydrophila* (32.35%), *Staphylococcus aureus* (20.58%), *Escherichia coli* (11.56%), *Vibrio vulnificus* (11.56%), *Edwardsiella tarda* (11.56%), and *Bacillus cereus* (8.82%). These isolates have also shown extracellular enzyme secretions like amylase (50%), protease (17.64%), cellulase (55.88%), and lipase (64.70%). These isolates underwent additional testing to determine their acceptability for use in various field situations and their capacity to grow in different pH and temperature ranges. The antibacterial activity of the isolates supports their potential as probiotics in fish culture, encouraging further exploration of their probiotic properties

Keywords: Probiotics, Freshwater fish, Gut microflora, Enzymes, Antibiotic resistance



ENHANCED IMMUNE PROTECTION IN TILAPIA THROUGH LECTIN-BASED ORAL AND INTRAPERITONEAL VACCINES

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Tilapia (*Oreochromis niloticus*) the second most cultivated fish globally, is highly susceptible to streptococcosis, primarily caused by *Streptococcus agalactiae* and *Streptococcus iniae*. Antimicrobial resistance to this disease has necessitated the development of effective preventive strategies such as vaccination. This study aimed to develop oral and injectable vaccines adjuvanted with lectin, a glycoprotein known to enhance antigen uptake and immune responses. A formalin-inactivated vaccine was prepared by culturing *S. agalactiae* and *S. iniae* in tryptic soy broth with NaCl at 28°C for 24 hours, followed by inactivation with 0.5% formalin. For oral vaccination, the inactivated vaccine was coated onto feed using lectin as an adjuvant and alkoxy glycerol (AKG) as a binder to stabilize the vaccine. For injectable vaccination, the inactivated vaccine was mixed with lectin and administered intraperitoneally at a dose of 100 µl/fish. Booster doses were administered orally for 7 days at 4- and 8-weeks post-vaccination, while intraperitoneal booster doses were given 21 days post-vaccination. Nonspecific immune responses, including superoxide dismutase (SOD), lysozyme, and myeloperoxidase, were analyzed in the serum of vaccinated fish (n=6) at 7, 14, 21, 28, 35, 42, 49, and 56-days post-vaccination. Specific IgM antibody titers were measured at 14-, 35-, and 49-day post-vaccination. Additionally, expression levels of immune-related genes (IgM, TCRβ, MHC I, MHC II, CD4, IFNγ, and IL8) were assessed in spleen and head kidney tissues. Both oral and injectable vaccines with lectin adjuvants demonstrated significantly enhanced nonspecific immune responses and elevated IgM antibody titers compared to control groups. The relative percentage of survival (RPS) was calculated as over



60% for orally vaccinated fish and 75% for intraperitoneally vaccinated fish. These findings highlight the efficacy of lectin as a vaccine adjuvant, offering a promising and sustainable strategy for managing streptococcosis in aquaculture.

Keywords: *Streptococcus agalactiae*, *Streptococcus iniae*, Lectin, Oral vaccine, *I.p.* vaccine, *Oreochromis niloticus*



SAB-P4

FATTY ACID BIOCONVERSION IN MARINE FISH:
IMPLICATIONS FOR SUSTAINABLE AQUAFEED PRODUCTION
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The rapid expansion of aquaculture is essential to meet the growing global demand for protein and lipids for human consumption. Consequently, the use of fish feed has also been increasing. Fishmeal (FM) and fish oil (FO) are widely used in aquafeeds, with FM serving as a key protein source and FO providing essential omega-3 and omega-6 highly unsaturated fatty acids (HUFAs), such as eicosapentaenoic acid (EPA), docosahexaenoic acid (DHA), and arachidonic acid (ARA). These fatty acids play a critical role in growth, metabolism, immune function, reproduction, and neural development, with EPA and ARA serving as precursors for eicosanoids that modulate immune responses. However, the increasing demand for FO, coupled with the decline in marine fishery resources, necessitates the search for sustainable alternatives such as plant-based oils. Plant oils are rich in polyunsaturated fatty acids (PUFA) such as alpha-linolenic acid (ALA) and linoleic acid (LNA) and some monounsaturated fatty acids (MUFA), palmitoleic acid, oleic acid, but lack HUFAs (EPA, DHA), which limit their direct use in aquafeed. However, certain fish species can synthesize HUFAs through the fatty acid bioconversion pathway. Wherein ALA and LNA are converted into EPA, DHA, and ARA through the action of desaturase ($\Delta 6$ and $\Delta 5$ desaturases) and elongase enzymes. These enzymes are responsible for fatty acid bioconversion. In general, freshwater teleosts possess a higher capability to biosynthesize HUFAs from their precursors ALA and LNA due to the presence of these enzymatic pathways, whereas most marine fish exhibit limited or a lack of ability to convert ALA and LNA to HUFAs. Interestingly, the bioconversion pathway has been identified in certain marine fish species, including Atlantic salmon (*Salmo salar*), rabbitfish (*Siganus* sp.), and Senegalese sole (*Solea senegalensis*). The ability of a fish species to convert C18 polyunsaturated fatty acids (PUFAs) into long-chain PUFAs



(LCPUFAs) is largely determined by its complement of fatty acyl desaturase (Fad) and elongase (Elovl) enzymes, which regulate fatty acid metabolism. Therefore, understanding these species-specific bioconversion pathways is essential for developing cost-effective and nutritionally optimized aquafeeds that minimize reliance on fish oil while ensuring optimal fish health and growth.

Keywords: Fatty acid bioconversion, Desaturase, Elongase, EPA, DHA, Marine fish



SAB- P5

**EMPOWERMENT OF COASTAL SCHEDULED CASTE
COMMUNITIES THROUGH SUSTAINABLE SEA CAGE
FARMING: A SUCCESS STORY FROM THOOTHUKUDI, TAMIL
NADU UNDER ICAR CMFRI, SCSP PROGRAM**

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Sea cage farming is an emerging sustainable mariculture. Under the Scheduled Caste Sub Plan (SCSP) of ICAR-Central Marine Fisheries Research Institute (CMFRI), various initiatives were implemented to empower Scheduled Caste (SC) community beneficiaries in Thoothukudi, Tamil Nadu. In 2019-20, the "Alangar" group under SCSP deployed 6-meter diameter HDPE cages in Mottaigopuram Sea for the culture of Asian Seabass. Over 11 months, they harvested 1090 kg of seabass (Rs. 440/kg), generating Rs. 4.796 lakhs. Following this success, the group received inputs for one more cage to upscale farming of fattening spiny lobster fattening. Juvenile lobsters of 80 g size stocked and fattened to 200-250g in five months, yielded 285 kg, generating Rs. 70,000 per person/harvest. In the next year, they have been given two numbers of rectangle type iron framed crab cages fitted with HDPE crab boxes and carried out mud crab fattening as and when water crabs are available. They sustainably harvest >500 g (XL) and >1 kg (XXL) size of mud crab during every 30-35 days fattening period and generated the gross revenue of Rs. 1.55 lakhs through mud crab fattening alone. In the next cycle, they stocked 550 assorted groupers, harvesting 356 kg after 12 months, generating Rs. 75,000. Over three years, the group completed two harvests of seabass, each one harvest of spiny lobster and grouper, with periodic crab harvests, resulting in Rs. 1.85 lakhs per person. Currently, they are farming Asian seabass, silver pompano, along with mud crab fattening. This case study highlights the success of sea cage farming as a tool for social empowerment, community development, and skill enhancement, serving as a model for sustainable aquaculture to achieve Blue Economy goals and equity.

Keywords: *Blue economy, sustainable, marine farming, livelihood, empowerment.*



SAB-P6

ISOLATION, SCREENING, AND PRELIMINARY CHARACTERIZATION OF ENZYME-PRODUCING BACTERIA FROM AQUACULTURE POND

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Aquaculture is one of the food production industries with the fastest rate of growth in the world. Sustainable methods and better pond management are becoming more and more important. Microbial enzymes as feed additives and bioremediation agents are a viable way to improve organic matter decomposition and preserve water quality in aquaculture systems. This study focuses on the isolation, screening, and preliminary screening of hydrolytic enzyme-producing bacteria from an aquaculture pond. Water and sediment samples were collected from an aquaculture pond in January 2025 near the School of Marine Science, CUSAT, and subjected to serial dilution and culture-based methods to isolate bacterial strains. The primary objective of the present study is to demonstrate the ability of enzyme-producing bacteria to degrade organic matter effectively in an aquaculture pond. Preliminary characterisation was done by morphological characterisation and biochemical tests. The results revealed that the following percentage of isolates from sediment and water samples showed positive results for various hydrolytic enzyme production: protease (52%), cellulase (52%), amylase (36%), lipase (44%). The findings demonstrate that organic matter can be biodegraded by native bacterial isolates, which can significantly increase nutrient cycling, reduce organic load, and promote pond health in aquaculture systems. Bacteria that produce extracellular enzymes play a vital role in the degradation of organic matter by breaking down complex organic compounds into simpler, more absorbable forms. These exogenous microbial enzymes may also be beneficial additions to fish feed formulations by enhancing digestion and making it easier to use alternative feed sources.

Keywords: Aquaculture, Enzyme-producing bacteria, Hydrolytic enzymes



SAB-P7

SPIRULINA AS A FUNCTIONAL FEED ADDITIVE: EFFECT ON GUT IMMUNE GENE EXPRESSION AND DISEASE RESISTANCE IN NILE TILAPIA

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Spirulina, a nutrient-dense cyanobacterium, has gained attention as a functional feed additive in aquaculture due to its potential immunomodulatory and growth-enhancing properties. This study evaluates the effects of dietary *Spirulina* supplementation on gut immune gene expression and disease resistance in Nile tilapia (*Oreochromis niloticus*) through a feeding trial followed by a bacterial challenge. In the feeding trial, Tilapia was fed a *Spirulina*-supplemented diet for two weeks, with gut samples collected at multiple time points (0, 1, 7, and 14 days) to assess changes in gut immune-related gene expression. Following the feeding period, the fish were subjected to a bacterial challenge by immersion in a *Streptococcus iniae* solution, a prevalent aquatic pathogen known to cause infections in Tilapia. Gut samples were collected at predetermined intervals post-challenge to analyze immune response dynamics induced by *Spirulina* supplementation. Quantitative real-time PCR (qRT-PCR) was employed to examine the expression levels of key immune-related genes. The differential expression of immune genes from the gut provides valuable insights into the immune-modulating effects of *Spirulina* supplementation in Tilapia, highlighting its potential role in boosting disease resistance and overall fish health. The findings contribute to the development of sustainable aquaculture practices through the use of natural dietary supplements. Further research is needed to optimize *Spirulina* inclusion levels and evaluate its long-term effects on fish performance.

Keywords: Feed additives, Gene expression analysis, Fish health, Immune response, Aquaculture



SAB-P8

PROBIOTIC-INDUCED IMMUNOMODULATION IN
OREOCHROMIS NILOTICUS: EFFECTS ON IMMUNE GENE
EXPRESSION AND DISEASE RESISTANCE

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Probiotics play a vital role in enhancing immunity and gut health in aquatic organisms, including fish. This study evaluates immune gene expression in *Oreochromis niloticus* (tilapia) fed a probiotic-supplemented diet. Fish were administered the probiotic diet for two weeks, with gut samples collected at 0, 1, 7, and 14 days to assess temporal changes in immune gene expression. On day 14, the fish were challenged via immersion with *Streptococcus iniae*, a Gram-positive bacterial pathogen, and additional sampling was conducted at predetermined intervals post-challenge to analyze immune response dynamics. RNA was extracted, complementary DNA synthesized, and quantitative PCR was performed. The results showed significant differential expression of immune-related genes in probiotic-fed fish compared to controls, particularly post-challenge. The upregulation of key immune genes suggests an enhanced immune response and improved disease resistance. These findings provide insights into the immunomodulatory effects of probiotics in tilapia, supporting their potential role in disease prevention and gut health improvement.

Keywords: Immune gene expression, Immunomodulation, *Oreochromis niloticus*, Probiotics, *Streptococcus iniae*



SAB-P9

COMPARATIVE GUT MICROBIOME ANALYSIS OF *FENNEROPENAEUS INDICUS* EXPERIMENTALLY CHALLENGED WITH WHITE SPOT SYNDROME VIRUS

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The gut microbiome plays a crucial role in pathogen resistance, immune modulation, and overall host health, making it a key focus in disease management of cultured shrimp. White Spot Syndrome Virus (WSSV) is one of the most lethal pathogens, causing high mortality and severe losses in shrimp aquaculture worldwide. This study conducted a comparative gut microbiome analysis of WSSV-infected and healthy *Fenneropenaeus indicus* using high-throughput sequencing. The results revealed significant shifts in bacterial diversity, with notable changes in beneficial genera and an increase in opportunistic pathogens in WSSV-infected shrimp. This study highlights microbial alterations associated with WSSV infection, providing insights into gut microbiome dysbiosis and its potential implications for shrimp health and disease resistance.

Keywords: *Fenneropenaeus indicus*, Gut microbiome, High-throughput sequencing, Microbial dysbiosis, White Spot Syndrome Virus (WSSV)



SAB-P10

PROBIOTIC POTENTIAL OF MANGROVE SEDIMENT MICROBES AGAINST AQUACULTURE PATHOGENS

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The aquaculture sector in India plays a vital role in food security, livelihoods, and economic growth, contributing significantly to global fish production. However, the same sector is currently plagued by an array of challenges that hamper overall growth and productivity, which include recurring disease outbreaks, compromised water quality, pollution, environmental degradation, inadequate regulatory frameworks, antimicrobial resistance, insufficient disease management and surveillance mechanisms. Infectious disease outbreaks pose a significant and immediate risk to the sustainability of the aquaculture industry, which calls for swift and effective countermeasures. Probiotics have emerged as a promising alternative, enhancing gut health, inhibiting pathogen growth, and improving water quality. Mangrove ecosystems harbour diverse microbial communities, where unique environmental pressures support resilient bacterial strains with exceptional probiotic potential, making them promising candidates for combating aquaculture pathogens. This study aims to assess the probiotic potential of bacteria isolated from mangrove sediments for their effectiveness against various aquaculture pathogens. The sediment samples were collected from Kannur district of North Kerala, and the isolation of the bacterial strains was carried out using the agar overlay method. A total of 33 potential strains could be isolated, which were taken for further screening. Around 20 isolates were subjected to mass culture, followed by preliminary screening of their antimicrobial activity using both crude extract and cell-free supernatant methods. From these 11 bacterial strains, demonstrating inhibitory activity was identified and prioritized. The findings highlight the successful identification of active bacterial strains with strong antimicrobial properties, which can be further explored for developing a potential probiotic consortium for aquaculture applications.

Keywords: Mangrove, Aquaculture, Probiotics, Antimicrobial activity



SAB-P11

EXPLORING THE ANTIBIOFILM POTENTIAL OF ACTINOMYCETES IN AQUACULTURE: A NOVEL APPROACH TO DISEASE MANAGEMENT

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A biofilm is a collection of microbial cells encased in a polysaccharide matrix and irreversibly attached to a surface. Biofilms pose a significant risk to global seafood production, which relies heavily on aquaculture. The growing threat of antibiotic-resistant biofilms necessitates the development of new antimicrobial strategies. Marine Actinomycetes offer benefits for aquaculture by producing bioactive compounds that inhibit biofilms and promote health. This study explored the ability of Actinomycetes from marine sediments to inhibit biofilms formed by aquaculture-related bacteria. Biofilm samples were collected in triplicate from five aquaculture systems. Screening of 15 Actinomycetes isolates revealed several with antibiofilm properties, including six with notable inhibition effects. A 96-well microtiter plate assay was used to assess the antibiofilm activity of Actinomycetes. DNA sequencing analysis and 16S rRNA gene PCR disclosed that the biofilm-forming bacteria comprised *Staphylococcus caprae*, *Priestia megaterium*, *Exiguobacterium* sp., and *Vibrio fluvialis*. In conclusion, Actinomycetes exhibit considerable potential for application in aquaculture due to their efficacy as anti-biofilm agents. These findings have significant implications for developing sustainable solutions to combat biofilm-related issues, and merit further research on commercialization and practical applications

Keywords: Biofilms, Aquaculture, Antibiotic resistance, Actinomycetes



SAB-P12

WASTE TO WEALTH APPROACHES IN FISH NUTRITION

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The "waste to wealth" approach in fish nutrition is transforming aquaculture by repurposing underutilized biomass into valuable feed ingredients, promoting sustainability and resource efficiency. In Kerala, the invasive *Eichhornia* plant, which disrupts waterways like the Water Metro, can be utilized as a substrate for black soldier fly (*Hermetia illucens*) larvae cultivation—an emerging protein-rich alternative to fishmeal. Additionally, microbial protein sources, such as methanol-utilizing single-cell protein bacteria, offer promising solutions for large-scale fish feed production. Another innovative strategy is the conversion of jellyfish biomass, driven by programs like Medusa, into high-protein feed ingredients, mitigating ecological imbalances caused by jellyfish overpopulation. Globally, shrimp shell waste is a significant concern, particularly in India, the world's second-largest shrimp producer. This byproduct is now being repurposed to extract chitosan, a compound with antioxidant properties and applications in targeted drug delivery. Moreover, chitosan is increasingly being incorporated into fish feed as a functional additive to enhance immune response and growth performance. By integrating circular economy principles into aquafeed production, these waste-to-wealth strategies not only reduce environmental impact but also create sustainable and economically viable solutions for the aquaculture industry. This review explores emerging innovations, their ecological and economic benefits, and advancements in bioprocessing technologies driving the future of sustainable fish nutrition.

