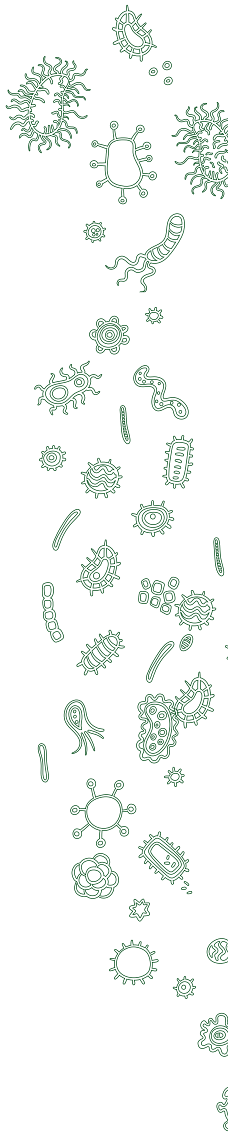
UAEU جامعة الإمارات العربية المتحدة
United Arab Emirates University

مركز خليفة للتقانات الحيوية والهندسة الوراثية
Khalifa Center for Genetic Engineering & Biotechnology

هيئة أبوظبي للزراعة والسلامة الغذائية
ABU DHABI AGRICULTURE AND FOOD
SAFETY AUTHORITY



Abstract Book

MICROBIOME: HUMAN, PLANT AND ENVIRONMENTAL HEALTH

applications and challenges

ABU DHABI NATIONAL EXHIBITION CENTER (ADNEC)
ABU DHABI, UNITED ARAB EMIRATES

NOVEMBER 21 – 22, 2023

SCAN ME!

WEBSITE

Get In Touch
uaemicrobiome@uaeu.ac.ae
www.uaemicrobiome2023.org

UAEMicrobiome23

uaemicrobiome

International Conference
"UAE Microbiome 2023"

uaemicrobiome2023

#UaeMicrobiome23

UAE
MICRO
BIOME
2023

The Book of Abstracts

International conference on
MICROBIOME: HUMAN, PLANT AND ENVIRONMENTAL HEALTH
applications and challenges

(UAE Microbiome 2023)

November 21 – 22, 2023

Location: Abu Dhabi National Exhibition Center (ADNEC),
Abu Dhabi, United Arab Emirates

Website: https://www.uaemicrobiome2023.org/
Email: uaemicrobiome@uaeu.ac.ae

Words from UAE Microbiome 2023 conference chair

I am delighted to welcome you all to explore the fascinating world of microbiomes and their impact on health, plants, and the environment. This conference serves as a platform for researchers, scientists, industry professionals, and enthusiasts to exchange knowledge, share groundbreaking discoveries, and discuss the latest advancements in this rapidly evolving field.

Microbiomes, the intricate communities of microorganisms that inhabit diverse ecosystems, have captured the attention of scientists worldwide. They play a pivotal role in shaping the health of humans, plants, and the environment. Understanding the complex interactions within microbiomes opens up new avenues for improving human well-being, enhancing agricultural practices, and promoting environmental sustainability. Throughout this conference, we will delve into a wide range of topics, including the human microbiome and its impact on disease prevention and treatment. We will explore the intricate relationship between plants and their microbial partners, uncovering the mechanisms that drive plant growth, resilience, and disease resistance. Additionally, we will examine the role of microbiomes in maintaining ecological balance, soil health, and the overall health of our planet.

The program features esteemed speakers who are at the forefront of microbiome research, bringing their expertise and insights to enlighten us all. Engaging panel discussions, interactive workshops, and poster presentations will provide ample opportunities for networking, collaboration, and the exchange of ideas.

I extend my gratitude to the organizers, invited speakers, our students, sponsors, and participants who have made this conference possible. Your contributions to advance microbiome research are invaluable in driving scientific progress and fostering innovation. I hope that this conference will inspire new collaborations, spark innovative research ideas, and pave the way for transformative discoveries. Together, let us unravel the mysteries of microbiomes and harness their potential for the betterment of human health, plant productivity, and environmental sustainability.

Once again, I extend a warm and enthusiastic welcome to the Microbiome Conference in Health, Plant, and Environment in Abu Dhabi.

Wishing you a fantastic and fruitful time at the conference!

Warm regards,
Prof. Dr. Khaled Amiri

Words from UAE Microbiome 2023 conference Co-chair

Welcome to the UAE Microbiome: Human, Plant, and Environmental Health Conference 2023. As we convene to explore the intricate relationships between microbiomes and the health of humans, plants, and our environment, we embark on a collective journey towards a more sustainable and healthier future.

This conference underscores the UAE's commitment to fostering cutting-edge research and innovation in these critical areas. At ADAFSA, we believe in the power of knowledge and innovation to shape the future of agriculture and food safety. That is why ADAFSA partnered with leading research institutions across the UAE, including the Khalifa Technology Center. This partnership is a catalyst for transforming scientific discoveries into practical applications. Together, we're fostering an environment of intellectual exchange and collaboration to drive research and development forward.

Without further ado, I would like to extend my sincere gratitude to all participants, esteemed speakers, and dedicated organizers for their invaluable contributions to this event. May our deliberations here lead to profound insights and collaborations that elevate the well-being of our planet and its inhabitants.

Warm regards
H.E. Dr. Mariam Al Suwaidi

Messages from UAE Microbiome 2023 conference organizing committee coordinator

I extend a warm welcome to all of you to the international conference, ***“Microbiome: Human, Plant, and Environmental Health - Applications and Challenges (UAE Microbiome 2023).”*** As a Conference Organising Committee Coordinator, I am both honored and delighted to witness the overwhelming response to this conference and to have the opportunity to bring together such a diverse and talented group of researchers from around the world, all working towards advancing our understanding of the microbiome and its relevance to one health. Your presence at this erence is a testament to your unwavering commitment to advancing knowledge and innovation in the microbiome, and I want to express my heartfelt appreciation.

The conference theme, “Microbiome and One Health,” is particularly fitting for this gathering, as we convene during COP2028 in Dubai. Moreover, the microbiome research community in the Middle East, especially in the UAE, is growing rapidly. Therefore, it is both compelling and essential to convene like-minded researchers to foster the exchange of innovative ideas and facilitate collaborative connections. This conference promises to be a platform for insightful discussions, meaningful collaborations, and the exchange of groundbreaking ideas, including various emerging aspects of the microbiome.

Our esteemed scientific committee, in collaboration with session chairs, has meticulously curated a lineup of engaging talks from several distinguished speakers and presenters. These sessions will cover a wide range of topics, spanning from cutting-edge research to practical applications of microbes. I strongly encourage you to actively participate in these sessions and to share your perspectives, as it is your contributions that will truly make this event exceptional.

Beyond the formal program, we have also organized various networking opportunities, poster sessions, and social events to facilitate connections and collaborations among participants. I urge you to make the most of these opportunities to expand your professional network and establish lasting connections.

I would like to extend my heartfelt gratitude to our sponsors, the dedicated members of the organizing committee, and our invaluable volunteers. Without their generous contributions, we would not have been able to achieve such a remarkable response, with a record number of abstract submissions and participants. Your unwavering dedication and hard work have been instrumental in shaping this event into what it is today. I eagerly anticipate the opportunity to meet each and every one of you and share in the excitement of UAE Microbiome 2023. I hope that you will not only find the conference content enriching but also renew old friendships, forge new collaborations with fresh ideas, and, above all, have a wonderful time in the UAE. Once again, I extend a warm welcome to UAE Microbiome 2023, and I look forward to embarking on this enlightening journey together.

Warm regards,
Sunil Mundra

Messages from UAE Microbiome 2023 conference scientific committee coordinator

It is with immense pleasure I welcome you all at the UAE Microbiome 2023 conference in Abu Dhabi. The microbiome, comprising a community of microorganisms such as bacteria, fungi, and viruses inhabiting specific environments, exerts significant influence over the One Health sector. Over recent years, research within various microbiome disciplines has witnessed remarkable growth, owing to their link to a multitude of intricate diseases affecting not only humans but also other animals, plants, and the broader environment. Consequently, it becomes imperative to bring together experts in this field, fostering a platform for the sharing of exciting discoveries, dialogue on challenges and constraints, and the exchange of groundbreaking concepts.

In my role as the coordinator of the Scientific Committee for this conference, I am thrilled by the overwhelming response from researchers across the microbiome spectrum. Our participants hail from diverse geographical locations and encompass a wide array of individuals, including esteemed scientists, representatives from biotechnology industries, educators, budding researchers, as well as enthusiastic and dynamic students.

I firmly believe that this conference will offer a unique opportunity for participants to learn from researchers working in various microbiome disciplines, ultimately advancing our understanding of the complexities of different microbiomes and their relevance to the One Health domain.

I wish to express my deep gratitude to all the committees for their efforts in bringing this exceptional platform to the United Arab Emirates.

Warm regards,
Dr. Mohammad Tauqeer Alam

هيئة أبوظبي للزراعة والسلامة الغذائية
ABU DHABI AGRICULTURE AND FOOD
SAFETY AUTHORITY

The Abu Dhabi Agriculture and Food Safety Authority (ADAFSA) is a governmental organization that safeguards the safety and quality of food and agricultural products in Abu Dhabi, UAE. Established in 2008, ADAFSA diligently monitors the entire food chain, from production to consumption, to uphold public health. It develops and enforces stringent food safety regulations, conducts thorough inspections of food establishments, and ensures adherence to international standards. Beyond its food safety mandate, ADAFSA also fosters sustainable agriculture and advances the growth of the agricultural sector in Abu Dhabi. The agency offers farmers technical expertise, training, and financial support to enhance their production and marketing capabilities. By guaranteeing the safety and excellence of food and agricultural products, ADAFSA assumes a vital role in safeguarding public health and bolstering the economic progress of Abu Dhabi.

مركز خليفة للتقانات الحيوية والهندسة الوراثية
Khalifa Center for Genetic Engineering & Biotechnology

His Highness Sheikh Mansour bin Zayed Al Nahyan, the Deputy Prime Minister and Minister of Presidential Affairs of the United Arab Emirates, inaugurated the Khalifa Center for Biotechnology and Genetic Engineering (KCGEB) in 2014. The researchers at the center diligently focus on the cultivation of agricultural crops endowed with the ability to withstand environmental stress within the UAE. This objective is accomplished by generating profound scientific knowledge through applied research. Furthermore, the center dedicates its efforts to cultivating crops possessing favorable agricultural characteristics, thereby augmenting the economic value of domestically produced crops. The KCGEB maintains a strong affiliation with UAE University, resulting in manifold benefits. Notably, this collaboration has significantly bolstered the country›s scientific and research capabilities in the fields of genomics, biotechnology, and genetic engineering. Moreover, the center has assumed a pivotal role in advancing the nation›s vision for 2021 and associated strategic plans pertaining to science and food security.