Keywords: Jellyfish, *Eichornia*, *Hermetia illucens*, Nutrition



SAB-P13

METHANOLIC EXTRACT OF *SARGASSUM WIGHTII* BOOST
IMMUNE SYSTEM AND SUPPRESS THE MULTIPLICATION OF
WHITE SPOT SYNDROME VIRUS (WSSV) IN INDIAN WHITE
SHRIMP *FENNEROPENAEUS INDICUS*

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Sargassum wightii collected and processed from Kanyakumari Coast and extracted with the polar solvent, methanol. The extract was screened against shrimp white spot syndrome virus (WSSV) through a shrimp *in vivo* model by monitoring the survival and PCR diagnosis. Based on the screening, the methanolic extract effectively suppressed WSSV multiplication. Further, artificial pellet feed was prepared by the incorporation of *S. wightii* methanolic extracts at the concentrations of 100 (SWD1), 200 (SWD2), 400 (SWD3), and 800 (SWD4) mg/kg of feed. The experimental and control (without *S. wightii* extract incorporation) diets fed to the *Fenneropenaeus indicus* weighed 10±1.3 g for 25 days, and at the termination of the feeding trials, they were challenged with virulent WSSV. The shrimp control group has succumbed to death 100 % and mostly PCR positive, whereas the experimental groups SWD3 and SWD4 groups had more than 70% survival and only 4% positive after two-step PCR detection, and the value differed significantly ($P<0.05$). The experimental diet had a significant impact ($P<0.001$) that improved the time of coagulase activity, improved increased haemocyte count compared to the control diet fed groups. The immunological parameters, which encompass prophenoloxidase activity and lysozyme activity, also appeared to have significantly increased ($P<0.001$) in experimental groups compared to control diet fed shrimp group. Based on the present findings, *S. wightii* active principles may help to develop the immunostimulant drug for boosting the immune system against WSSV infection in cultivable shrimps.

Keywords: Antiviral, *Fenneropenaeus indicus*, Immunostimulants; *Sargassum wightii*, WSSV



SAB-P14

INTEGRATED BIOREMEDIATION AND SUSTAINABLE SHRIMP
FARMING: CO-CULTIVATION OF *GRACILARIA FOLIIFERA*
(FORSSKAL) BORGESON, 1932 AND *PENAEUS VANNAMEI*
(BOONE, 1931)

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A 60-day study evaluated the co-culture of *Gracilaria foliifera* seaweed with *Penaeus vannamei* shrimp in pond systems. Using a completely randomized design, three treatments were tested based on the timing of seaweed introduction: T1 (day 0), T2 (day 30), and T3 (day 60), each compared to shrimp monoculture controls. Nutrient absorption was highest in T2, where *G. foliifera* achieved the most significant uptake of Total Ammonia Nitrogen (76.6%) and Nitrite (66.9%). Shrimp growth performed best in T1, with a weight gain of 438.41%, followed by T2 (222.34%) and T3 (127.94%), with T1 also exhibiting the highest specific growth rate (2.8%). Seaweed growth was most pronounced in T2, showing a 26.39% increase in biomass. Additionally, co-culture reduced oxidative stress in shrimp, as indicated by lower enzyme activity and blood glucose levels in T2. Proximate analysis revealed that T1 had the highest moisture and protein content, while T2 recorded the highest crude fat levels. Overall, introducing seaweed at day 30 (T2) optimized nutrient absorption, enhanced growth, and reduced stress, making it the most effective co-culture strategy for bioremediation and sustainable shrimp farming.

Keywords: Co-culture, Nutrient absorption, Shrimp, Bioremediation, Seaweed, Sustainable aquaculture



SAB-P15

INTEGRATING RESEARCH AND RESCINDABLE FISHING
ADAPTIVE TO ENGAGE JELLYFISH FISHERIES AS A
SUSTAINABLE APPROACH TO BLUE ECONOMY: AN INDIAN
SCENARIO

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Blue economy emphasizes the sustainable utilization of marine resources to drive economic growth while ensuring environmental sustainability. Among marine resources, commercial fisheries, mariculture, deep-sea fishing, ornamental fisheries, seaweed culture, renewable energy, tourism, shipping, seabed mining, Jellyfish fisheries have emerged as an important yet underutilized component with significant ecological and economic potential. During bloom seasons, jellyfish adversely impact marine ecosystems and fisheries, disrupting livelihoods dependent on traditional fish stocks. However, their commercial potential remains largely untapped, with exports currently limited to a few coastal regions of India. In the Indian seas, 35 species are said to be found (29 scyphozoans and 6 cubozoans), where only 4 species are found to be edible, which are processed for export. Traditionally considered a nuisance due to their blooms, jellyfish are now being explored for their contributions to fisheries, pharmaceuticals, cosmetics, and biotechnology. They serve as a valuable food source in various Asian markets and are rich in bioactive compounds with medical applications, having a potential use in collagen extraction and anti-aging products. Expanding jellyfish fisheries could mitigate the ecological disruptions caused by blooms while creating new economic avenues for coastal communities. This review paper explores the potential of jellyfish as a fisheries resource in India, emphasizing its role in the fisheries sector, global market expansion, urgent need for scientific monitoring, processing infrastructure, and policy integration.

Keywords: Blue economy, Jellyfish, Jellyfish fisheries, Jellyfish bloom, Policies, India



SAB-P16

ENRICHMENT AND ISOLATION OF SULFUR-OXIDIZING
BACTERIAL CONSORTIA FROM DIFFERENT AQUATIC
ECOSYSTEMS FOR THE BIOREMEDIATION OF HYDROGEN
SULFIDE IN AQUACULTURE SYSTEMS

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Intensification of aquaculture practices leads to environmental deterioration, especially water and sediment qualities, which directly contribute to disease outbreaks and mortality in cultured animals. In an aquaculture system, hydrogen sulfide is a lethal pollutant produced at the anoxic bottom sediment by the activity of sulfur-reducing bacteria. The micromolar concentration of sulfide is toxic for eggs, fries, and adults of aquaculture organisms causing disease and mortalities, leading to massive crop loss. Bioremediation is the best method to mitigate the pollutants in aquaculture practices without making any environmental impacts. To resolve the sulfide toxicity in aquaculture, sulfur-oxidizing bacteria can be enriched and isolated from the aquatic ecosystems and used as bio-augmenters to convert the toxic sulfide to harmless forms such as sulfate or elemental sulfur. In the present study, sediment and water samples were collected from different aquatic systems, and the sulfur oxidation activity of the bacterial community was screened by a pH reduction test using sulfur-based inorganic media. The enriched consortia sub-cultured and the sulfur oxidation activity was quantified by measuring the substrate utilization rate, and by-product formation using standard protocols. A total of 6 different SOB consortia were enriched and isolated in ATCC medium 152, which can work under three salinity ranges such as 0 ppt, 15 ppt, and 25 ppt. All the SOB consortia enriched utilized sulfide and thiosulfate as their energy source in the ATCC media, and sulfate ion was produced as the by-product. The study was significant because it focused on eco-friendly approaches to mitigate sulfide toxicity in aquaculture systems using enriched SOB consortia as a bioaugmentor.

Keywords: Hydrogen sulfide toxicity, Bioremediation, Sulfur-oxidizing bacteria



SAB-P17

MINI ECO AQUAPONICS: THE FUTURE OF SUSTAINABLE HOME AQUACULTURE

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This study introduces an innovative mini recirculatory aquaponics system designed for small glass aquarium tanks, offering an affordable and eco-friendly alternative. Utilizing repurposed materials such as discarded PVC pipes, the system eliminates the need for conventional water pumps, instead employing a low-energy air pump for water circulation. This approach significantly reduces energy consumption while ensuring ease of operation. The system integrates polar white cichlid aquaculture with mint plant cultivation, creating a self-sustaining ecosystem where fish waste provides essential nutrients for plant growth, and plants, in turn, purify the water. Key water quality parameters, including pH, dissolved oxygen, and ammonia levels, are carefully monitored to maintain a balanced environment conducive to aquatic and plant health. This presentation will examine the design, functionality, and outcomes of the project, demonstrating its practicality, affordability, and ecological advantages. By making aquaponics accessible for small-scale urban applications, this system encourages sustainable living while contributing to greener indoor environments.

Keywords: Mini recirculatory aquaponics, Sustainable aquaculture, Water quality management, Ecological benefits, Urban sustainability



SAB-P18

DIETARY ANALYSIS OF NILE TILAPIA IN AN INTRODUCED ECOSYSTEM: A CASE STUDY FROM VELIAKKULAM LAKE

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Native to tropical and subtropical regions of Africa and the Middle East, the Nile tilapia (*Oreochromis niloticus*) has been introduced to over 50 countries across all continents except Antarctica. The Nile tilapia is regarded as a "potential pest" for amphibians and juvenile fish species in the indigenous ecosystem. Currently, the dominant fish species in Veli-Akkulam Lake is the invasive Nile tilapia. The samples were taken in Veli-Akkulam Lake, on the southwest coast of Kerala (Sept 2023 to May 2024), using a cast net. This research aims to analyze the stomach contents of Nile tilapia in Veli-Akkulam Lake to determine their feeding habits and their impact on the native aquatic ecosystem. A total of 55 Nile tilapia specimens were collected for diet content analysis. The gut contents were examined using frequency of occurrence, the points method, and Gastro Somatic Index (GaSI). The study results are summarized as Chlorophyceae was identified as the most preferred food item (25%), followed by Bacillariophyceae (21%), detritus and insects (13%), insect remains (7%), Ostracoda (1 %), and Cyanophyceae (1%). Carnivory was observed in mid-sized and larger fish, with few small-sized fish consuming insect remains and chironomid larvae. Bacillariophyceae was the most frequent food item overall (35%), followed by Chlorophyceae (23%) and miscellaneous items (18%). The feeding intensity analysis revealed that most fish were in moderate condition (51%), 22% were in poor condition, and only 5% had empty stomachs; the rest of the percentage were in Good, full gorged. Gorged and full stomachs were absent in small-sized fish but present in mid-sized and larger fish. The GaSI increased with fish size, whereas the Relative Gut Length showed minimal variation, with slightly higher values in mid-sized fish. These findings support the notion that Nile tilapia, as an omnivorous species with significant trophic plasticity, can pose a considerable threat to native species like *Etroplus suratensis* in invaded ecosystems.

Keywords: Nile -Tilapia, Chlorophyceae, Bacillariophyceae, Omnivorous, Plasticity



SAB-P19

EFFECTS OF MICROPLASTIC POLLUTION ON SMALL-SCALE FISHING COMMUNITIES AND POTENTIAL BLUE ECONOMY SOLUTIONS

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Microplastic pollution is a serious and widespread threat to marine ecosystems and the livelihoods of small-scale fishing communities globally. These small plastic pieces, easily consumed by marine organisms, build up in the food web, threatening twice: depleting fish populations and human health through contaminated seafood. Proven effects on fish stocks are growth impairment, reproductive failure, and changed behavior, having a direct consequence on smaller catches and financial insecurity for fishers. The concerned communities tend to be deeply dependent on the coastal resources and have limited diversified sources of income. These are exposed the most. To solve the crisis, solutions in the Blue Economy are needed. Encouragement of circular economy concepts, waste minimization, and recycling, as well as rewarding biodegradable fishing equipment, is fundamental. Local microplastic monitoring and cleanup activities can be empowering for local people, and sustainable tourism practices that place a premium on environmental responsibility provide alternative economic opportunities for local people, and sustainable tourism practices that place a premium on environmental responsibility provide alternative economic opportunities. In the end, meaningful mitigation will demand coordinated policy structures and strong international cooperation. It is only through these cooperative efforts that we can protect the long-term viability of small-scale fisheries and secure the resiliency of coastal communities in a prosperous Blue Economy.

Keywords: Microplastics, Small-scale fisheries, Blue economy, Pollution, Coastal communities



SAB-P20

A PRELIMINARY EXPERIMENTATION USING MIXED ALGAL DIETS TO UNRAVEL ITS EFFECT ON THE ANTIOXIDANT BIOMARKERS OF ARTEMIA FRANCISCANA METANAUPHII

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Artemia metanauplii is a premier choice among popular live feeds used in hatcheries. Characterized by their small size, filter-feeding behavior, and high carotenoid content, *Artemia nauplii* meet most of the desired criteria for an ideal live feed. The present study evaluates the beneficial effects of mixed algae-based enrichment on the antioxidant biomarkers of *Artemia metanauplii*. Marine microalgae—*Tetraselmis gracilis*, *Thalassiosira weissflogii*, and *Isochrysis galbana*—were cultivated in F/2 nutrient-enriched sterile saline water (salinity: 30 ppt). *Artemia nauplii*, hatched from dry cysts (OSI Brand), were incubated in sterile saline until they moulted into Instar II. The algal cultures were mixed in a 1:1 ratio to prepare the enrichment media (cell density: 25×10^4 cells/mL): *Tetraselmis* + *Isochrysis* (Diet-I), *Thalassiosira* + *Isochrysis* (Diet-II), and *Tetraselmis* + *Thalassiosira* (Diet-III). Instar II *Artemia* were incubated in the enrichment media (treatment groups) or sterile saline (control) for 1.2 hours. The enriched biomass from both the treatments and control was then macerated in PBE buffer (pH: 7.4) and centrifuged to obtain the fraction used for analyzing total antioxidant capacity (TAC), lipid peroxidation index (LPx), and H₂O₂ content. The tissue concentration of soluble protein (50.11 µg/100 mg wet wt.) and TAC (84.67%) were found to be significantly higher ($p < 0.05$) in the batch enriched with Diet-III. However, the indices of lipid peroxidation (LPx) and H₂O₂ showed no significant differences between the control and treated batches or among the treated batches themselves. Thus, the combination of microalgae appears to be a promising strategy for improving the antioxidant profile of enriched *Artemia metanauplii*.

Keywords: *Artemia franciscana*, *Tetraselmis gracilis*, *Thalassiosira weissflogii*, *Isochrysis galbana*



SAB- P21

MELANOPHORE INDEX AS AN INDICATOR OF CHROMIUM TOXICITY IN *CYPRINUS CARPIO*

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Potassium dichromate ($K_2Cr_2O_7$) is a highly toxic hexavalent chromium compound that poses significant risks to aquatic organisms. This study investigates melanophore deformities in *Cyprinus carpio* (common carp) following exposure to two sublethal concentrations (6.45 ppm and 12.90 ppm) over various durations (0, 24, 48, 72, 96, and 120 hours). Melanophores, responsible for pigmentation and stress responses in fish, were analyzed for morphological changes induced by chromium toxicity. The melanophore index (MI), a quantitative biomarker used to assess changes in the number, size, and distribution of melanophores, was employed to evaluate stress responses and the environmental impacts on pigmentation. The MI serves as a sensitive, non-invasive method for detecting toxicity, providing valuable insight into the physiological and cellular disruptions caused by chromium exposure. Results revealed a concentration- and time-dependent increase in deformities, including cellular fragmentation, aggregation, and dispersion, with severe structural damage observed at 120 hours in the higher concentration group. These findings demonstrate the potential of potassium dichromate to disrupt melanophore patterns and highlight its broader implications for physiological processes in aquatic species, affecting fish health, population stability, and ecosystem balance. From a societal perspective, this study underscores the importance of mitigating industrial pollution to ensure safe water resources, protect biodiversity, and safeguard fisheries essential for food security and livelihoods. The hazardous impact of chromium pollution on aquatic life necessitates strict environmental monitoring and remediation strategies to reduce heavy metal contamination in aquatic ecosystems. Future research should explore long-term physiological effects and potential mitigation strategies to protect aquatic life.