UAEU
جامعة الإمارات العربية المتحدة
United Arab Emirates University

The United Arab Emirates University (UAEU) is a distinguished and research-intensive university located in Al Ain, Abu Dhabi, UAE. Established in 1976 by the late Sheikh Zayed Bin Sultan Al Nahyan, UAEU holds the distinction of being the UAE›s first and oldest national university, renowned as one of the top educational institutions in the region. The university provides a wide range of undergraduate and graduate programs across diverse fields, encompassing engineering, business, humanities, social sciences, and natural sciences. UAEU is dedicated to delivering a world-class education to its students while driving research and innovation to contribute to the development of the UAE and beyond. The Biology Department, founded in 1977, has experienced significant evolution. In 2019, the department updated its curriculum to incorporate two areas of specialization: Cellular and Molecular Biology (CMB) and Ecology and Organismal Biology (EOB), granting BSc, MSc, and PhD degrees. With cutting-edge research laboratories and equipment, the department boasts a strong research orientation, with faculty members securing competitive research grants and conducting both fundamental and applied research security in various disciplines of biology.

MEET THE SPEAKERS

Prof. Peer Bork
Director European Molecular Biology Lab
(EMBL), Heidelberg, Germnay

Prof. Leho Tedersoo,
University of Tartu,
Estonia

Prof. Trevor Lawley
Sanger Institute,
UK

Prof. Alexandre S. Rosado
King Abdullah University of Science
and Technology, Saudi Arab

Dr. Kasthuri J Venkateswaran,
The National Aeronautics and Space
Administration (NASA) – Jet Propulsion
Laboratory (JPL), Pasadena, CA, USA

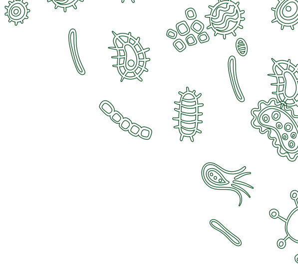
Prof. Jingyuan Fu,
University Medical Centre Groningen,
Netherlands

Dr. Shivaji Sisinthy
Director of Research, L V Prasad Eye
Institute, Hyderabad, India

Dr. Souhaila Al Khodor
Director of Maternal and Child Health
Program. Sidra Medicine, BBK University,
Doha, Qatar

Prof. Shady Amin
New York University Abu Dhabi, UAE

Prof. Hani El-Nezamy
Deputy Director of the School of Biological Sciences
University of Hong Kong

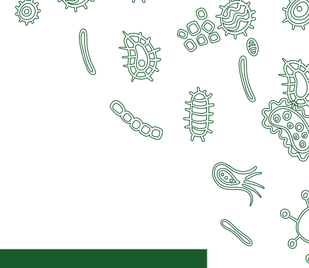


HIGHER COMMITTEE		
Prof. Khaled Amiri	Director of KCGEB, and Chair of Department of Biology, UAEU	Coordinator
HE Maryam Hareb Al Suwaidi	Deputy Director General for Affairs, ADAFSA	Co-Coordinator
Dr. Saeed Ali Al Yammahi	Director of Research and Development Department, ADAFSA	
Dr. Sunil Mundra	Department of Biology, UAEU	
Dr. Mohammad Tauqeer Alam	Department of Biology, UAEU	
Salwa Sultan	Department of Biology, UAEU	

COMMITTEES ORGANIZATION

STEERING COMMITTEE		
Prof. Khaled Amiri	Director of KCGEB, and Chair of Department of Biology, UAEU	Coordinator
Dr. Sunil Mundra	Department of Biology, UAE	Co-Coordinator
Prof. Ranjit Vijayan	Department of Biology, UAEU	
Dr. Mohammad Tauqeer Alam	Department of Biology, UAEU	
Dr. Khaled Hazzori	KCGEB	
Dr. Manish Roorkiwal	KCGEB	
Eng. Safa Hashem	ADAFSA	

ORGANIZING COMMITTEE		
Dr. Sunil Mundra	Department of Biology, UAEU	Coordinator
Dr. Mohammad Tauqeer Alam	Department of Biology, UAEU	Co-coordinator
Prof. Khaled El-Tarabily	Department of Biology, UAEU	
Prof. Synan Abu Qamar	Department of Biology, UAEU	
Prof. Sabir Bin Muzaffar	Department of Biology, UAEU	
Dr. Yusra Al Dhaheri	Department of Biology, UAEU	
Dr. Khalid Muhammad	Department of Biology, UAEU	
Eng. Safa Hashem	ADAFSA	
Asma Al Blooshi	KCGEB	
Salwa Sultan	Department of Biology, UAEU	
Shaikha Al Ameri	KCGEB	



SCIENTIFIC COMMITTEE

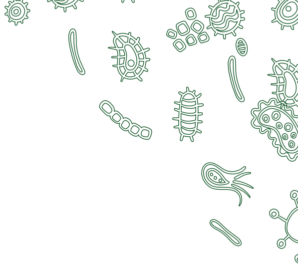
Dr. Mohammad Tauqeer Alam	Department of Biology, UAEU	Coordinator
Dr. Sunil Mundra	Department of Biology, UAEU	Co-Coordinator
Prof. Khaled El-Tarabily	Department of Biology, UAEU	
Dr. Khaled Hazzori	KCGEB	
Dr. Manish Roorkiwal	KCGEB	
Prof. Munawwar Khan	Zayed University, Dubai, UAE	
Prof. Ahmed Yousef	Khalifa University, Abu Dhabi	
Prof. Habiba Al Safar	Khalifa University, Abu Dhabi	
Prof. Dr. Heribert Hirt	KAUST, Saudi Arabia	
Prof. Mohammad Issa El Mouzan	King Saud University, Saudi Arabia	
Prof. Abdullah M. Al-Sadi	Sultan Qaboos University, Oman	
Prof. Ramesh P. Arasaradnam	University of Leicester, UK	
Dr. Tiago Magalhaes	G42 Healthcare, Abu Dhabi	
Dr. Thulani Makhalanyane	University of Pretoria, South Africa	