Keywords: Potassium dichromate, Melanophore index, *Cyprinus carpio*, Melanophore deformities, Aquatic ecosystem



SAB- P22

IMPACT OF COVID-19 ON AQUACULTURE: CHALLENGES AND RESILIENCE

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The global aquaculture industry was severely disrupted by the COVID-19 pandemic, which had an impact on livelihoods, supply chains, market access, and production. Transportation restrictions and lockdown procedures decreased the supply of labour, feed, and seed, which had an effect on farming operations and productivity. The demand for high-value aquatic species fell rapidly as a result of restaurant closures and export restrictions, which resulted in higher stock retention and financial losses. Due to their limited financial resilience and reliance on live markets, small-scale farmers were especially at risk. Seafood exports were impacted by global trade and logistics disruptions, resulting in lower profits for major producers such as Ecuador, Vietnam, and India. Direct consumer sales were made possible by the crisis, which also hastened the adoption of digital platforms for e-commerce and seafood marketing. The pandemic underscored the importance of sustainable and localized supply chains to enhance resilience in the sector. Recovery efforts should focus on strengthening policies for smallholder farmers, improving market diversification, and fostering innovations in aquaculture technology. Increasing investment in biosecurity, disease management, and sustainable practices will be essential for building a more resilient aquaculture industry in the post-pandemic era.

Keywords: Covid-19, Aquaculture, Lockdown, Challenges



SAB-P23

FISHING RESTRICTIONS AND SUSTAINABLE LIVELIHOOD: CHALLENGES FACED BY SMALL-SCALE CRAB FARMERS IN BANGLADESH

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Fishing restrictions are widely implemented to protect marine and coastal ecosystems, yet their socioeconomic implications for small-scale fishers and aquaculture farmers remain underexplored. This study conducts a systematic literature review (SLR) to examine the impact of fishing restrictions on the sustainable livelihoods of small-scale crab farmers in Bangladesh. The review synthesizes existing research on the economic, environmental, and social challenges associated with fishing bans, focusing on how these policies affect income stability, resource access, and long-term sustainability. Findings indicate that while fishing restrictions contribute to biodiversity conservation, they create financial hardships, intensify resource competition, and push farmers toward unsustainable practices. The study highlights gaps in policy implementation, weak enforcement of regulations, and a lack of alternative livelihood strategies as critical barriers to sustainability. It emphasizes the need for integrated policy approaches that balance conservation goals with economic resilience, including sustainable aquaculture, improved governance, and targeted support programs. This review contributes to the broader discourse on fisheries management and offers insights for policymakers aiming to enhance both ecological preservation and the well-being of small-scale crab farmers.

Keywords: Sustainable livelihoods, Small-scale fisheries, Crab farming, Fishing restrictions, Bangladesh



SAB-P24

GREEN SYNTHESIS OF ZINC OXIDE NANOPARTICLES FOR ENHANCING FISH HEALTH AND WATER QUALITY IN AQUACULTURE

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To meet the demands of aquaculture, sustainable practices have paved the way to explore novel technologies to enhance fish health and water quality. In this regard, Zinc oxide nanoparticles are a promising tool currently gaining attention. This study investigates the green synthesis of ZnO nanoparticles using aqueous extract from the mango panicles. Hundred grams of fresh mango panicles were sampled and treated with 250 mL warm water kept at 70°C for 30 minutes. The extract was filtered, and the volume was reduced to 100 mL. These concentrated extracts were used to synthesize ZnO nanoparticles by reacting with zinc nitrate solution. The pH of the solution was adjusted with a dilute NaOH solution. The precipitate obtained were purified and dried followed by calcination. The formation of ZnO nanoparticles were confirmed by analysis using UV-VIS spectroscopy and XRD. Results showcase the potential of aqueous extract of mango panicles for developing ZnO nanoparticles that can be used to improve fish growth rates, immune response, and water quality by reducing waterborne pathogens.

Keywords: Zinc Oxide nanoparticles, Green synthesis, Aquaculture, Sustainable aquaculture practices



SAB-P25

INSTITUTIONAL BARRIERS TO SUSTAINABLE MARINE FISHERIES IN INDIA: A CRITICAL ANALYSIS WITH SPECIAL REFERENCE TO KERALA

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India's marine fisheries sector contributes to 39% of national fish production and supports nearly 3.52 million people. The institution is marked by economic instability, falling inshore fish stocks endangering coastal ecosystems, and over-reliance by communities. Overfishing, driven by motorized fleets and trawlers, has depleted resources, with 90% of fish stocks fully or overexploited. Unregulated market chains, ineffective port infrastructure, and subpar cold storage facilities cause post-harvest losses and lower profitability for small-scale fishermen. In Kerala, the issues are exacerbated by infrastructure deficiencies, failed modernization efforts, widespread non-compliance to rules (primarily The Kerala Marine Fishing Regulation Act, 1980) and climate vulnerabilities. Gaps in the implementation of statutory norms and government initiatives, as well as flaws in relevant policies and statutes, combined with government mismanagement, further undermine sustainability. While initiatives like the Pradhan Mantri Matsya Sampada Yojana (PMMSY) aim to promote responsible fishing, gaps in implementation persists, with fishers lacking viable alternatives during fishing bans. Overfishing, regulatory loopholes, and socio-economic vulnerabilities pose serious challenges to the sustainability of India's marine fisheries system, especially in Kerala. Therefore, there is a strong need for institutional reforms and decentralized governance to balance Sustainable development with livelihood needs of dependent people. This study explores, in-detail, the various provisional, procedural, administrative, policy-related and other institutional challenges to sustainability in this sector in Kerala and their possible solutions. The research employs a mixed-methods approach, combining qualitative interviews with stakeholders with quantitative fisheries data analysis to examine the institutional barriers affecting sustainable marine fisheries in Kerala.

Keywords: Resource depletion, Sustainability, Institutional barriers, Kerala



SAB-P26

GENETICALLY MANIPULATED SEAWEED FOR SUSTAINABLE COASTAL AQUACULTURE

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Seaweeds, macroscopic marine algae, are a vital alternative source of food, feed, fuel, and livelihood. With an 8% annual growth rate, seaweed aquaculture is expanding due to rising demand, depleted natural stocks, and intensive farming challenges. However, issues like poor phycocolloid-producing strains, disease susceptibility, environmental variability, and low thermal tolerance hinder industry progress. To address these challenges, genetically manipulated seaweeds (GMS) are developed through genetic engineering or induced variation. Techniques such as hybridization, parthenogenesis-induced morphological changes, and mutagenesis-mediated variations are employed. Hybridization, the most studied method, combines protoplasts of different species, as demonstrated by Fujita and Migita (1987) using Polyethylene Glycol (PEG) in *Porphyra* sp. With global demand rising, seaweed farmers advocate for GMS adoption, while scientists strive to develop and commercialize superior strains, particularly in India. Overexploitation of natural resources and the need for sustainable raw materials drive this innovation. GMS can strengthen seaweed-based industries, enhance carbon sequestration, and support marine biodiversity restoration, aligning with the blue economy. Moreover, integrating GMS into aquaculture can reduce reliance on wild fishmeal, promoting sustainability. Responsible development and regulation of GMS are essential to maintaining ecological balance, food security, and economic viability in the evolving marine sector.

Keywords: GMS, PEG, Genetic engineering, Blue economy



SAB-P27

RECYCLING WATER HYACINTH FOR SUSTAINABLE INCOME AND ENVIRONMENTAL CONSERVATION

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This study explores the transformation of *Eichhornia crassipes*, commonly known as water hyacinth, an invasive exotic aquatic species, into a valuable resource. The water hyacinth is converted into handmade paper through a multi-step process. Initially, the plant is collected and cleaned, followed by the removal of leaves, inflorescences, and roots. The stalks are then chopped into small pieces and boiled until they turn brown. After cooling, the boiled stalks are pulped and mixed with corn starch as a binding agent. Finally, the pulp is diluted with water, strained into frames, and left to dry under the sun, resulting in handmade paper. A comparative analysis reveals that producing paper from water hyacinth offers significant environmental benefits over traditional wood pulp methods. Specifically, the water hyacinth process requires substantially less water and energy, utilizing only 1.5 liters of water and 0.1365 kWh of energy to produce an 80 GSM A4 sheet. The traditional wood pulp methods demand 15-20 liters of water and 1.82 kWh of energy for the same output. By harnessing water hyacinth for paper production, the pressure on trees is significantly alleviated, and the ecological harm caused by this invasive species can be mitigated.

Keywords: Water hyacinth, Handmade paper, Invasive species



SAB-P28

EVALUATION OF FISH GUT ASSOCIATED BACTERIA FOR AQUACULTURE PROBIOTIC PROPERTIES

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Global fish consumption is projected to exceed 200 million tonnes by 2030, driving the need for sustainable aquaculture practices. This study explores the probiotic potential of 177 bacterial isolates from the gut of economically significant fish species in India: *Loligo duvaucelii* (Squid), *Rastrelliger kanagurta* (Indian Mackerel), and *Sardinella longiceps* (Oil Sardines), collected from Vizhinjam, Kerala a prominent fishing area in South India. Three isolates (IM23, IM30, OS40) demonstrated overall probiotic potential, exhibiting antagonistic activity against fish pathogens (*V. vulnificus*, *V. alginolyticus*, *A. salmonicida*, *A. caviae*, *E. tarda*). The isolates produced extracellular digestive enzymes (Protease, Amylase, Lipase, Cellulase, Pectinase), indicating their ability to enhance nutritional digestion and absorption in fish. High siderophore synthesis was observed. Good cell surface hydrophobicity (23%–48%) was seen, suggesting moderate to high intestinal attachment potential by MATH assay. The isolates exhibited considerable pH and bile tolerance, with auto-aggregation <40% after 24 hours and co-aggregation against *A. salmonicida* and *V. vulnificus* ranging from 32.11% to 47.69%. Strong biofilm formation was seen in IM23 and IM30. Safety assessments confirmed no hemolytic activity on 5% sheep blood agar and susceptibility to 13 commonly used antibiotics. These findings highlight the potential of these fish gut-associated bacteria as probiotics in aquaculture. Further in vivo studies are to be followed to validate their efficacy in aquaculture systems.

Keywords: Aquaculture, Probiotics, Fish-gut associated bacteria



SAB-P29

GREEN SYNTHESIS AND CHARACTERIZATION OF COPPER OXIDE NANOPARTICLES FOR CONTROLLING HARMFUL ALGAL BLOOM IN AQUACULTURE

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The productivity of aquaculture poses a significant threat from harmful algal blooms (HABS). They also pose a significant threat to the quality of fish products and human health. Considering their impact on human health, the ecosystem, and economic stability, managing HABs in aquaculture is essential. Copper oxide nanoparticles are shown to exhibit algicidal activity via algal cell membrane disruption, reactive oxygen species generation, and inhibition of photosynthesis. This study aims to develop copper oxide nanoparticles CuO-NPs via a green synthetic route to control HABs in aquaculture. Hundred grams of fresh leaf sampled from *Polygala javana* was treated with 250 mL hot water kept at 70°C for 30 minutes. The extract was filtered and concentrated to 100 mL. Concentrated aqueous extract from *P. javana* was used to synthesize CuO-NPs at room temperature. CuO-NPs formation was confirmed by UV-Vis absorbance studies. Plasmonic absorbance confirmed the formation of CuO-NPs. The stability of CuO-NPs in various saline conditions was assessed. CuO-NPs synthesized using *P. javana* extract showcased excellent stability in various saline conditions. This study confirms the potential of aqueous extract from *P. javana* in synthesizing stable CuO-NPs. Stability of synthesized CuO-NPs highlights the potential in developing methods for sustainable aquaculture practices.

Keywords: *Polygala javana*, Green synthesis, Copper oxide nanoparticles, HABs,



Polar Biology, Ecology, Climate Change, and Ocean Health

Invited Talks



PEC IT-1

POLLUTION PROFILING OF KERALA'S COASTAL SEDIMENTS: THE ROLE OF MICROPLASTICS AND TRACE ELEMENTS

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Plastic pollution are pervasive environmental concerns, particularly in coastal regions. This study investigates the distribution and abundance of microplastics (MPs) in the coastal beach sediments of South-western India particularly Kerala, along with assessing their co-occurrence with trace elements and surrounding environmental conditions. Coastal sediments were collected from 66 sampling sites across 590 km of coastline using systematic quadrat sampling. MPs were extracted by density separation and wet peroxide digestion, followed by characterization using optical microscopy and Raman spectroscopy. The concentration of 20 trace elements were analyzed using ICP-MS, adhering to the EPA 3050B protocol. Sediment pH, conductivity, and particle size were also determined. Results revealed widespread MP contamination, with a state average of 125.83 particles/kg (IQR=144.44). MPs were predominantly fibers (76%), followed by fragments and films, with PET identified as the dominant polymer type. Concurrently, the concentration of all trace elements tested remained within the standard limits. Positive correlations between MP abundance, population density, and pH suggest human activity as a key driver of pollution. PCA highlighted the influence of urbanization on MP and trace element distribution. The findings emphasize the need to implement regular beach clean-up and waste management activities in the coastal regions to regulate the input of microplastics due to the aging of plastic debris. It further reduces the environmental risks caused by the toxic chemicals associated with microplastic on the health of living organisms thriving in the coastal ecosystems.

Keywords: Coastal pollution, ICP-MS, Microplastics, Sediments, Trace elements



PEC-IT 2

ARCTIC TERN MIGRATION AND MY COOPERATION WITH HATHA'S LAB

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Arctic Terns (*Sterna paradisaea*) are known for the longest migration on earth. They fly every year from the Arctic, where they breed, to the Antarctic, where they winter. Every year, there is a small colony of Arctic Terns near the Norwegian Arctic science town of Ny-Ålesund on Svalbard. Several nations have a scientific base in Ny-Ålesund, including the Netherlands and India. Here, they all contribute to Arctic science. The development of geolocators has made it possible to track the entire migration route of this species. For the Arctic Tern, the Netherlands is the southern border of their breeding range, and these birds even fly a longer distance than their northern counterparts. While nesting, the Arctic Terns fiercely defend their nests by attacking visitors to their colony, drawing blood from their head and bombarding faeces on their coats. Mohamed Hatha of the Cochin University of Science and Technology (CUSAT) in India became interested in the Arctic Tern interacting with their intestinal microbes. He spent a lifetime studying microbes and their effect on the natural environment. He had a particular interest in collecting and analysing faeces of the Arctic Tern while looking at, e.g. antibiotic-resistant genes. Students of Hatha have collected faeces from the rain coats of my students and were able to do their microbial studies. Now, Mohamed Hatha is retiring. It is time to show a bit of our field work, and I hope to inspire a new generation of Indian students to study this magnificent bird.

Keywords: Arctic tern, Migration, Microbial community



PEC-IT3

EMERGING ANTIMICROBIAL RESISTANCE AND ONE HEALTH SURVEILLANCE

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Antimicrobial resistance (AMR) is a significant global health threat, and One Health surveillance systems aim to address this by integrating data from humans, animals, food, and the environment. To build efficient One Health surveillance systems for AMR, integrated surveillance on both national and regional level is a key factor. This involves combining data from human health, veterinary health, and environmental sources to obtain a comprehensive overview of AMR status and emerging risks. Standardized methods for sampling, testing, and reporting are essential to ensure data consistency and comparability. This process demands extensive collaboration among sectors and disciplines, including public health, veterinary medicine, environmental science, and policy-making. Implementing One Health surveillance systems faces several challenges, including high costs and resource requirements for comprehensive surveillance across multiple sectors and the difficulty in integrating diverse data sources and ensuring interoperability between different systems. While public health data has been the primary focus, many regions still lack diagnostic capabilities, necessitating training and infrastructure upgrades. Variability in regulations and policies across countries and sectors can also hinder effective collaboration. Despite the challenges, One Health surveillance systems offer significant benefits, such as enhanced understanding of the complex dynamics of AMR across sectors and improved ability to detect and respond to emerging threats. Additionally, improved data can inform policy decisions and public health interventions. In regions where seafood and aquaculture are vital industries, the marine environment plays a crucial role in the spread and persistence of AMR. Antibiotic residues and resistant bacteria can enter marine ecosystems through wastewater and agricultural runoff, and the use of antibiotics in aquaculture contributes to this issue. Humans can be exposed to resistant bacteria through seafood consumption and recreational activities in



contaminated waters. Integrating marine environmental data into One Health surveillance systems can help better understand and mitigate the impact of AMR on human health and the environment, leading to improved interventions.

Keywords: Antimicrobial resistance, One health surveillance, Antibiotic resistant bacteria, Marine ecosystems



FERMENTING FUTURE: ENGINEERING YEAST FOR SUSTAINABLE PRODUCTION OF SHARK-FREE SQUALENE

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Squalene is a natural triterpene predominantly isolated from Sharks with diverse applications in pharmaceuticals and cosmetics. It can also be used as a potent antioxidant and anticancer agent. Every year several thousand sharks are killed for extraction of industrially important squalene. *Pichia pastoris*, a methylotrophic yeast, is considered a sustainable alternative and promising host for the biosynthesis of valuable compounds due to its capability for high protein expression, robust growth characteristics, and ease of genetic manipulation. This study focuses on enhanced squalene production from the *P. pastoris* strain through various processes and metabolic engineering methods. Comparative analysis of squalene synthesis from *P. pastoris*, treated with various inhibitory compounds, was analysed through HPLC. The impact of Terbinafine hydrochloride on squalene titer was analyzed, which resulted in a yield of 20 mg/L. The current study also investigated the susceptibility of *P. pastoris* towards terbinafine and the impact of this inhibitor on the morphology of yeast cells. The effect of terbinafine on the fatty acid composition of *P. pastoris* was also analyzed through GC-MS. To enhance squalene biosynthesis, pathway engineering techniques targeting critical genes such as tHMG (truncated HMG CoA reductase), ERG 9 (Farnesyl pyrophosphate synthetase), and ERG20 (Squalene synthase) were adopted. Analysis of the single gene effect on increased squalene titer was done through overexpressing genes coding rate-limiting enzymes on the pathway, such as tHMG, ERG9, and ERG20. Vector was constructed using a bi-directional HTX promoter (weak promoter) with two key genes (ERG9 and ERG20) cloned at the ends of the promoter through Gibson cloning.

Keywords: Squalene, *Pichia pastoris*, HPLC, Terbinafine hydrochloride, GC-MS, Metabolic engineering, Cloning

Oral Presentations



PEC-O1

AMUNDSEN AND NANSEN BASINS OF THE CENTRAL ARCTIC OCEAN HARBOURS A DISTINCT PARTICLE-ATTACHED AND FREE-LIVING BACTERIAL COMMUNITY STRUCTURE

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The Central Arctic Ocean (CAO) is among the least studied yet most rapidly changing marine environments on Earth, with unique hydrographic and climatic conditions that shape its pelagic microbial community diversity. In the present study, we have investigated the spatial distribution patterns of particle-attached (PA) and free-living (FL) bacterial community structures across the Amundsen and Nansen basins of the Central Arctic Ocean through a 16S rRNA-based amplicon sequencing approach. The preliminary findings suggest that Proteobacteria and Bacteroidota were the dominant bacterial phyla identified in the samples. The PA and FL bacterial community composition across both basins was significantly different. Bacterial taxa belonging to gamma-proteobacteria were found to be highly abundant in the PA fraction, whereas taxa belonging to Alpha-proteobacteria were highly abundant in the FL fraction across both basins. Among the studied physicochemical variables, C-DOM, salinity, and temperature played a critical role in determining the bacterial community structure and distribution patterns in the Amundsen and Nansen basins of the Arctic Ocean. With rapidly changing climate-induced environmental conditions like reduction in sea-ice cover and water mass characteristics in the CAO, the present study underscores the importance of continuous monitoring to understand the ecosystem dynamics better.

Keywords: Central Arctic Ocean, Bacterial community structure, 16S rRNA



PEC-O2

ARCTIC MARINE *STREPTOMYCES* SP. AS A POTENT SOURCE OF ANTICANCER DRUGS

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Marine Actinomycetes are a valuable source of unique bioactive compounds with diverse applications, particularly as antitumor and cytotoxic agents. Efforts to uncover rare marine Actinomycetes have increasingly focused on unique and extreme locations like the Arctic Ocean. Actinomycetes isolated from such environments have attracted significant attention as a substantial number of antitumor agents derived from marine sources originate from actinobacteria. Being recognised as prolific producers of secondary metabolites, these microorganisms, especially those belonging to the genus *Streptomyces*, contribute significantly to the discovery of novel pharmaceutical compounds. The sediment samples for this study were collected from Kongsfjorden, an Arctic Fjord (79°N, 12°E), located at Ny-Ålesund, Svalbard, in June 2023. A total of 50 Actinomycetes were isolated from the study stations and purified, with 20 isolates selected for further screening to evaluate their anticancer properties through the MTT assay using the NCIH-460 lung cancer cell line. Isolate AK34, identified as *Streptomyces* sp., exhibited significant cytotoxic activity against the lung cancer cell line, showing 99.2% cytotoxicity at a 50µg/mL concentration. Bioassay-guided fractionation was subsequently carried out, and the resulting fractions were screened, identifying FF3 (99%) and FF4 (99%) as the most active. Further HPLC purification was performed to isolate and characterise the active compounds. These findings underscore their potential as promising candidates for further exploration in the development of chemotherapeutics, particularly for lung cancer treatment.

Keywords: Arctic, Kongsfjorden, *Streptomyces*, Cytotoxic, NCIH-460



PEC-O3

HEAVY METAL TOLERANCE OF ARCTIC BACTERIA ISOLATED FROM RAUDFJORDEN, MAGDALENFJORDEN, AND ST. JONSFJORDEN SEDIMENTS

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Arctic fjords are increasingly exposed to heavy metal contamination, which can influence microbial communities and their resistance mechanisms. This study investigates the ability of bacteria isolated from sediment samples in Raudfjorden, Magdalenfjorden, and St. Jonsfjorden to tolerate heavy metals and resist antibiotics. Bacterial strains were tested for tolerance to zinc (Zn), mercury (Hg), copper (Cu), and lead (Pb) using three methods: spot plate assay, well diffusion method, and tube dilution method. Among the metals tested, mercury was the most toxic to the bacterial cells. Tolerance levels varied among different bacterial strains, with one isolate, *Psychrobacter fozii*, showing resistance to all tested metal concentrations. Antibiotic resistance tests against 30 different antibiotics revealed that many of the metal-resistant bacteria were also resistant to multiple antibiotics, suggesting a link between metal tolerance and antibiotic resistance. The bacterial strains were identified using 16S rRNA sequencing. These findings highlight the presence of bacteria in Arctic fjords that can survive in environments contaminated with both heavy metals and antibiotics, raising concerns about the spread of resistance in these remote regions. Further research is needed to understand the ecological impact and risks associated with these resistant bacteria.

Keywords: Arctic fjords, Heavy metal contamination, Bacterial tolerance, Antibiotic resistance



VARIABILITY OF METHANE PRODUCTION IN KONGSFORDEN: INSIGHTS FROM AN ARCTIC FJORD

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Approximately 18% of the current global warming can be attributed to the methane-induced greenhouse effect (Forster 2007). This study presents the first report on concentration of dissolved methane using Gas chromatography in the samples collected from Kongsfjorden, an Arctic fjord in the Svalbard Archipelago. Methane concentration in Kongsfjorden varied from 4.89 to 17.89 (aveg: 9.89 ± 4.22) nmol/L with higher concentration in the bottom samples. It indicates the input from the seabed and its subsequent oxidation by methanotrophs in the deeper layers. Samples were found to be saturated with respect to methane, with saturation levels ranging from 125 to 484 (Aveg: 272 ± 118) %. Concentration was found to be low near glaciers, likely due to reduced microbial activity. The temperature increase in June may enhance the microbial activity, favoring the methane production in near-surface sediments. However, methane sources linked to oxygen minimum zones in the water column were not evident, as no OMZ ($<20 \mu\text{M O}_2$) was observed. The highest methane concentration was observed in the mid-section of the fjord, possibly influenced by the runoff from the Bayelva river, which transports nutrients and other minerals in turbid waters. Environmental settings in coastal waters and sediments influence the production and processing in the production and processing of organic carbon that can be modified by global warming, which is more pronounced in polar regions (IPCC, 2014).

Keywords: Methane, Arctic fjord, Organic matter, Kongsfjorden



PEC-O5

BIOACCUMULATION IN MARINE FISHERIES IN INDIA, AND POSSIBLE IMPACTS OF CLIMATE CHANGE

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Marine fisheries are an important source of nutrition to a substantial number of world's population. However, they also bioaccumulate a suite of chemicals, organic and inorganic. Hence, consumers are, concomitantly, exposed to these chemicals as well. India is a major exporter of fisheries, both marine catch, and coastal aquaculture. Here, I will present a review on the available information on contaminants such as mercury and select persistent organic pollutants (POPs) reported in marine fisheries in India. This work will highlight the dearth of data on chemicals in fisheries, even though long-term population studies elsewhere have shown that exposure to contaminants may mitigate the beneficial effects of fish consumption. Further, this work will employ results from a bioaccumulation model to show that climate change effects, such as seawater warming can increase chemical bioaccumulation in marine fish to 20% or more. This necessitates measures to curb marine pollution, as it is invariably linked to human exposure to pollutants via bioaccumulation and fish consumption.

Keywords: Marine pollution, Bioaccumulation, Exposure, Climate change



PEC-O6
MONSOON-MEDIATED PRODUCTIVITY CHANGES IN THE
SOUTHEASTERN ARABIAN SEA DURING THE LATE
DEGLACIAL TO HOLOCENE

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Understanding the response of surface ocean productivity, carbon export and carbon burial to climate change is vital for the projection of biological feedback in a high CO₂ world. Here we have utilized a 4.82 m long sediment core (SK313 GC01) collected from the southeastern Arabian Sea (SEAS) to determine the sedimentary carbon components organic carbon (OC) and calcium carbonate (CaCO₃) contents their mass accumulation rate (MAR), burial rates and estimate empirically paleoproductivity to better understand the climate-productivity link during the late deglacial to Holocene interval since 14.4 kilo years Before the Present (kyr BP). We note that productivity was the highest during the Bølling–Allerød (B/A) warm event, a step-wise decreased productivity during the Younger Dryas (YD) cold period, the lowest productivity during the early Holocene, and increased and stabilized productivity during the mid-late Holocene time interval. These productivity variations seem to be driven by the varying strengths of Indian summer monsoon-induced upwelling in the study area and therefore monsoon induced forces played a key role in millennial-scale productivity changes in the SEAS. Our estimate of the paleoproductivity condition of the present study gives clarity to understand the regional picture of productivity changes along with the other published records from the Arabian Sea. Data compilation reveals a striking regional similarity of productivity on millennial timescale, suggesting a strong role of Indian summer monsoon and associated forcing factor in driving basin-wide productivity changes in the Arabian Sea.

Keywords: Marine sediments, Organic carbon, Calcium carbonate



PEC-O7

DISTRIBUTION OF MICROPLASTICS IN THE COCHIN ESTUARY, BARMOUTH, AND COASTAL WATERS DURING MONSOON AND POST-MONSOON PERIODS

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Rivers and estuaries are considered major causeways for the entry of various components of terrestrial origin into the Ocean. Plastics and microplastics have emerged as the leading components of terrestrial origin entering the ocean via these channels. In the present study, quantitative and qualitative assessments of microplastics were conducted in water and sediment from the Cochin estuary, Barmouth, and coastal waters during the monsoon and post-monsoon seasons. The sediment exhibited a higher abundance of microplastics when compared to water during both the monsoon and the post-monsoon seasons. In the sediment, an increasing pattern of microplastic abundance was observed from the estuary to Barmouth and further to coastal waters during both seasons. The average microplastic abundance observed during the monsoon was as follows: Estuary (323 ± 115 particles/kg) < Bar mouth (600 particles/kg) < Coastal (770 ± 444 particles/kg) and during the post-monsoon: Estuary (376 ± 98 particles/kg) < Bar mouth (590 particles/kg) < Coastal (443 ± 86 particles/kg). Water samples showed a similar pattern of microplastic abundance during the monsoon period as follows: Estuary (1.53 ± 0.55 particles/L) < Bar mouth (2.13 particles/L) < Coastal (2.99 ± 0.48 particles/L). During the post-monsoon period, the bar-mouth station exhibited higher abundance as: Estuary (1.77 ± 0.71 particles/L) < Coastal (1.83 ± 0.25 particles/L) < Bar mouth (2.23 particles/L). Fiber was the dominant morphotype in all the stations. The study results show that land-based pollutants like microplastics directly reach the estuary and are ultimately transported and accumulated in the coastal waters via Barmouth.

Keywords: Plastic pollution, Estuary, Seasonal variation, Monsoonal effects

Poster Presentations



PEC-P1

DIVERSITY AND BIOPROSPECTING OF CRYOSPHERE MICROBES FROM NY – ALESUND ARCTIC

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The cryosphere harbors an extraordinary diversity of microbes with immense biotechnological potential. In this study, sediment samples were collected from Ny-Ålesund, Arctic, specifically from Kongsfjorden and Krossfjorden. Out of ten collected samples, two (KR-3 and KG-4) were selected to study the diversity and bioprospecting of bacteria uncultured bacterial diversity was studied by amplicon sequencing targeting the V3-V4 regions of 16s rRNA genes. This study revealed the presence of Proteobacteria and Actinobacteria as dominant phyla. Culturable bacteria from the sediment samples were isolated by dilution and plating method using 11 different culture media (SCA, AIA, NA, ISP-3, ISP-4, ISP-5, LB-CAS, GYM, M1, M5, KA), incubated at 4°C and 28°C. Maximum colonies were observed on AIA, M1, and M5 media. From both samples, 465 mesophilic and 310 psychrophilic colonies were recovered, from which 65 mesophilic and 52 psychrophilic bacterial cultures were selected for further bioprospecting. Siderophore production was positive in 188 cultures, highlighting their bioprospecting potential for plant growth promotion and biocontrol applications. Pigment characterization of selected yellow and orange pigments demonstrated enhanced pigmentation at 4°C. These findings underscore the rich bacterial diversity of Arctic environments and their potential in biotechnology.

Keywords: Arctic, Metagenomics, Bacterial diversity, Bioprospecting, Psychrophiles



PEC-P2

ENVIRONMENTAL DRIVERS AND DEPTH-WISE VARIABILITY
IN MESOZOOPLANKTON COMMUNITY STRUCTURE IN THE
GLACIALLY INFLUENCED KROSSFJORDEN, SVALBARD
ARCHIPELAGO

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Arctic marine ecosystems, particularly the semi-enclosed fjordic basins of Svalbard, are highly sensitive to climate-driven changes that can rapidly reshape plankton communities and disrupt ecosystem trophodynamics. This research examines the community structure of mesozooplankton in Krossfjorden, a glacially affected fjord on the western coast of Spitsbergen in the Svalbard Archipelago, during the spring of 2023. Sampling was carried out at specific depths (up to 200 m) in the inner, middle, and outer regions of the fjord. Concurrently, important physicochemical parameters, temperature, salinity, PAR, nutrients, and dissolved oxygen were recorded. The results showed large spatial heterogeneity in mesozooplankton biomass and abundance, with the innermost fjord having the highest values (444 mg m^{-3} and 964 ind. m^{-3} , respectively). The mesozooplankton communities were dominated by a limited number of taxa, including copepods, ostracods, polychaetes, decapod larvae, chaetognaths, and ctenophores. Elevated silicate and ammonia concentrations in the fjord likely reflected high primary productivity due to the preceding *Phaeocystis* sp. bloom. Altogether, the spring season is a pivotal period in Arctic fjords, marked by the onset of phytoplankton blooms, nutrient cycling, and significant impacts on marine species' life cycles, providing critical insights into ecosystem responses to climate change.

Keywords: TLC, HPTLC, FT-IR, Anti-inflammatory potential, Secondary metabolites



PEC-P3

BIOSURFACTANT PRODUCING PSYCHROTROPHIC BACTERIA FROM KONGSFJORD, ARCTIC: SCREENING, OPTIMIZATION AND CHARACTERIZATION

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Biosurfactants are microbial-derived, surface-active biomolecules produced by numerous microorganisms. The biosurfactants have unique properties like specificity, low toxicity, and biodegradability. These remarkable properties aid them to play a significant role in a wide range of applications in food, pharmaceuticals, cosmetics, agriculture, and environmental remediation. The present study focuses on screening, optimization and characterization of a novel biosurfactant-producing bacterial strain from Kongsfjord, Arctic sediments. A total of forty bacterial strains (AT1-AT40) were isolated, and each strain was further screened for biosurfactant production by drop collapse test, oil spread test, parafilm test, and emulsification activity. Among them, two isolates showed positive results with good surface and emulsification activity; AT16 (75%), and AT29 (70%), and these strains were selected as the most promising biosurfactant producers. The selected isolates were further characterized by their colony morphologies, Gram staining, motility and biochemical tests, and the enzyme production was also performed. The One-Factor-At-a-Time (OFAT) method was also employed to determine optimal growth conditions by varying one parameter (such as temperature, pH, carbon source, nitrogen source, and media) while keeping others constant for maximum biosurfactant yield. Results revealed that AT16 shows both proteolytic and lipolytic activity, while AT29 had only shown promising lipolytic activity. The optimization revealed that the optimized condition for higher biosurfactant production was at temperature (20°C), pH (6), and carbon and nitrogen sources was glucose and yeast extract, respectively. This study highlights the potential of psychrotrophic bacteria in biosurfactant and enzyme production and their use in various cost-effective industrial and bioremediation applications.