REGISTRATION AND EVENT MANAGEMENT COMMITTEE

Prof. Synan Abu-Qamar	Department of Biology, UAEU	Coordinator
Dr. Yusra Al Dhaheri	Department of Biology, UAEU	Co-coordinator
Dr. Mayank Gururani	Department of Biology, UAEU	
Dr. Naeema Al Shamsi	Department of Biology, UAEU	
Samira Al Dashti	Department of Biology, UAEU	
Eng. Safa Hashem	ADAFSA	
Eng. Khawla Al Wahshi	ADAFSA	
Rawan Al Junaibi	KCGEB	
Halima Al Meqbali	Department of Biology, UAEU	

LOGISTICS AND TRANSPORT COMMITTEE

Prof. Khaled El-Tarabily	Department of Biology, UAEU	Coordinator
Dr. Oliver Manlik	Department of Biology, UAEU	Co-Coordinator
Dr. Mohammad Yusuf	Department of Biology, UAEU	
Dr. Mohammad Enan	Department of Biology, UAEU	
Dr. Gaber Ramadan	Department of Biology, UAEU	
Shaikha Al Ameri	KCGEB	
Aisha Al shamsi	KCGEB	



FINANCE COMMITTEE

Prof. Sabir Bin Muzaffar	Department of Biology, UAEU	Coordinator
Dr. Sunil Mudra	Department of Biology, UAEU	Co-Coordinator
Raja Al Maskari	Department of Biology, UAEU	
Nasr M Khalifa	KCGEB	
Salwa Sultan	Department of Biology, UAEU	
Dr. Mohammed Taher	Department of Biology, UAEU	

MEDIA AND OUTREACH COMMITTEE

Dr. Khalid Muhammad	Department of Biology, UAEU	Coordinator
Prof. Ranjit Vijayan	Department of Biology, UAEU	Co-Coordinator
Prof. Mohammed Ali Al-Deeb	Department of Biology, UAEU	
Dr. Igor Kryvoruchko	Department of Biology, UAEU	
Dr. Amit Kumar	Department of Biology, UAEU	
Dr. Mohamed Ibrahim Lotfy	Department of Biology, UAEU	
Eng. Khawla Al Wahshi	ADAFSA	
Hussain Al Shamsi	ADAFSA	
Nabila Ahmed	ADAFSA	
Naganeeswaran Sudalaimuthu-asari	KCGEB	
Rafeea Al-Qemzi	UAEU publication department	
Mariam Al Nuaimi	KCGEB	

Day 1:

Tuesday, November 21, 2023

8:00 AM - 8:45 AM	Arrival and Registration	**LOCATION** **Between Hall A and B**
8:45 AM - 9:00 AM	**Welcome note - Khaled Amiri,** Chair, UAE Microbiome 2023	**Hall B**
	SESSION 1: HUMAN AND ANIMAL MICROBIOME **SESSION CHAIRS: Mohammad Tauqeer Alam and Khaled Hazzouri**	**LOCATION**
9:00 AM - 9:40 AM	**I1: Invited talk: Trevor Lawley,** Wellcome Sanger Institute and Microbiotica, Cambridge, UK. ***Talk title: Making Medicines from the Human Microbiome.***	**Hall B**
9:40 AM - 9:55 AM	**O1: Farah Al-Marzooq,** United Arab Emirates University, United Arab Emirates. ***Talk title: Deciphering salivary microbiome signature in Crohn's disease patients with different factors contributing to dysbiosis.***	
9:55 AM - 10:10 AM	**O2: Maha Al-Asmakh,** Qatar University, Qatar. ***Talk title: Metagenomic Analysis of Oral Microbiome during pregnancy.***	
10:10 AM - 10:25 AM	**O3: Abiola Senok,** Mohammed Bin Rashid University of Medicine and Health Sciences, United Arab Emirates. ***Talk title: Investigating the microbial community contaminating mobile phones: A metagenomic sequencing and microbial genotyping study from the United Arab Emirates.***	
10:25 AM - 10:45 AM	**Tea break**	**LOCATION** **Hall A**
10:45 AM - 11:25 AM	**I2: Invited talk: Jingyuan Fu,** University Medical Center Groningen, The Netherlands. ***Talk title: Individual specificity of the human gut microbiome: a new player in personalized medicine.***	**LOCATION** **Hall B**
11:25 AM - 11:40 AM	**O4: Ahmed A. Shibl,** New York University Abu Dhabi, United Arab Emirates. ***Talk title: Multiomics reveals distinct oral microbial functions and metabolic profiles contributing to host phenotypes.***	
11:40 AM - 11:55 AM	**O5: Areej A. Alhhamzi,** Taibah University Saudi Arabia. ***Talk title: Gut Microbiota Profile among Advanced Colorectal Cancer.***	
11:55 AM - 12:10 PM	**O6: Sarma PVSRN,** University of Hyderabad, India. ***Talk title: Dissecting and understanding the seed microbiome differences between cultivated groundnut and wild germplasm accessions.***	
12:10 PM - 1:15 PM	**Lunch**	**LOCATION** **Hall A**