Keywords: Biosurfactants, Psychrotrophic bacteria, Enzyme, Bioremediation



PEC-P4

BIOGEOCHEMICAL COMPOSITION OF SEDIMENTS IN ARCTIC FJORD (KONGSGJORDEN)

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The Arctic is warming four times the global average, driving significant changes in ecosystems and carbon cycling processes. The total sediment transport to the Arctic Ocean is estimated to be $324 - 884 \times 10^6 \text{ t yr}^{-1}$. Of this total, a maximum of about 56% can be considered monitored, while the rest is based on different estimates. The monitoring network in the high Arctic is limited, and the fate of carbon reaching the sea and bedload remains poorly understood. Due to increasing glacial melting, runoff, and precipitation, organic matter will accumulate in fjord sediments. We examined the biochemical composition of fjord sediments from Kongsfjorden (Svalbard) through the application of Elemental Analyzer-Isotopic Ratio Mass Spectroscopy, High-Performance Anion Exchange Chromatography-Pulse Amperometric Detection, and the Phenol-Sulfuric Acid (PSA) method. These fjord sediments collected in May 2024 showed total carbohydrate content from 0.089 to 1.692 $\mu\text{g/g}$. Monosaccharides such as fucose, galactose, arabinose, glucose, glucosamine, rhamnose, xylose, mannose, galacturonic acid, glucuronic acid, and mannuronic acid were recorded with their diagnostic ratios. Glucose was the dominating sugar at all stations, followed by galactose. Higher abundance of galactose in offshore stations indicated a higher marine contribution to the organic matter than in coastal stations. Higher content of galactose and rhamnose compared to fucose and ribose indicated bacterial contribution and potentially degraded contribution from phytoplanktonic organic matter in the sediments. This study of fjord sediment organic matter aids in understanding its fate amid changing Arctic conditions.

Keywords: Arctic warming, Carbon cycling, Fjord sediments, Kongsfjorden



PEC-P5

THE SOUTHERN OCEAN CARBON CYCLE; MICROBIAL INTERACTION AND CLIMATE CHANGE IMPLICATIONS

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The Earth's biosphere is largely composed of cold ecosystems, where microorganisms dominate. The Southern Ocean plays a crucial role in the global carbon cycle, influencing oceanic heat and carbon sequestration, and thereby impacting atmospheric CO₂ levels. Microbial communities in this region regulate global biogeochemical cycles, including carbon sequestration, with the Antarctic Circumpolar Current (ACC) facilitating gas exchange with the atmosphere. This process enables the ventilation of CO₂ from the deep ocean to the atmosphere, rendering the Southern Ocean (SO) a key region for carbon cycling. Microbial communities drive primary productivity and carbon sequestration by supporting phytoplankton photosynthesis and respond to changes in hydrographic conditions. Understanding their role is key to comprehending the Southern Ocean's carbon cycle. Nevertheless, substantial knowledge gaps remain regarding the intricacies and functionality of microbial assemblages in the SO. The remote and extreme environment of the Southern Ocean poses substantial challenges to observational and modelling efforts, and consequently, perpetuates significant uncertainties in our understanding of the oceanic carbon cycle in this region. Future investigations into the vertical distribution of bacterial communities in the Southern Ocean could explore their roles in the carbon cycle and elucidate the contributions of these communities to carbon degradation, methanogenesis, and methanotrophy. This review could enhance our understanding of carbon cycling and microbial interactions in rapidly changing, high-latitude regions, informing the development of more accurate regional and global carbon cycle models.

Keywords: Southern Ocean, Carbon cycle, Methanotrophy



PEC-P6

CHEMICAL CHARACTERIZATION OF PARTICULATE ORGANIC MATTER FROM KONGSFJORDEN, ARCTIC REGION

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Marine POM, which is mostly phytoplankton derived, constitutes a driving force for the biological pump, one of the mechanisms controlling the uptake of atmospheric CO₂ by the marine environment. Burial of the marine fraction of POM in sediments eliminates CO₂ assimilated by phytoplankton during photosynthesis from the present CO₂ pool. However, shelf regions also receive significant loads of terrestrial POM, which may partially undergo mineralization in seawater, releasing CO₂ to the water column. Kongsfjorden, a high-Arctic fjord in Svalbard, serves as a critical site for studying the dynamics of particulate organic matter (POM) under rapidly changing environmental conditions. Influenced by glacier meltwater, Atlantic water inflow, and seasonal variability, POM in Kongsfjorden reflects a complex interplay of terrestrial and marine sources. This study employs advanced analytical techniques to biochemically characterize the POM collected in spring in May 2024 across the fjord's environmental gradient. Total carbohydrate content is quantified using a Phenol-Sulfuric Acid colorimetric assay. Stable isotopic compositions ($\delta^{13}\text{C}$ and $\delta^{15}\text{N}$) and total organic carbon (TOC) and nitrogen (TN) concentrations are measured using Elemental Analyzer-Isotope Ratio Mass Spectrometry (EA-IRMS). Monosaccharide composition was measured using High-Performance Anion Exchange Chromatography-Pulse Amperometric Detection (HPAEC-PAD). The results indicate that $\delta^{13}\text{C}$ of the POM samples varied from -24.8 to -27.03 ‰ with similar values at different locations (inner to outer) of the fjord at each depth. $\delta^{15}\text{N}$ varied from 1.4 to 5.7 ‰. TOC ranged from 3.4 to 13.4 % and TN from 0.4 to 5 %. However, the C: N ratio showed an increasing trend (1.1 to 5.9) from outer to inner fjord, indicating a marine to terrestrial transition. Preliminary results indicate significant variability in carbohydrate content and composition along the fjord, with



higher contributions of marine-derived sugars in offshore waters and increased terrestrial influence near glacial outflows. With these results, we aim to understand the nature, sources, and transformation of POM along depth during spring in Kongsfjorden.

Keywords: Stable isotopic composition, Carbohydrates, Total organic carbon, Total nitrogen, Stratification



PEC-P7

ISOLATION AND CHARACTERIZATION OF EXOPOLYSACCHARIDES FROM ARCTIC SEDIMENT-DERIVED EXTREMOPHILES

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Exopolysaccharides (EPS) are high-molecular-weight polysaccharides secreted by microorganisms into their extracellular environment. Because of their rheological properties, bacterial exopolysaccharides have great industrial potential as emulsifiers, bioflocs, and thickening agents. However, EPS produced by marine bacteria, particularly those from extreme environments, remains underexplored. Marine bacteria from habitats such as deep hydrothermal vents, polar oceans, deep sediments, and methane reservoirs possess unique enzymatic mechanisms that enable survival under harsh conditions, making their EPS promising candidates for applications in the cosmetics, food, beverage, and dairy industries. This study involves the isolation, screening, and molecular characterisation of bacterial isolates with the potential to produce EPS from Arctic fjord sediments. The bacteria for the study were revived from the Marine Microbial Culture Collection (MMCC) housed in the Department of Marine Biology, Microbiology and Biochemistry, CUSAT. Colonies with distinct morphologies were selected and subjected to primary screening tests. A total of 20 bacterial strains were screened for EPS production using the Congo Red Agar test and the Aniline Blue test. The EPS producing positive isolates were mass cultured using the nutrient broth medium supplemented with high glucose content. EPS extraction was carried out through solvent precipitation using ethanol and isopropanol, followed by protein removal via trichloroacetic acid (TCA) treatment. The crude EPS was further purified through dialysis and lyophilization. The nutraceutical potential of the purified EPS was evaluated through different assays. The outcomes from this study would highlight the potential of Arctic bacteria in novel EPS production, which has significant potential in the nutraceutical industry.

Keywords: Exopolysaccharides, Arctic, Marine bacteria, Emulsifiers



UNVEILING THE CRYOPROTECTIVE POTENTIAL OF ANTARCTIC MARINE SEDIMENT BACTERIA

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Antarctica, the coldest and most extreme environment on our planet, presents polyextreme conditions that challenge microbial life. Bacteria inhabiting the marine sediments of Antarctica endure multiple stressors, including high salinity, subzero temperatures, and limited nutrient availability. Despite these harsh conditions, these bacteria produce specialized exopolysaccharides (EPS) that help prevent freezing and enhance survival. As a part of this study, we isolated bacterial strains from marine sediment samples collected from Quilty Bay in the Larsemann Hills, Antarctica. The strains were screened for EPS production using Congo Red Agar. EPS was extracted from mass cultures through cold ethanol precipitation and purification using various chromatographic techniques. The structural characterization of the purified EPS was performed using Fourier Transform Infrared Spectroscopy (FT-IR), Nuclear Magnetic Resonance (NMR), and Gas Chromatography-Mass Spectrometry (GC-MS) to determine monosaccharide composition and linkage patterns. Furthermore, we assessed the cryoprotective activity of EPS through freeze-thaw cycle experiments using *E. coli* DH5 α cells. We expect the EPS to exhibit significant cryoprotective properties, improving cell viability during freeze-thaw cycles. The structural analysis can reveal unique monosaccharide compositions and glycosidic linkages contributing to the cryoprotective function. This work could suggest the potential application of Antarctic bacterial EPS in biotechnological fields, particularly in cryopreservation techniques.

Keywords: Antarctica, Marine bacteria, Exopolysaccharide, Cryoprotectant



PEC-P9

INTER SENSOR VALIDATION AND PERFORMANCE
EVALUATION OF COLOURED DISSOLVED ORGANIC MATTER
(CDOM) IN SOUTHERN INDIAN COASTAL WATERS

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Water quality is critical for marine ecosystems, with Coloured Dissolved Organic Matter (CDOM) influencing light penetration, primary production, and thermal dynamics. As an optically measurable fraction of Dissolved Organic Matter (DOM), CDOM plays a crucial role in global carbon cycling. Its high variability due to biogeochemical processes and seasonal changes necessitates accurate detection for ecosystem monitoring. Field-based CDOM assessment is resource-intensive and time-consuming, posing challenges for large-scale monitoring. Remote sensing enables efficient CDOM monitoring by providing timely data with broad spatial and temporal coverage. Despite the increasing availability of satellite-derived CDOM data, their accuracy varies across sensors, requiring inter-sensor validation. This study aims to validate and compare the performance of CDOM retrieval from satellites (MODIS- Aqua, OCM-3, and Sentinel-3B) using remote sensing reflectance, employing a previously evaluated algorithm for improved accuracy. Satellite-retrieved CDOM varied across MODIS-Aqua ($0.03\text{--}0.13\text{ m}^{-1}$), Sentinel-3B ($0.03\text{--}0.17\text{ m}^{-1}$), and OCM-3 ($0.034\text{--}0.32\text{ m}^{-1}$). Sentinel-3B showed the highest correlation with in situ CDOM (440), ($R^2=0.5399$; $N=29$), followed by MODIS- Aqua ($R^2=0.5242$; $N=22$) and OCM-3 ($R^2=0.5035$; $N=21$). Inter-sensor validation at common stations ($N=13$) showed MODIS-Aqua had the best agreement with in situ a CDOM (440), with the lowest RMSE (0.1355), the highest Pearson correlation (0.639), and $R^2=0.4092$. Additionally, satellite-retrieved CDOM was validated with Hyperspectral radiometer retrieved CDOM, where MODIS-Aqua again exhibited the stronger correlation ($R^2=0.5218$; $N=10$) than Sentinel-3B ($R^2=0.4943$; $N=10$)



and OCM-3 ($R^2=0.3031$; $N=10$), confirming its higher reliability for CDOM estimation. These findings suggest that MODIS-Aqua provides the highest accuracy and performance in retrieving CDOM in the Southern Indian coastal waters, outperforming Sentinel-3B and OCM-3.

Keywords: CDOM, Satellite, Hyperspectral radiometer, Performance evaluation



PEC-P10

**PHYTOCHEMICAL DIVERSITY AND BIOACTIVE POTENTIAL:
AN ECOLOGICAL PERSPECTIVE ON PLANT-DERIVED
EXTRACTS**

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A qualitative phytochemical screening confirmed the presence of diverse secondary metabolites, including phenols, tannins, saponins, alkaloids, terpenoids, flavonoids, glycosides, steroids, and carbohydrates, across different solvent extracts. Quantitative analysis revealed that ethyl acetate and methanolic extracts exhibited significantly higher concentrations of these bioactive compounds. Notably, the ethyl acetate extract was enriched with alkaloids, terpenoids, and flavonoids, while the methanolic extract predominantly contained phenols and tannins. Advanced characterisation techniques such as thin-layer chromatography (TLC) and high-performance thin-layer chromatography (HPTLC) unveiled a broad spectrum of phytoconstituents, with ethyl acetate and methanolic extracts displaying the highest diversity of compounds. HPTLC analysis at 254 nm and 366 nm confirmed the presence of multiple bioactive molecules, while ferric chloride derivatisation reinforced the abundance of flavonoids in both extracts. Further functional group analysis through FTIR identified key phytochemical signatures in the ethyl acetate extract, including alkenes, aromatics, esters, amines, alkyl halides, alkyl aryl ethers, ketones, phenols, and alcohols. Beyond its chemical richness, the ethyl acetate extract demonstrated notable anti-inflammatory potential, as evidenced by protein denaturation and protease inhibition assays. These findings underscore the ecological significance of these plant-derived extracts, shedding light on their role as natural reservoirs of medicinally relevant compounds. Comprehensive phytochemical profiling through HPTLC and FTIR enhances our understanding of nature's biochemical wealth, reinforcing the importance of biodiversity in sustaining pharmaceutical and therapeutic advancements.

Keywords: TLC, HPTLC, FTIR, Anti-inflammatory potential, Secondary metabolites



EXPLORING SECONDARY METABOLITES AS ANTIOXIDANT AND ANTI-INFLAMMATORY AGENTS: *IN VITRO* INVESTIGATION AND ECOLOGICAL SIGNIFICANCE

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Many secondary metabolites derived from plants play a crucial role in ecological balance and have been recognised as promising candidates for exhibiting antioxidant, anti-inflammatory, antimicrobial, anticancerous, antidiabetic, and immunomodulatory properties. This study explores the pharmacological importance of plant products and their vital role in ecosystem functioning and disease treatment. *Dodonaea viscosa* (L.) Jacq. (Sapindaceae) commonly known as 'Virali', have been reported for use as traditional medicine in folklore practices. To substantiate this claim, the present study evaluated the screening and quantification of bioactives using standard protocols. Also, the antioxidant activity of ethanolic leaf extract was evaluated by DPPH assay, and anti-inflammatory activity by COX and Lox assays. RAW 264.7 was used as the cell line for the anti-inflammatory study. The phytochemical profiling in various leaf extracts of this plant reveals the presence of major secondary metabolites. The quantitative estimation of the major compound in ethanolic extract shows a higher number of phenolic compounds (80.53 mg GAE/g), followed by tannin content (58.60 mg/g). The results for antioxidant and anti-inflammatory effects were compared using ascorbic acid and diclofenac as reference compounds, respectively. The ethanolic extract of *D. viscosa* leaves was found to be very effective in scavenging DPPH radical ($IC_{50} = 10.06 \mu\text{g/ml}$). In both COX ($IC_{50} = 197.33 \mu\text{g/ml}$) and LOX assay ($IC_{50} = 120.49 \mu\text{g/ml}$), the maximum percentage inhibition was observed at a higher concentration (500 $\mu\text{g/ml}$) of $80.63 \pm 0.25 \mu\text{g/ml}$ and $74.28 \pm 0.24 \mu\text{g/ml}$, respectively. The results obtained in the present study highlight the ecological importance of these compounds and their potential application in medicine.