SESSION 2: Human and animal microbiome

SESSION CHAIRS: Ranjit Vijayan and Tiago Magalhaes

		LOCATION
1:15 PM - 1:55 PM	**I3: Invited talk: Souhaila Al Khodor,** Sidra Medicine, Doha, Qatar. ***Talk title: Can the Salivary Microbiome Predict Chronic Diseases? Lessons Learned from the Qatari Population.***	**Hall B**
1:55 PM - 2:25 PM	**I4: Invited talk: Hani El-Nezami,** School of Biological Sciences, The University of Hong Kong. ***Talk title: Gut Microbiome: A potential target for the prevention and treatment of liver diseases.***	
2:25 PM - 2:45 PM	**Tea break**	**Hall A**
2:45 PM - 3:25 PM	**I5: Invited talk: Shivaji Sisinthy,** Prof Brien Holden Eye Research Institute, L V Prasad Eye Institute, Hyderabad, India. ***Talk title: Implications of the gut microbiome on diseases of the human eye.***	**Hall B**
3:25 PM - 3:55 PM	**Flash talks** **F1: Michael Olbrich,** Khalifa University, United Arab Emirates. ***Talk title: MBECS: Microbiome Batch Effects Correction Suite.*** **F2: Natasha Barnes,** CSIR-National Institute of Oceanography, India ***Talk title: Impact of trace metal deposition on marine microbial communities.*** **F3: Raza Muhammad,** Chulalongkorn University, Thailand. ***Talk title: Influence of environment and diet on gut microbiota variation in two subspecies of Macaca fascicularis.*** **F4: Shahana Seher Malik,** United Arab Emirates University, United Arab Emirates. ***Talk title: Decoding microbiome and their antibiotic resistance patterns in a UAE wastewater treatment plant: a wake-up call for effective measures.*** **F5: Haneen Abdullah Al-Saadi,** Sultan Qaboos University, Oman. ***Talk title: In vitro detoxification of aflatoxin B1 by bacterial isolates from the gut of the rice weevil (Sitophilus oryzae L.) (Coleoptera: Curculionidae).*** **F6: Duaa Ahmed Elhag,** Sidra medical and research center, Qatar. ***Talk title: Dynamics of the vaginal microbiome and cytokines levels in women with Gestational Diabetes.***	
3:55 PM - 5:00 PM	**Tea break** + Poster session (F1-F6 and P1-P70)	**Hall A**
5:00 PM - 6:00 PM	**Confernece inaugration ceremony**	**Hall B**
6:00 PM - 7:00 PM	**Plenary talk: Peer Bork,** Director, European Molecular Biology Laboratory (EMBL), Heidelberg, Germany. ***Talk Title: Microbiome analysis for human and planetary health.***	**Hall B**

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Day 2:
Wednesday, November 22, 2023

SESSION 3: Environmental (soil and plant) microbiome
SESSION CHAIRS: Sunil Mundra and Abdullah Al-Sadi

LOCATION

9:00 AM - 9:40 AM
I6: Invited talk: Alexandre S. Rosado,
King Abdullah University of Science and Technology (KAUST),
Kingdom of Saudi Arabia.
Talk title: Making Medicines from the Human Microbiome.

9:40 AM - 9:55 AM
O7: Laura Zucconi,
University of Tuscia, Italy.
Talk title: Unraveling Antarctic Soil Microbial Communities and Environmental Shifts.

9:55 AM - 10:10 AM
O8: Raeid Abed,
Sultan Qaboos University, Oman.
Talk title: Extremophilic microbiome in the Arabian deserts: novel diversity, metabolic processes and a great potential for biotechnology

10:10 AM - 10:25 AM
O9: Shankar Manoharan,
Indian Institute of Technology Jodhpur, India.
Talk title: Ecological engineers of the thar desert: a long-read metagenomics perspective.

Hall B

10:25 AM - 10:45 AM
Tea break
LOCATION
Hall A

10:45 AM - 11:25 AM
I7: Invited talk: Leho Tedersoo,
University of Tartu, Estonia.
Talk title: Diversity and global change vulnerability of the Earth soil mycobiome.

LOCATION

11:25 AM - 11:40 AM
O10: Muhammad Ishtiaq Ali,
Quaid-i-Azam University Islamabad, Pakistan.
Talk title: Exploring the Potential of Organic Waste-derived Biochar for Soil Bioremediation in Diesel-contaminated Environments.

11:40 AM - 11:55 AM
O11: Munawwar Ali Khan,
Zayed University, United Arab Emirates.
Talk title: Halotolerant plant growth-promoting bacteria isolated from avicennia marina alleviate saline stress in radish (raphanus sativus l).

11:55 AM - 12:10 PM
O12: Maged SAAD,
King Abdullah University of Science and Technology (KAUST), Saudi Arabia.
Talk title: Unlocking Nature's Blueprint: The Saudi Soil BioAtlas and its Transformative Impact on Ecosystems towards a Greener Saudi Arabia.

Hall B

12:10 PM - 1:15 PM
Lunch
LOCATION
Hall A

SESSION 4: Environmental (soil and plant) microbiome

SESSION CHAIRS: Synan AbuQamar and Khalid Muhammad

LOCATION

Hall B

1:15 PM - 1:55 PM **I8: Invited talk: Kasthuri J Venkateswaran**
NASA Jet Propulsion Laboratory, California Institute of Technology, Pasadena, CA, USA.
Talk title: Microbes in Space: Lessons Learned.