Keywords: Secondary metabolites, Antioxidant, Anti-inflammatory, COX



EVALUATION OF OCM-3 CHLOROPHYLL-A CONCENTRATIONS: A COMPARATIVE STUDY WITH MODIS AND SENTINEL-3A USING IN-SITU DATA

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Chlorophyll-a (Chl-a) is a key indicator of phytoplankton biomass and ocean health, reflecting primary productivity and ecosystem status. Monitoring coastal systems requires understanding biophysical variations, where daily satellite observations provide an efficient solution. High-resolution multispectral data help detect chemical, biological, and physical changes, making remote sensing vital for marine ecosystem monitoring. Since the launch of CZCS in 1978, satellite sensors like SeaWiFS, MODIS, MERIS, and Sentinel-3 have improved global ocean colour monitoring. These sensors provide valuable insights into marine dynamics across broad spatial and temporal scales. Satellite remote sensing, a reliable method for estimating surface Chl-a, utilises sunlight absorption and scattering in blue and green spectral bands. This study evaluates OCM-3's performance by comparing its Chl-a estimates with MODIS-Aqua and Sentinel-3A, validated against in situ measurements from the southern Indian coastal waters. All the sensors exhibit a slight underestimation of Chl-a. Among the three sensors, OCM-3 demonstrated the strongest correlation with in-situ data, achieving an R² value of 0.5363, followed by MODIS-Aqua (R² = 0.4451) and Sentinel-3A OLCI (R² = 0.4135). For Chl-a concentrations below 1 mg/m³, OCM-3 demonstrated a stronger correlation with in-situ measurements compared to MODIS-Aqua and Sentinel-3A. However, at high Chl-a concentrations >1 mg/m³, the Sentinel-3A demonstrated the best performance, with the highest correlation and a more responsive slope. MODIS-Aqua showed moderate accuracy, while OCM-3 exhibited the lowest accuracy, significantly underestimating Chl-a concentrations when values exceeded 1 mg/m³. The



differences in sensor performance highlight the need for region-specific algorithm improvements to enhance the accuracy of chlorophyll-a retrievals, particularly for OCM-3. Existing global algorithms may not fully account for the complex optical properties of the southern Indian coastal waters, where factors such as coloured dissolved organic matter (CDOM) and non-algal particles (NAP) can influence chlorophyll-a estimations.

Keywords: Chlorophyll-a (*Chl-a*), Ocean health, MODIS-Aqua, Sentinel-3A



PEC-P13

SEASONAL VARIATION AND ABUNDANCE OF PHYTOPLANKTON IN THE COASTAL WATERS OF KANNUR COAST

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Phytoplankton diversity and abundance in the coastal waters of Kannur were studied over one year, from April 2024 to March 2025. A total of 75 species of phytoplankton, belonging to 40 families and six classes, were identified. The dominant taxonomic group was Bacillariophyceae (76%), followed by Dinophyceae (21%) and Chlorophyceae (14%). Seasonal variations in phytoplankton diversity were observed throughout the study. During the pre-monsoon season, the dominant species included *Ceratium breve*, *Pyrophaeus steini*, *Ditylum brightwellii*, and *Chaetoceros curvisetum*. In the monsoon season, *Odontella mobiliensis*, *Cladopyxis hemibrachiata*, and *Protoperidinium oceanicum* were predominant. The post-monsoon season was characterized by the presence of *Ditylum brightwellii*, *Odontella brightwellii*, *Pyrophaeus steini*, and *Odontella sinensis*. The average phytoplankton cell density recorded in the study area was 19,390 cells/L, with the highest density observed during the pre-monsoon season (21,280 cells/L) and the lowest during the monsoon season (17,440 cells/L). Shannon diversity index (H' loge) was highest in the post-monsoon season (3.25) and lowest in the monsoon season (2.8). BIOENV analysis indicated that phytoplankton diversity in the coastal waters was influenced by physicochemical parameters, particularly temperature, salinity, and dissolved oxygen. Correlation analysis further revealed that pH ($r = 0.76$) and temperature ($r = 0.53$) had a significant effect on the abundance of Cyanophyceae.

Keywords: Phytoplankton, Abundance, Diversity, Coastal waters



PRIMARY SCREENING AND CHARACTERIZATION OF COLD-ADAPTED ENZYME PRODUCTION AND ANTIBIOTIC RESISTANCE PROFILES OF BACTERIA ISOLATED FROM ARCTIC SEDIMENTS

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The Arctic region provides a habitat for a distinct variety of microorganisms that have evolved unique metabolic adaptations to thrive in such cold conditions, including the production of cold-adapted enzymes. The biotechnological potential of Arctic microbes, particularly for enzyme production and medical use, remains underexplored. This study focuses on isolating and characterizing psychrotrophic bacteria from Arctic sediments, assessing their enzyme activity and antibiotic resistance. A total of forty bacterial strains (AT1-AT40) were isolated, and each bacterial strains were further characterized using biochemical tests, Gram staining, and hanging drop motility methods. The enzyme production potential of these isolates was assessed by screening for the production of six hydrolytic enzymes. The result revealed that lipolytic and proteolytic activity was shown by 73% and 45% of strains, respectively. Only a limited number of strains exhibited amylolytic (13%) and cellulolytic activity (23%). Additionally, the antibiotic resistance test results demonstrated that most of the strains were resistant to antibiotics such as Erythromycin, Streptomycin, Amoxicillin, Nalidixic acid, Vanomycin, and Ciprofloxacin. None of the strains has shown resistance towards Tetracycline. These findings highlight our knowledge of the potential biotechnological value of cold-adapted enzymes in various industrial applications and also provide an insight into the significance of Arctic bacteria in their prospective uses in biotechnology and medicine applications.

Keywords: Arctic, Psychrotrophic bacteria, Enzyme, Antibiotic resistance



Marine Microbiology and Antimicrobial Resistance

Invited Talks



MAR-IT 1

MICROBIAL DIVERSITY AS A TOOL FOR ENVIRONMENTAL CHANGES DETECTION

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Climate change is unarguably a critical existential threat to humanity in our present and maybe in our future. The microbial community is sensitive to changes in its living environment, reflecting the structure and function of the aquatic ecosystems. Changes in environmental factors impact the abundance of microorganisms, potentially affecting microbial metabolism. Microbial diversity can be commonly used as a bioindicator of ecosystems functioning. However, there is a lack of sensitivity of microbial diversity indicators in the case of moderate and chronic environmental degradation, such as atmospheric deposition of pollutants, agricultural practices, diffuse pollution by wastewater and long - term climate change. The advent of novel molecular tools, a more depth understanding of these changes has been demonstrated. Here we will present our data on the potential of microbial diversity as a powerful tool in study of environmental changes along the Adriatic Sea coast.

Keywords: Climate change, Microbial diversity, Novel molecular tools, Adriatic Sea coast



MAR-IT 2

ANTIMICROBIAL PEPTIDES OF MARINE AND TERRESTRIAL ANIMALS AS PROMISING TEMPLATES FOR CREATING OF NEW ANTIBIOTICS

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Antimicrobial peptides (AMPs) are important effector molecules of the innate immune system of both and marine animals. AMPs have a variety of primary structures and adopt different conformations. They possess a potent antimicrobial activity and a wide range of effects on host cells including immunomodulatory, antitumor, corticostatic activity, etc. These features determine the prospect of AMPs application in medicine, mainly as novel anti-infective drugs, considering their fast and multitargeting antimicrobial action, and an array of other host defense functions. However, there are some limitations for introducing of AMPs into medicine: relatively low stability, some toxicity for host cells, susceptibility to host or microbial proteases. There are several ways for overcoming these limitations. The main purpose of our study was exploring of varied approaches for developing new antimicrobials on a base of selected natural AMPs: modifying the peptides' structure, combining AMPs with conventional antibiotics or antiseptics; using as immune modulators. In a course of our previous search for new AMPs we have isolated a set of peptides from immune cells of varied aquatic and terrestrial animals and studied their activities: arenicins of the lug worm *Arenicila marine*, aurelins of the jelly fish *Aurelia aurita*, acipensins of the sturgeons *Acipenser gueldenstaedtii* and *Acipenser stellatus*, beta-defensins of the pond turtle *Emys orbicularis*, protegrins of the domestic pig *Sus scrofa*, bactenecin 3.4 of the goat *Capra hircus*, micaecilin and ricaecilin of the limbless amphibia *Microcaecilia unicolor* and *Rhinatremma bivittatum* (the last two structures were deduced by use of bioinformatics methods), etc. The listed peptides were applied in our study. The structural variants of AMPs were developed,



chemically synthesized and their biological activity was explored. It was shown that the synthetic analogues of natural AMPs exerted the potent antimicrobial activity against multidrug resistant strains of *Klebsiella pneumonia*, *Acinetobacter baumannii*, *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Stenotrophomonas maltophilia*, etc. We have developed a set of structural modifications of marine peptide beta-hairpin arenicin 1 and of the terrestrials' AMP - proline-rich bactenecin 3.4. The best index of selectivity of the peptides towards bacteria versus host cells was obtained for bactenecin 3.4 variant. For increasing the effectiveness of AMPs we examined their combined use with conventional antibiotics, antiseptics or nanomaterials to reveal the cases of synergistic effects of the antimicrobial action. The combined preparations consisted of i) AMPs with the best selectivity indexes, ii) AMPs with the wound healing activity and iii) low amounts of other antimicrobials, were elaborated, and their effectiveness were proved in *in vivo* experiments (infected skin wound in mice). The data obtained confirm the idea on the great prospects of a practical use of AMPs of animal origin and provide the successful examples of improving the effectiveness of natural peptides for optimizing their features for medical application.

Keywords: Antimicrobial peptides, Drug-resistance, Antimicrobial activity, Wound-healing activity



MAR-IT3

ANALYSIS OF ANTIMICROBIAL RESISTANCE GENES (ARGs) BY
ELEMENT BIOSCIENCES' AVITI AND ILLUMINA'S NOVASEQ
6000

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Antimicrobial resistance is an emerging global challenge. High throughput sequencing (HTS) technologies often characterize the abundance and diversity of antimicrobial resistance genes. Illumina's NovaSeq 6000 has led the way in this regard. However, AVITI - a recently available platform based on Avidite chemistry and isothermal rolling circle amplification technology from Element Biosciences presents an alternative approach. It has some key advantages including higher base call accuracy (~99.99% for AVITI vs. ~99.9% for NovaSeq 6000), less duplicate reads, and lower cost per million reads. These factors are important in accurately characterizing the ARGs. Higher base call accuracy may allow more reliable calls for the presence or absence of key single nucleotide polymorphism (SNPs) which must be established to determine the presence of certain ARGs such as fluoroquinolones. Less number of duplicate reads means more efficient use of the sequencing cell space. A reduced cost of sequencing per million reads may allow detection of rare ARGs at lower cost. It may also allow collection of sufficient information to build metagenome assembled genomes (MAGs) or determine the presence or absence of antibiotic-resistant bacteria (ARB). We sequenced the extracted genomic DNA from five environmental samples of varying microbial community complexity using AVITI and NovaSeq 6000 HTS technologies, analyzed the resulting 2x150 bp reads by AMR++ 3.0 bioinformatic pipeline, and evaluated the presence and abundance of class, genes, and mechanisms of antimicrobial resistance (AMR). Various technology performance scores including mean quality score, duplicate percentage, and cost per million reads



were compared for evaluating the two methods. The metagenomic library (Quantabio sparQ DNA Library) was prepared only once and used to obtain the sequence reads from both the platforms. Rarefaction curves obtained at the level of AMR classes, genes, and mechanisms were evaluated to determine the sufficiency of the depth of sequencing. AMR++ 3.0 pipeline was employed to determine the presence of SNPs to establish the presence of selected ARGs. The phylogenetic diversity and presence of other bacterial functions were determined using additional tools from K-base. Overall, both the platforms allowed a deeper and comprehensive characterization of ARGs. With sufficient depth of sequencing, both platforms effectively characterized most of the ARGs. However, normalized to per million reads, AVITI was superior in establishing the presence of rare species, rare ARGs, and selected functional gene groups. On a per million reads basis, AVITI was also less expensive. This study highlights the importance of sequencing approach and depth in establishing the presence of rare ARGs.

Keywords: Antimicrobial resistance, High throughput sequencing, Single nucleotide polymorphism

Oral Presentations



MAR-O1

SCREENING OF MANGROVE-ASSOCIATED ACTINOMYCETES FOR POTENTIAL ANTIMYCOBACTERIAL COMPOUNDS

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Multidrug-resistant tuberculosis (MDR-TB) is a form of TB caused by bacteria resistant to the most effective first-line TB drugs, rifampicin and isoniazid. MDR-TB is treatable and curable by second-line drugs, but the options are limited and require extensive chemotherapy. A general approach to counter antibiotic resistance is to introduce new molecules into the treatment pipeline to replace ineffective ones. The marine ecosystem, harbouring various organisms, is becoming a hot spot for identifying novel drug leads. Marine Actinomycetes are prolific producers of secondary metabolites that show a wide range of biological activities, including antimicrobial and anticancer. As part of our marine drug discovery program, we screened around 45 Actinomycetes isolated from sediments collected from mangroves against *Mycobacterium smegmatis*. Among them, one isolated MSM40 has shown potential antimicrobial activity against *Mycobacterium smegmatis*. The 16S rRNA gene sequence (1300 bp) analysis of the isolate MSM40 identified it as a member of the genus *Streptomyces*, showing the highest sequence similarity to the type strain *Streptomyces werraensis* NBRC 13404. The antimicrobial activity of MSM40 against *Mycobacterium smegmatis* highlights its potential as a valuable source for isolating an antimycobacterial compound, which could serve as a promising candidate for developing a drug to combat *Mycobacterium* infections.

Keywords: Mangrove Actinomycetes, Marine bioprospecting, *Mycobacterium smegmatis*



MAR-O2

ENHANCING *NANNOCHLOROPSIS* SP. GROWTH THROUGH SYMBIOSIS: THE ROLE OF *STUTZERIMONAS STUTZERI* IN NITROGEN-STRESS CONDITIONS

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Nannochloropsis is a genus of microalgae, significant for its high content of valuable compounds like omega-3 fatty acids, specifically eicosapentaenoic acid, making it a promising resource for various industries. Enhancing microalgal growth and stability using beneficial bacteria, particularly for *Nannochloropsis* sp. presents a promising approach for optimizing microalgal applications. This study explores the growth-promoting properties of the phycosphere bacterium *Stutzerimonas stutzeri* and investigates its impact on the growth of *Nannochloropsis* sp. in a co-culture setup. Additionally, the study examines the influence of *S. stutzeri* under nitrogen-stress conditions to assess its potential as a microbial growth promoter in nutrient-limited conditions. The results show that the co-culture with *S. stutzeri* significantly increased microalgal growth compared to control cultures without bacterial interaction, suggesting a mutually beneficial relationship between *S. stutzeri* and *Nannochloropsis* sp. Moreover, *S. stutzeri* markedly enhances the growth of *Nannochloropsis* sp., especially under nitrogen-limited conditions. The observed growth enhancement is attributed to several microalgae-growth-promoting traits exhibited by *S. stutzeri*, such as nitrogen fixation, phosphate solubilization, production of essential enzymes, secretion of phytohormones such as indole-3-acetic acid (IAA), and tolerance to abiotic stress. These traits collectively contribute to enhanced nutrient uptake, greater stress resilience, and increased algal productivity. These findings highlight the potential of *S. stutzeri* as an effective microbial partner for *Nannochloropsis* sp., particularly in nitrogen-limited environments. The study provides valuable insights into microalgae-bacteria interactions and their applications in sustainable algal cultivation, with promising implications for biotechnology, aquaculture, and biofuel production.

Keywords: *Nannochloropsis* sp., Nitrogen stress, Growth-promoting traits



MAR-O3

MULTIDRUG-RESISTANT AND BIOFILM-ASSOCIATED *KLEBSIELLA PNEUMONIAE* IN WATER SOURCES: A GROWING THREAT TO PUBLIC HEALTH

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The growing threat of antimicrobial-resistant *Klebsiella pneumoniae* presents a major global health crisis, with multidrug-resistant strains increasingly prevalent in both clinical and environmental settings. This study investigated antibiotic resistance, biofilm formation, and virulence potential in *K. pneumoniae* isolates from the coastal regions of Cochin, India. Isolates were cultured, identified by the spread plate method using CHROM agar, and subjected to antibiotic susceptibility testing via the Kirby-Bauer disc diffusion method. Biofilm formation was quantified using a modified microtiter plate adhesion assay and visualised using a scanning electron microscope. Hypervirulent strains were confirmed by K1 serotype. All isolates demonstrated resistance to at least five antibiotics, with extended-spectrum β-lactamase (ESBL) production primarily attributed to the *bla_{TEM}* gene. Resistance was observed against critically important antibiotics, including beta-lactams, macrolides, and colistin, while aminoglycosides showed lower resistance rates. Hypervirulent strains displayed significantly higher antibiotic resistance and biofilm formation. A high prevalence of antibiotic resistance genes (*bla_{TEM}*, *bla_{SHV}*, *bla_{OXA}*) and virulence factors was observed, suggesting a substantial risk of severe infections. This study underscores the urgent need for continuous surveillance and targeted public health interventions to mitigate the spread of environmental hypervirulent multidrug-resistant *K. pneumoniae*.