1:55 PM - 2:10 PM **O13: Khaled Masmoudi**
United Arab Emirates University, United Arab Emirates.
Talk title: Harnessing Plant-Microbiome Interactions for Abiotic stress mitigation in Date Palm.

2:10 PM - 2:25 PM **O14: Majed D. Alotaibi,**
Abu Dhabi Agriculture and Food Safety Authority, United Arab Emirates.
Talk title: Microorganisms Activity for Degrading Chemical Contaminants Displayed in Recycled Water Used for Managed Aquafer Recharged.

LOCATION

2:25 PM - 2:45 PM **Tea break** — **Hall A**

LOCATION

Hall B

2:45 PM - 3:25 PM **I9: Invited talk: Shady Amin,**
New York University Abu Dhabi, United Arab Emirate.
Talk title: The role of the microbiome in coral adaptation to climate change.

3:25 PM - 3:55 PM **Flash talks**

F7: Aditi Pandit,
University of South Bohemia, Czech Republic.
Talk title: Unveiling the Diversity and Specificity of Orchid Mycorrhizal Fungi Associations: Insights from Geographic Regions and Methodological Comparisons.

F8: Balamurugan Sadaiappan,
United Arab Emirates University, United Arab Emirates.
Talk title: Unveiling the microbial tapestry: global diversity and biogeographic patterns of mangrove microbiomes.

F9: Mohamed T. El-Saadony,
Zagazig University, Egypt.
Talk title: Wheat microbiome promotes the defense responses against Fusarium culmorum colonization.

F10: Al Anoud A. Alshamsi,
United Arab Emirates University, United Arab Emirates.
Talk title: Mangrove (Avicennia marina) growth and development are further enhanced by the use of halotolerant plant growth-promoting actinobacteria in conjunction with fish emulsion.

F11: Amal Khalaf Alghamdi,
King Abdullah University of Science and Technology, Saudi Arabia.
Talk title: The Mangrove-Associated Bacteria for Crop Plant Sustainability.

F12: Fabiana Canini,
University of Tuscia, Italy.
Talk title: Responses of soil microbial communities to the spread of invasive alien species in coastal sand dunes.

F13: Komal Shoukat,
Government College Women University, Pakistan.
Talk title: Characterization of Plant Growth Promoting Rhizobacteria (PGPR) for Enhancing Drought Tolerance in Mung Bean Under Variable Moisture Regimes

LOCATION
Hall B

3:55 PM - 5:00 PM **Tea break** + Poster session (F7-F12 and P71-P146)

LOCATION
Hall A

5:00 PM - 5:30 PM **Panel discussion: How to bridge microbiome innovation, funding, and geographical expansion to the UAE?**

Panelist
Khaled Amiri,
Director KCGEB and Chairmen Department of Biology, UAE University
Jeremy Lim,
Co-founder and CEO of AMILI
Johan van Hylckama Vlieg,
Co-founder and CSO of Freya Biosciences
Peter Luke,
Biotech Investor
Sunil Mundra,
Department of Biology, UAE University
Session moderator:
Mohammad Tauqeer Alam,
Department of Biology, UAE University
Session introducer:
Caroline Souchet,
Investment Manager, CE-Ventures

LOCATION
Hall B

5:30 PM - 6:00 PM **Closing ceremony**

CONFERENCE VENUE

The UAE Microbiome Conference 2023 will be held in the Abu Dhabi National Exhibitions Company (ADNEC), which is one of the leading event venues in Abu Dhabi (UAE) and the wider Middle East region. The multi-award-winning venue boasts a state-of-the-art facility with over 133,000 square meters of floor space, making it one of the largest exhibition centers in the Middle East. With its strategic location in the heart of the capital city of Abu Dhabi, make it as an excellent place to host events. There are several hotels located within walking distance of ADNEC, making it easy for attendees to stay close to the venue

TRAVELLING TO UAE BY AIR

If you are travelling to UAE by air and need to access ADNEC, there are several options available to you, depending on which airport you are arriving at. Public transportation options are available in UAE but may take longer and require more transfers and may not be as comfortable.

From Abu Dhabi International Airport (AUH): The Abu Dhabi International Airport is the closest airport to ADNEC, located just a 15-minute drive away. You can take a taxi from the airport directly to ADNEC, or you can rent a car and drive yourself. There are also public transportation options available, including buses and the Abu Dhabi Metro, which has a station at ADNEC.

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Abu Dhabi International Airport

Dubai International Airport

Sharjah Airport

IMPORTANT DATES TO REMEMBER

Abstract submission starts:	June 1, 2023
Registration starts:	July 15, 2023
Abstract submission closes:	August 21, 2023
Abstract acceptance date:	September 25, 2023
Early-bird Registration ends:	October 9, 2023
Late Registration ends:	November 6, 2023

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The United Arab Emirates (UAE) is a popular tourist destination known for its stunning architecture, luxurious shopping malls, and cultural heritage. Here are some of the top attractions that tourists can enjoy during their visit to the UAE.

Attraction in Abu Dhabi (www.visitabudhabi.ae)

Abu Dhabi is the capital city of the United Arab Emirates and one of the most popular tourist destinations in the Middle East. The city boasts numerous attractions such as Sheikh Zayed Grand Mosque, Qasr Al Watan, Ferrari World, Louvre Abu Dhabi, Abu Dhabi Corniche.