Keywords: Bacterial pathogens, *E. coli*, *Klebsiella*, Hypervirulent genes, Antibiotic-resistant genes, Biofilm



MAR-O4

GREEN SYNTHESIS OF ZINC OXIDE NANOPARTICLES (ZNO-NPS) USING OCIMUM TENUIFLORUM EXTRACT: A SUSTAINABLE STRATEGY TO CONTROL AEROMONAS HYDROPHILA BIOFILMS IN AQUACULTURE

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Aeromonas hydrophila is a multidrug-resistant, zoonotic bacterium causing ulcerative disease, fin rot, and hemorrhagic septicemia in fishes. It reduces market value and raises production costs associated with intensive disease management. Its ability to form biofilm boosts its survival and antibiotic resistance, making new antimicrobials crucial. ZnO-NPs are promising for their antimicrobial and antibiofilm properties, but conventional synthesis is costly and harmful to the environment. This study employed a green synthesis method to produce sustainable, cost-effective ZnO-NPs and evaluated their antimicrobial and antibiofilm properties against *A. hydrophila*. ZnONPs were synthesized by treating zinc nitrate hexahydrate with the methanolic extract of *O. tenuiflorum* leaves. The nanoparticles were characterized by FTIR spectroscopy, X-ray diffraction, and scanning electron microscopy. An MTT assay was conducted to determine antimicrobial activity and minimum inhibitory concentration against *A. hydrophila*. Antibiofilm activity was evaluated using the Congo red agar method. Characterization revealed ZnO-NPs with FTIR peaks at 443 cm^{-1} (Zn-O stretching), 1633 cm^{-1} (O-H bending), and 3391 cm^{-1} (O-H stretching). XRD confirmed the crystalline nature, while SEM showed hexagonal structures sized 80–90 nm. ZnONPs exhibited antimicrobial activity with a MIC of $80\text{ }\mu\text{g/mL}$ against *A. hydrophila*. Congo red assay demonstrated significant biofilm inhibition at equivalent concentrations. Green synthesis of ZnO-NPs using *O. tenuiflorum* offers an environmentally sustainable approach to producing effective antimicrobial and antibiofilm agents. These findings support their potential for combating antimicrobial resistance and biofilm-related infections in aquaculture.

Keywords: *A. hydrophila*, ZnO-NP'S, *Ocimum-tenuiflorum*, Antibiofilm



MAR- O5

AN IMAGE ASSISTED MONITORING SYSTEM FOR EARLY-STAGE DETECTION OF BIOFILMS

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Biofilm is defined as an assemblage of microorganisms attached to an inert or living surface, embedded within a self-produced extracellular matrix. The ability to form a protective matrix that shields the bacteria within them makes it resistant to antimicrobial agents, thereby making it difficult to eradicate. This leads to persistent infections, biofouling, and operational inefficiency of equipment and surfaces in diverse industrial sectors. The biofilm formation in drinking water systems, cooling towers, desalination plants, sea-water intake pipelines, aquaculture systems, and underwater sensors poses serious threats, as it contributes to microbial contamination, clogging, corrosion, and reduced efficiency. Early and accurate detection of biofilm is indispensable for its proper management. The present study investigates the development of a real-time detection and removal kit for rapid identification, quantification, and remediation of biofilms in drinking water conduits. This kit includes the Salt Agglutination Test (SAT) assay and Crystal Violet (CV) assay integrated with an image analyser to monitor the biofilm density, agglutination patterns, and levels of contamination. Based on this analysis, a variable UV-C light lamp is incorporated for disrupting the biofilm formation. This study employs the effectiveness of a detection kit using biofilm-forming marine bacterial strains isolated from marine invertebrates. The nine bacterial strains (*Halomonas meridiana*, *Halomonas piezotolerens*, *Psychrobacter celer*, *Pseudomonas songnensis*, *Shewanella fidelis*, *Stutzerimonas decontaminans*, *Halomonas aquamarina*, *Halomonas lionensis*, *Psychrobacter celer*) were assessed for biofilm formation by SAT assay to evaluate the cell surface hydrophobicity, further quantified by CV assay and eventually removed on exposure to UV radiation at specific wavelength. The detection accuracy can be further enhanced by integrating AI analysis for precise and high-throughput results. The results obtained from SAT and CV assays, and UV



treatments can be processed using AI algorithms to analyse the biofilm formation patterns and UV–UV-mediated biofilm disruption. The formulated technology, thus, envisages the possibility of integrating traditional biofilm detection assays and AI to monitor, detect, and remove biofilms. This would facilitate optimisation of antifouling strategies in maritime industries, desalination, and water treatment plants.

Keywords: Biofilm, CV assay, Image-based, Marine bacteria, SAT assay, Ultraviolet



MAR-O6

PREVALENCE, ANTIBIOTIC RESISTANCE, BIOFILM
FORMATION, AND GROWTH PROFILE OF *VIBRIO MIMICUS*
ISOLATED FROM SEAFOOD SOLD IN RETAIL MARKETS IN
COCHIN, KERALA

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The marine environment harbors diverse bacterial communities, including opportunistic pathogens such as *Vibrio mimicus*, which pose significant risks to seafood safety and public health. This study investigates the prevalence, antibiotic resistance, biofilm formation, and growth profile of *V. mimicus* in seafood samples collected from retail markets in Cochin, Kerala, India, between April 2021 and March 2024. A total of 100 seafood samples were screened, revealing a *V. mimicus* prevalence of 7%. Antibiotic susceptibility testing demonstrated high resistance to ampicillin, penicillin, cefotaxime, and cefepime, whereas complete susceptibility was observed for chloramphenicol, imipenem, ciprofloxacin, and tetracycline. The multiple antibiotic resistance (MAR) index ranged from 0.13 to 0.50, highlighting the potential risk of antimicrobial-resistant strains. Environmental growth assessments indicated that *V. mimicus* exhibited significant variations in response to pH and salinity, with optimal growth observed at 37°C. Notably, a majority of multidrug-resistant isolates were strong biofilm producers, enhancing their survival and persistence in seafood processing environments. Despite the low prevalence, the presence of multidrug-resistant and biofilm-forming *V. mimicus* strains underscores the need for stringent monitoring and sustainable seafood safety measures to protect consumer health.

Keywords: *Vibrio mimicus*, Seafood safety, Antimicrobial resistance, Biofilm formation, Foodborne pathogens



MAR-O7

EVALUATION OF *SPIRULINA SUBSALSA* PHOTOSYNTHETIC EFFICIENCY UNDER INDUSTRIAL SEWAGE TREATMENT

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On the Earth's surface, three parts are covered with brackish water and one part is covered with fresh water. The population expansion and industrial development have deteriorated the quality of freshwater reservoirs around the world and have caused freshwater shortages in certain areas. The discharge of industrial effluents containing toxic heavy metals (cadmium (Cd), mercury (Hg), and chromium (Cr)) into the environment has a serious impact on human, animal, and aquatic life. Hence, *Spirulina subsalsa* is a photosynthetic filamentous prokaryotic cyanobacterium and has the ability the reduction of metal pollutants. So, in this study is more useful to assess the basic photosynthetic efficiency parameters and the toxicity mitigation possibilities of *S. subsalsa* under wastewater sewage treatment. The collected wastewater sewage from near Kurnool industrial area, Andhra Pradesh, this of Industrial wastewater sewage (IWS) incubated at laboratory conditions ($28\pm4^{\circ}\text{C}$) and filtered for the treatment. After filtration of this industrial wastewater, the sewage maintained with *Spirulina* nutrient media for further treatment and analysis. The results (growth of cyanobacterial species, lipid peroxidation, and photosynthetic pigments) are concluded that have the ability to reduce the wastewater sewage pollutants of the selected study area.

Keywords: *Spirulina subsalsa*, Industrial wastewater, Photosynthetic pigments

Poster Presentations



MAR- P1

BIOFILM FORMATION AND ENZYME ACTIVITIES OF BACTERIA ASSOCIATED WITH SEA URCHIN IN A SEAMOUNT OF THE SOUTHEAST ARABIAN SEA

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The interaction between marine organisms and their associated microbiome is vital for host health, physiology, and adaptation to environmental changes. Intrinsic host factors, environmental conditions, and the core microbial community shape this dynamic relationship. This study investigated the microbial diversity and functional potential of seamount-dwelling sea urchins through culture-based techniques. Specifically, we analyzed the microbiota associated with various parts of the sea urchin, *Stereocidaris indica*, collected from a seamount in the eastern Arabian Sea. Additionally, we assessed the biofilm formation capacity and enzymatic activity of these bacterial communities. A total of 115 bacterial isolates were obtained from the gut, coelomic fluid, and peristomial membrane of *S. indica*. Of these isolates, nearly 50 % showed biofilm formation above a median level of 0.2 a.u. The expression profile of enzymes associated with sea urchin bacteria was analysed spectrophotometrically using dye-conjugated enzyme substrates. The bacterial isolates which showed above median level of enzyme expression, were in the order of tyrosinase (69 no's; median $0.11\mu\text{g } 100\mu\text{l}^{-1}$) > phosphatase (63 no's; median $0.14\mu\text{M ml}^{-1}\text{min}^{-1}$) > aminopeptidase (60 no's; median $0.55\mu\text{M ml}^{-1}\text{min}^{-1}$) = lipase (60 no's; median $0.22\mu\text{M m}^{-1}\text{min}^{-1}$) > β -glucosidase (58 no.s; median $0.19\mu\text{M ml}^{-1}\text{min}^{-1}$) = laminarinase (58 no's; median $0.92\mu\text{g }\mu\text{l}^{-1}$). Ongoing studies are focused on the molecular phylogeny of these bacterial isolates to gain a deeper understanding of their role in host-microbe interactions.

Keywords: Deep Sea, Seamount, Sea urchin, Microbiome, Enzyme expression, Biofilm



MAR- P2

QUANTITATIVE ANALYSIS OF PHENOL DEGRADATION BY MARINE BIOFILM-ASSOCIATED BACTERIA ON POLLUTANT PLASTIC SURFACES

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Phenol is a soluble organic pollutant in the marine environment. Major sources of phenol and its derivatives polluting the marine environment are industrial effluents, oil spills, and plastic leachates. Phenol poses a serious threat to marine life, disrupting metabolic functions, causing oxidative stress, and bioaccumulating in the food chain. The increasing accumulation of plastics is also a critical concern as it has long-term persistence and effects in the marine environment. Pollutant plastic surfaces in marine environments create an ecosystem for bacterial biofilms, including those individuals with high potential in bioremediation. This unique ecosystem is known as the 'plastisphere'. The study aims to isolate and identify phenol degraders residing on pollutant plastics collected from the Cochin coast and quantify their phenol degradation efficiency. Plastics with pre-formed biofilm were collected from polluted environments, and isolates were cultured on sterile plastic substratum in Minimal Salt Medium (MSM), in which phenol is the sole carbon source. Quantitative analysis of phenol degradation efficiency is by giving the known concentration of Phenol and extraction of the medium at an interval of 12 hours to know the rate of degradation.

Keywords: Marine biofilm, Plastic pollution, Phenol degradation



MAR-P3

PLASMID-MEDIATED ANTIMICROBIAL RESISTANCE IN VIBRIOS: A CHALLENGE TO SUSTAINABLE SHRIMP FARMING

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Nowadays, shrimp-culture methods frequently use antibiotics to ensure the sustainable production of healthy and disease-free shrimp. Serious antimicrobial resistance (AMR) could develop across environmental bacteria as a result of this. Given the serious effects of AMR worldwide, the goal of the study was to find out the prevalence of antimicrobial-resistant vibrios and other pathogens in infected shrimp (*Litopenaeus vannamei*) from two brackish-water cultured farms in various regions. Diverse species of vibrios viz. *V. alginolyticus*, *V. parahaemolyticus*, *V. cholerae*, *V. mimicus*, *V. fluvialis*, *Aeromonas hydrophila*, *A. salmonicida*, and *Shewanella algae* were recovered from the shrimps on TCBS medium. With a MAR index of 0.60, *V. alginolyticus* was found to be the most resistant isolate, followed by *V. mimicus* (MAR index 0.54) and *V. parahaemolyticus* (MAR index 0.42). The isolates from farm 1 had a Shannon Wiener diversity index, H', of 1.506, while those from farm 2 had an H' of 1.69. Among the 35 antibiotics of 15 different classes tested, the isolates were often resistant to tetracyclines, beta-lactams, and cephalosporins. All the isolates from both the farms were susceptible to erythromycin, ciprofloxacin, and cefazolin, whereas none of them were sensitive to tetracycline and ampicillin. Plasmid curing resulted in a significant alteration in the MAR index and an increased altered resistance phenotype. Plasmid-borne AMR was found to be common among the bacteria from the shrimp samples examined in the study, raising serious public health concerns. By implementing a multifaceted “One-Health” approach, the authorities may be able to reduce the usage of antibiotics and open the door for the development of innovative alternative solutions.

Keywords: Antimicrobial resistance, *Litopenaeus vannamei*, Plasmid curing, Shrimp, *Vibrio*



MAR-P4

METAGENOMIC INSIGHTS INTO MICROBIAL DIVERSITY AND FUNCTIONAL POTENTIAL OF SEDIMENTS IN THE COCHIN ESTUARY

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The Cochin Estuary, the lower reach of the Vembanad wetland ecosystem, is a monsoonal tropical estuary that harbours a rich diversity of flora and fauna. The eutrophic, phosphorus-rich sediments support a diverse microbial community with pivotal roles in nutrient cycling and estuarine productivity. The present study investigates the microbial diversity at two selected stations: S1 (Latitude: 9.9642° N, Longitude: 76.2829° E) and S2 (Latitude: 9.9658° N, Longitude: 76.2433° E) in the Cochin Estuary using a whole-genome metagenomic approach. Sediment samples were collected from both stations, and the metagenomic DNA was extracted using the QIAGEN Power Soil Kit. The extracted DNA was quality-checked and quantified before whole-genome metagenomic sequencing library preparation using the KAPA DNA Hyper Prep Kit. Sequencing was performed on the Illumina NovaSeq X Plus platform. The raw reads were quality-checked to remove low-quality reads and adapter sequences. The filtered reads were then assembled de novo using the metaSPAdes assembler. Taxonomic and functional annotation was performed using MEGAN, based on comparisons with reference databases. A total of 232 microbial species were identified across two stations, with 130 unique species in S1, 72 in S2, and 29 shared species. Phylum-level composition revealed that Actinobacteria dominated S1, followed by Proteobacteria, and Chloroflexi, whereas Proteobacteria dominated S2, followed by Chloroflexi, and Bacteroidetes. At the genus level, *Bifidobacterium* (59.3%) and *Prevotella* (8.89%) were predominant in S1, while *Desulfosarcina* (16.42%) dominated S2. Functional gene prediction analysis revealed higher genomic complexity and metabolic potential in S2, which contained 6,283 genes compared to 3,603 in S1, along with a greater proportion of



genes exceeding 1,000 bp. These findings suggest distinct microbial community structures and functional adaptations across the two stations. Overall, the study highlights the spatial heterogeneity in microbial diversity and functional potential within the Cochin Estuary sediments.