SHEIKH ZAYED GRAND MOSQUE

Attraction in Al Ain

Al Ain is a city located in the Emirate of Abu Dhabi, United Arab Emirates. It is the second-largest city in the emirate, after Abu Dhabi, and is known for its rich cultural heritage, stunning natural beauty, and modern infrastructure. Places to visit in Al Ain are Al Ain Oasis, Jebel Hafeet, Qasr Al-Muwaji and Al Ain Fort.

AL AIN FORT

Attraction in Dubai

Dubai is a city known for its luxurious shopping centers, ultramodern architecture, and lively nightlife scene. The city is home to some of the world's most iconic landmarks, such as Burj Khalifa, Dubai Mall, Palm Jumeirah, Dubai Miracle Garden, Desert Safari, Dubai Museum of Future etc.

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The process of obtaining a visa for the United Arab Emirates (UAE) can vary depending on the applicant's nationality and the purpose of their visit. It's important to note that citizens of some countries, including GCC countries, may be eligible for visa-free entry or a visa on arrival in the UAE. However, it's always best to check the latest visa requirements and regulations before you travel. Please visit this link (https://visitabudhabi.ae/en/plan-your-trip/essential-info/getting-a-visa) for more information. The conference organizer can issue the letter for the VISA application after completing the registration and payment of the fee.

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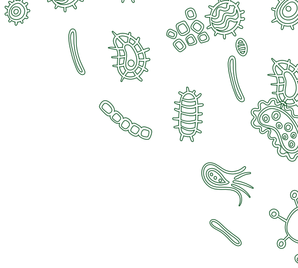

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UAE Microbiome 2023 Organisers

Plenary talk: Microbiome analysis for human and planetary health

Bork, P.[1]

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ABSTRACT

Environmental sequencing, that is metagenomics, has become a major driver for uncovering microbial biodiversity and increasingly also for molecular functionality on our planet. Based on computational methods and resources, often developed in our group, here I (i) introduce into our work on the gut microbiome, arguable the best-studied microbial community, serving as a model for other habitats. Metagenome-wide association studies enable bioinformatics-driven hypothesis generation, which we complement with collaborators by experimental approaches *in vitro*, *ex vivo* and *in vivo*, to pave the way for diagnostics and medication guidance. I (ii) further show how to apply the underlying concepts to other habitats, like ocean and soil, to arrive at a basic understanding of microbial life in context on earth. For this, we have developed a planetary-scale microbial resource that we are starting to mine, e.g. for gene evolution at global sale or fluxes of molecular functions across habitats. We complement analysis of public data with an ambitious, continental-scale international expedition that traverses European coastlines (TREC). It crosses various scales and brings molecular biology to ecosystems research in an unprecedented way, with extensive measurements of environmental factors. Analyzing and integrating respective data will provide base-line knowledge to prepare for applications. In analogy to microbial diagnostics and treatment for human health, we foresee microbiome-informed bioindicator and remediation strategies towards improving planetary health.

Keywords: Metagenomics, Gut microbiome, Gene evolution, Bioindicators

I1: Making Medicines from the Human Microbiome

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ABSTRACT

The human body is an ecosystem colonized by diverse microbes with beneficial functions that impact our growth and development, disease resistance and clinical response to life saving medicines. Pathogenic imbalances in the human microbiome, caused by things like antibiotics, infection, poor diet, genetics, can lead to a variety of diseases and poorly understood syndromes. High resolution metagenomic methods can now be used to profile the microbiome composition and functions to identify bacterial strains that are ‘beneficial” or “pathogenic” to human health. The development of technologies to target culture bacteria from the human microbiome allows us to isolate specific bacterial strains directly from patients for experimental validation and mechanistic studies. Based on these technologies and methods we developed a “patient first” microbiome discovery platform to develop orally delivered live bacterial products (medicine made from defined consortia of bacterial strains) to treat patients with cancer or autoimmune disease.

Keywords: Pathogenic imbalances, High resolution metagenomics, “Patient first” platform

I2: Individual specificity of the human gut microbiome: a new player in personalized medicine

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ABSTRACT

The human gut microbiome refers to the collective genomes of tens of thousands of the microorganisms that reside in the human gut. Through an investigation of a prospective, population-based LifeLines cohort, we have revealed a remarkable inter-individual variation in the microbial composition and functional profile. Systematic genetic and epidemiological association analyses have identified over 200 genetic, host, dietary, and environmental factors that contribute to the individual specificity of the gut microbiome. Additionaly, we have conducted comprehensive omics integration analyses to recover the role of the gut microbiome, its interaction with the host's genetics and environment, in the human metabolism and immune response. Our findings have prompted a reconsideration of the definition of complex traits, which may result from interactions among genetics, the gut microbiome, and the environment. It is evident that the gut microbiome is emerging as a significant player in personalized medicine.

Keywords: Gut Microbiome Specificity, Microbial interaction

I3: Can the Salivary Microbiome Predict Chronic Diseases? Lessons Learned from the Qatari Population

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ABSTRACT

The human microbiome comprises various microorganisms found in the gut, oral cavity, skin, and reproductive organs. It forms a complex and balanced ecosystem consisting of trillions of microbes. Despite being the second most diverse ecosystem after the gut, the Salivary Microbiome (SM) remains relatively unexplored in terms of its diagnostic and prognostic role, particularly in chronic diseases such as Cardiovascular Diseases (CVD), Type 2 Diabetes (T2D), and Hypertension (HTN). This study aims to elucidate significant microbial markers present in saliva that can predict chronic diseases within the Qatari population.