Keywords: Cochin estuary, Metagenomics, Microbial diversity, Sediment microbiome, Functional annotation



MAR-P5

INFLUENCE OF AQUACULTURE ON ANTIMICROBIAL RESISTANCE IN AQUATIC ENVIRONMENTS

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Antimicrobial resistance (AMR) in aquatic environments poses significant risks to ecosystem health and public safety. This study investigates the presence of antimicrobial-resistant bacteria in an aquaculture farm and a nearby natural water body, both located at Vypin, Ernakulam district. Water and sediment samples from both sites were analyzed. Water quality parameters were assessed, revealing a pH of 7.2, salinity of 10 ppt, total hardness of 3225 mg/L, ammonia of 0.19 mg/L for water collected from the natural water body whereas the aquaculture farm water had a pH of 7.5, salinity of 9 ppt, total hardness of 2675 mg/L, ammonia of 0.12 mg/L for water collected from the aquaculture farm. Nitrite and sulphide levels were below the detectable limit for both water samples. Total organic carbon (TOC) in the sediment sample was 6.07% for the natural water body and 3.67% for the aquaculture farm. Total plate count was performed to estimate the bacterial load. Colony counts were recorded for all samples. This was followed by antimicrobial sensitivity testing using the Bauer-Kirby disk diffusion method, assessing resistance against multiple antibiotic classes, including Beta-lactams, tetracyclines, aminoglycosides, sulphonamides, and nitrofurans confirmed the presence of resistant bacterial strains, indicating potential AMR contamination from aquaculture activities. The presence of AMR highlights the urgent need for stricter antimicrobial regulation in aquaculture to prevent environmental contamination

Keywords: Antimicrobial resistance, Aquaculture, Water quality, Environmental impact



MAR-P6

A COMPARATIVE STUDY OF ANTIBIOTIC RESISTANCE IN THE BACTERIAL ISOLATES FROM A HOSPITAL EFFLUENT-EXPOSED SITE AND A NORMAL OPEN-SOURCE AQUATIC SYSTEM

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The increasing presence of antimicrobial-resistant bacteria in aquatic environments, particularly in areas receiving hospital effluents, poses a significant threat to aquatic health and food safety. This study compares bacterial load, physicochemical parameters, total organic carbon (TOC), and antibiotic resistance patterns in a hospital effluent-exposed site (Kothad) and a normal site water and sediment sample (Vypin) to assess the impact of hospital discharge on microbial communities. Water samples from both sites were analyzed for pH, salinity, alkalinity, hardness, calcium, magnesium, ammonia, nitrite, and sulfide levels to evaluate environmental influences on microbial proliferation. Total hardness showed 3025 mg/l in Kothad and 3225 mg/l in Vypin. Magnesium concentration was notably higher in Vypin (3041 mg/l) than in Kothad (2845 mg/l). The results of the total plate count revealed a higher bacterial load in sediment samples compared to water samples, with Kothad sediment containing 4.30×10^6 CFU/gm and water containing 1.45×10^4 CFU/ml, whereas Vypin sediment showed 3.20×10^6 CFU/ml and water 4.00×10^3 CFU/ml. Antibiotic susceptibility testing was conducted using β -lactams, cephalosporins (first to fourth generation), carbapenems, aminoglycosides, macrolides, quinolones, tetracyclines, sulfonamides, and nitrofurans. Isolates from Kothad displayed a higher degree of resistance, particularly to some of the antibiotics. The findings emphasize the need for stricter wastewater treatment measures to mitigate the spread of AMR bacteria from hospital effluents into aquatic systems.

Keywords: Hospital effluent, Bacterial load, Antimicrobial resistance (AMR), Aquatic pollution



MAR-P7

ANTIBIOTIC RESISTANCE PROFILING OF SELECTED
BACTERIAL PATHOGENS FROM NATURAL AQUATIC
ENVIRONMENTS IN VYPIN AREA, ERNAKULAM DISTRICT,
KERALA

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The impact of antimicrobial resistance (AMR) on the environment and public health is substantial. Aquatic environments can be a source of drug-resistant bacteria that can be directly transmitted to humans, causing infections and treatment failure. The present study aimed to assess the prevalence of antibiotic-resistant bacteria in water and sediment samples in the natural aquatic environment in the Vypin area. The physicochemical analysis of water samples indicated a pH of 7.2, salinity of 10 ppt, alkalinity of 60 mg/L, and bicarbonate concentration of 60 mg/L. The recorded calcium and magnesium levels were 184 mg/L and 3041 mg/L, respectively, contributing to a total hardness of 3225 mg/l. Ammonia was detected at 0.19 mg/L, while nitrite and sulfide remained below detectable limits (BDL). The total organic carbon (TOC) content of the sediment was measured at 6.07%. The result of the total plate count showed a bacterial load of 5.50×10^5 CFU/gm in sediment and 1.09×10^4 CFU/mL in water. Key bacterial species, including *Escherichia coli*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, and *Klebsiella pneumoniae*, were isolated. Antibiotic sensitivity test was conducted using a panel of antibiotics from various classes, including β -lactams, first-generation cephalosporin, third-generation cephalosporin, fourth-generation cephalosporin, carbapenems, aminoglycosides, macrolides, quinolones, tetracyclines, sulfonamides, and nitrofurans to evaluate bacterial resistance patterns. The result of the antibiotic sensitivity test revealed that the pathogenic bacteria were resistant to many of the antibiotics tested. The presence of antibiotic-resistant pathogenic bacteria in a natural system highlights potential public health risks and the need for effective monitoring and management strategies to mitigate AMR proliferation.

Keywords: Bacterial pathogens. Antibiotic resistance, Environmental monitoring



MAR-P8

PROBIOTICS AND ENZYMATIC PROFILING OF ACTINOMYCETES FROM KALLADA RIVER SEDIMENTS: A BIOTECHNOLOGICAL PERSPECTIVE

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Microorganisms are a diverse group of organisms widely used as a source of essential compounds in pharmaceutical, agricultural, and food industries. Among them, Actinomycetes are abundant in freshwater, marine, and terrestrial ecosystems. They are primarily nonpathogenic, gram-positive bacteria and play a crucial role in drug discovery, with over 90% of antibiotics being derived from them. This study focuses on the isolation of potential Actinomycetes and evaluating their probiotic activity. Samples were collected from four stations along the Kallada River in the Kollam district of Kerala, India. A total of 25 isolates were obtained. Isolates were subjected to antimicrobial analysis, enzymatic and probiotic assays, like pH tolerance and salt tolerance. Bacteria exhibited antimicrobial activity against 10 pathogens, namely *Vibrio proteolyticus*, *Edwardsiella tarda*, *Bacillus cereus*, *Escherichia coli*, *Staphylococcus aureus*, *Vibrio harveyi*, *Vibrio vulnificus*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, and *Vibrio alginolyticus*. Hydrolytic assay confirmed the presence of enzymes like cellulase, lipase, and amylase. The bacteria could tolerate acidic pH of 1-3 and salt concentration up to 10%. DNA sequencing was performed to identify the species of potential Actinomycetes. The findings suggest that Actinomycetes from the Kallada River hold promise for the development of novel probiotics, antimicrobial agents, beneficial enzymes, and other therapeutic applications, particularly in aquaculture.

Keywords: Probiotics, Enzymes, Actinomycetes, River, Antibiotic resistance



MAR-P9

PREVALENCE OF ANTIBIOTIC RESISTANCE AMONG
AQUACULTURE PATHOGENS FROM TRADITIONAL PADDY
CUM PRAWN CULTURE FARMS AND FEEDER CANAL ALONG
THE COCHIN BACKWATERS

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The Cochin estuary, a region experiencing rapid urbanization, faces significant threats of organic pollution. The traditional aquaculture ponds along the estuary, directly connected via feeder canals, suffer from poor water quality and facilitate the dissemination of AMR bacterial pathogens. This study investigated the incidence of antibiotic-resistant bacteria in water and sediment from traditional aquaculture ponds (paddy-cum prawn culture and the perennial ponds) and the feeder canal along the Cochin backwaters. Field measurements included temperature, pH, salinity, and dissolved oxygen, following standard protocols. Total and fecal coliform levels ranged from 40 to >1100 MPN/100mL. Heterotrophic plate counts in water and sediment samples of the feeder canal were 1.18×10^5 CFU/mL and 1.144×10^7 CFU/g, respectively. All samples tested positive for targeted pathogens. Representative strains were confirmed by 16S rRNA gene sequencing. The major bacterial pathogens identified were *Escherichia coli*, *Vibrio* sp., and *Aeromonas* sp. Antibiotic susceptibility testing performed using the Kirby-Bauer method revealed that most isolates were resistant to tetracycline, azithromycin, and nitrofurantoin. The presence of antibiotic residues, if any, in the water samples from the feeder canal and perennial pond was also analyzed. In conclusion, the detection of antibiotic-resistant bacterial pathogens in the aquaculture environments underscores a significant public health risk, particularly concerning seafood consumption, and emphasizes the need for improved water quality management and antibiotic stewardship.

Keywords: Antibiotics, Antibiotic resistance, Aquaculture pathogens, Cochin Estuary



MAR-P10

INVESTIGATING THE PROBIOTIC EFFICIENCY OF ACTINOMYCETES ISOLATED FROM SEDIMENT SAMPLES OF ASHTAMUDI LAKE, KOLLAM

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Actinomycetes are Gram-positive bacteria. They are best known for their ability to produce antibiotics and play a crucial role in decomposing organic materials. Actinomycetes play a major role in inhibiting the growth of pathogens. For inhibiting the growth of pathogens, the biological properties used in Actinomycetes include antimicrobial, probiotic, and enzymatic activity. Nowadays, probiotic and enzymatic activity are more promoted rather than antimicrobial activity for further treatment, which is more efficient. This study investigated the biotechnological potential of Actinomycetes isolated from Ashtamudi Lake sediments, focusing on antimicrobial, enzymatic, and probiotic properties. The isolates displayed broad-spectrum antimicrobial activity, inhibiting ten pathogenic bacteria relevant to human and aquaculture health. Enzymatic assays confirmed the production of cellulase, amylase, and lipase, demonstrated by hydrolysis assays. Furthermore, the isolates exhibited robust probiotic characteristics, tolerating up to 10% salt concentration and acidic pH levels as low as 1-3. These results suggest that Ashtamudi Lake Actinomycetes represent a valuable resource for developing novel antimicrobial agents, industrial enzymes, and probiotics for aquaculture and pharmaceutical applications.

Keywords: *Actinomycetes, Antimicrobial resistance, Enzymatic activity (cellulase, amylase, lipase), Probiotic activity (salt tolerance, pH tolerance), Ashtamudi Lake*



MAR-P11

FIRST REPORT ON THE GC-MS BASED ANTIBACTERIAL
ACTIVITY SCREENING OF BROWN SEAWEED (*PADINA*
PAVONICA (LINNAEUS) THIVY) OBTAINED FROM
KODIYAGHAT, SOUTH ANDAMAN, IN VARIOUS ORGANIC
SOLVENTS

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Seaweeds endure harsh marine conditions and harmful bacteria, seemingly protected by diverse bioactive compounds. This work presents a pioneering investigation into the antibacterial activity of brown seaweed, *Padina pavonica* (Linnaeus) Thivy, with an emphasis on understanding the solvent efficiency in extracting the antibacterial components, which are characterized using GC-MS. The extract was obtained with acetone, chloroform, ethyl acetate, and hexane were tested against five bacterial strains, *Staphylococcus aureus*, *Proteus mirabilis*, *Citrobacter freundii*, *Salmonella typhimurium*, and *Salmonella paratyphi* B by agar well diffusion method. The findings revealed that only the crude extract obtained using ethyl acetate had an inhibitory effect on all five pathogens tested. Further testing with different concentrations (25 µl, 50 µl, 100 µl of 100mg/ml extract) of crude extract prepared in ethyl acetate has shown a maximum zone of inhibition against *P. mirabilis* (30 ± 0.81 mm) and the minimum inhibition zone in *S. paratyphi* B (8.66 ± 0.47 mm). The compounds identified using GC-MS include 1-Butene, 1-(methylthio)-, (Z)-, n-hexadecanoic acid, hexadecanoic acid ethyl ester, Oleic Acid, and Octadecanoic acid, all of which are known to exhibit confirmed antibacterial properties. The findings confirm that brown seaweed, *Padina pavonica* (Linnaeus) Thivy, can be further researched for the purification of antibacterial compounds.

Keywords: Seaweeds, *Padina pavonica*, Antibacterial, Bioactive, GC-MS, Marine algae



MAR-P12

ACTINOMYCETES FROM MANGROVE SEDIMENTS OF COCHIN: A POTENTIAL SOURCE OF BIOACTIVE COMPOUNDS

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Mangrove ecosystems, positioned at the interface of terrestrial and marine environments, harbour diverse microbial communities with significant biotechnological potential. This study aimed to isolate and characterize bacteria and Actinomycetes from sediment samples collected at three mangrove sites in Ernakulam District, Kerala, namely Pukkad (PKD), Pallippuram (PLP), and Puthuvype (PTY). Sediment samples were collected employing sterile techniques, stored in cooler bags, and transported to the lab, and subsequently cultured on Actinomycetes Isolation Agar (AIA), Starch Casein Agar (SCA), and Zobell Marine Agar (ZMA) to promote bacterial growth. Environmental parameters such as salinity and temperature were recorded to assess their influence on microbial diversity. A total of 25 morphologically distinct pure bacterial strains, identified as Actinomycetes, were successfully isolated. Mass production of these strains using A1BFE+C media was carried out for crude extract preparation and subsequent biochemical compound isolation. The findings highlight the potential of mangrove-associated microbes, particularly Actinomycetes, in producing bioactive compounds with antimicrobial, anticancer activities. This study reinforces the significance of mangrove ecosystems as reservoirs of microbial diversity with promising applications in drug discovery and biotechnology.

Keywords: Mangrove ecosystems, Actinomycetes, Antimicrobial



MAR- P13

ANTIBIOFILM ACTIVITY OF ACTINOMYCETES IN THE FOOD INDUSTRY

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Microorganisms living in communities within extracellular polymeric substances (EPSs) that contain proteins, lipids, DNA, and polysaccharides are known as bacterial biofilms. In the industries, biofilms stand for both good and bad qualities. When improper clean-up and control measures are used in the food industry, spoilage and pathogenic bacteria can form biofilms on food industry surfaces, which can result in food deterioration and disease transmission. Samples from Actinomycetes have shown antibiofilm effectiveness against a variety of foodborne pathogens in the past. In this study, we identified Actinomycetes antibiofilm activity in our investigation and numerous antibiofilm chemicals were present in several samples. The biofilm samples were collected from different equipment used in the food industry. When 15 actinomycete isolates were tested for antibiofilm activity, many of them showed inhibitory action, and six of them showed notable inhibition of biofilms. Additionally, the isolates ability to inhibit and destroy biofilms remained consistent across a range of temperatures. All of the Actinomycete samples showed efficacy against foodborne pathogen biofilms that were produced on the surface of polystyrene, which is frequently used in industrial equipment, and stainless-steel coupons. Utilizing DNA sequencing analysis, PCR for the 16S rRNA gene, and the 96-well microtiter plate method. To round up, Actinomycetes have the potential and efficiency to be employed in food industry equipment and environments to improve food safety since they can be used as anti-biofilm agents.

Keywords: Food industry, Antibiotic resistance, Actinomycetes, Biofilms



MAR- P14

ANTIBIOFILM ACTIVITY OF ACTINOMYCETES AGAINST BIOFILM ISOLATED FROM NATURAL ENVIRONMENT

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A biofilm consists of a collection of microorganisms that adhere to a surface, creating a slimy matrix composed of extracellular polymeric substances. It is crucial to manage biofilms in natural settings such as lakes, as they can lead to the corrosion of submerged items like metal pipes, harm underwater instruments and ships. To mitigate this issue, submerged metals are often coated with chemical compounds, which can inadvertently endanger aquatic life. To address this concern, there is a need to substitute chemical compounds with natural materials. This research investigates the inhibitory activity of Actinomycetes on biofilms. Biofilm samples were collected from different locations at the CUSAT jetty. When tested for antibiofilm activity, fifteen Actinomycete isolates demonstrated varying levels of inhibition, with seven exhibiting significant biofilm inhibition. The effectiveness of the Actinomycetes was evaluated using the 96-well microtiter plate assay. All Actinomycetes displayed effectiveness against biofilms found on items submerged in aquatic environments. DNA sequencing analysis and PCR allowed for the identification of certain biofilm-forming organisms, including *Enterococcus faecalis* and *Bacillus subtilis*. This study reveals that Actinomycetes hold promise for use in protecting items that are regularly submerged in water bodies, as they serve as excellent agents against biofilm formation.

Keywords: Biofilm, Actinomycetes, Lakes, Antibiofilm



MAR- P15

BIOGENESIS OF SILVER NANOPARTICLES FROM THE BACTERIAL FLORA ISOLATED FROM COASTAL WATERS OF KANNUR

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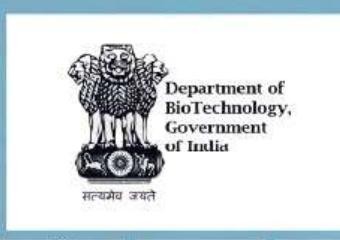
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In the present study, the population of culturable heterotrophic bacteria in the coastal waters of Kannur was determined. The bacterial count ranged from 3.5×10^2 to 4.35×10^4 CFU/mL. A total of 120 bacterial cultures were isolated from the water samples. BIOENV analysis showed that bacterial populations in the coastal waters were influenced by physicochemical parameters such as temperature, salinity, and dissolved oxygen. All isolates were screened for their potential in the biogenic synthesis of silver nanoparticles, and four demonstrated extracellular synthesis. These were analyzed using UV-VIS spectroscopy, which revealed an absorption peak near 420 nm, confirming the formation of monodispersed silver nanoparticles. The four isolates that exhibited extracellular synthesis of silver nanoparticles were purified for further characterization.

Keywords: Bacterial population, Silver nanoparticle, Coastal waters

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