Saliva samples were collected from 2974 Qatari participants, obtained from Qatar BioBank. The cohort was categorized into three groups based on their CVD risk scores: High (HR), moderate (MR), and low (LR). Participants were also classified as non-diabetic, pre-diabetic, or diabetic based on their HbA1C levels, and their blood pressure determined whether they fell into the Normal, Elevated, Stage 1, or Stage 2 category. The composition of the SM was analyzed using 16S-V1-V3-rDNA libraries, which were sequenced and evaluated through the QIIME-pipeline. Machine Learning (ML) techniques were employed to identify SM-based predictors of chronic diseases.

Our findings revealed that Desulfobulbus, Prevotella, and Tissierellaceae were common indicators of an increased risk for CVD, while Anaerotruncus and Enterobacteriaceae were associated with T2D. Bacteroides and Atopobium were identified as significant members of the hypertensive groups. This study represents the first extensive assessment of the SM in a large Qatari population cohort. Furthermore, it sheds light on specific microbial signature changes associated with chronic diseases. Overall, this research represents a significant stride towards utilizing saliva as a diagnostic marker for various diseases.

Keywords: Salivary Microbiome, Machine learning, Qatari, Qatar biobank, Diabetes

I4: Gut Microbiome: A potential target for the prevention and treatment of liver diseases

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ABSTRACT

Hepatocellular carcinoma (HCC) is the fifth most prevalent cancer and the third leading cause of all cancer-related deaths in the world. More than 600,000 deaths are reported globally each year. Approximately 75% of HCC patients are concentrated in Asia, but a recent trend of rising rates of HCC has been reported in several developed countries including Europe and the United States. Standard treatments involve high costs. For example, molecular targeted therapy using Sorafenib as recommended by NCCN/AASLD/JSH/ESMO Guideline is expensive, with an average cost ~US$6,000 per month, so it can only be performed in countries with extensive financial resources for healthcare services. Meanwhile, probiotics, bacterial cocktails, may be commonly found in dairy food products, and the cost is only ~US$86.00 per month for buying patented commercial products such as VSL#3. Thus, probiotics-based therapeutics may offer a cheaper approach in HCC intervention. Using our experience from studies on probiotic-aflatoxin interaction we want to demonstrate the problems associated with compiling evidence in support of health claims for probiotics. This presentation describes a series of studies showing the path from laboratory-based findings *in vitro* and animal experiments to confirm the *in vitro* findings *in vivo* , to field studies in human subjects. We demonstrated that oral feeding of a novel probiotic mixture “Prohep”, which comprised viable *Escherichia coli strain Nissle* 1917 (EcN), heat-inactivated Lactobacillus rhamnosus strain GG (LGG) and VSL#3, was effective in reducing subcutaneous HCC growth in C57BL6/N mice, especially when given 1 week in advance of tumor injection than in treatment model (probiotics administered at the same day of injection). This study is first to provide evidence to demonstrate oral feeding of probiotics mixture may have beneficial effect to subcutaneous liver cancer development. IL-17+cells were important in promoting tumor growth and that Prohep feeding affect tumor growth and angiogenesis via IL-17 modulation in tumor microenvironment. Moreover, our study for the first time demonstrated that modulating the composition of the gut microbiota may have a significant impact on the progress of extra-intestinal tumors. While the role of probiotics in the development of gut-related disorders is well documented, our study was the first one to show such an impressive response, by the use of probiotics, in hepatocellular carcinoma. Furthermore, we proposed a mechanism by which the altered bacterial community impacts the progression of HCC, which makes us believe that we could apply the same principles in other cancers.

Keywords: HCC, Probiotics-based therapeutics, Prohep, Gut microbiota

I5: Implications of the gut microbiome on diseases of the human eye

Shivaji, S.[1]

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ABSTRACT

Microbiome refers to the trillions of bacteria, fungi and viruses that share our body space. The gut with 100 trillion bacteria and approximately 3.3 million genes is the most enormous of the human microbiomes. The gut bacterial microbiome aids in digestion, immune protection and in the production of vitamins and anti-inflammatory molecules. But, under conditions of high-fat diet, excessive sugar intake, sedentary lifestyle, excessive antibiotics use, diseased conditions etc. the balance in the microbiome tilts from a preponderance of 'beneficial' to 'harmful' bacteria. This imbalance in the gut microbiome is referred to as "dysbiosis".

Dysbiosis has been implicated in several intestinal diseases like obesity, Crohn's disease, inflammatory bowel disease, Diabetes Mellitus etc., and neurological diseases like Alzheimer's, Parkinson's diseases etc. But little is known about the role of gut microbiome dysbiosis and ocular infectious diseases. Using fecal material from healthy controls and from individuals with bacterial keratitis, fungal keratitis, uveitis and diabetic retinopathy, DNA was extracted, and bacterial microbiomes were generated. Analyses of the microbiomes indicated dysbiosis in the gut microbiomes in individuals with ocular diseases at the phylum and genera level compared to the control microbiomes. Dysbiosis was also confirmed by PCoA analysis. Functionally, the gut microbiomes of the diseased individuals showed an increase in bacteria with pro-inflammatory (*Prevotella copri*) and pathogenic bacteria (*Treponema* Spp.) and simultaneous decrease in probiotic (*Lactobacillus ruminis*) and anti-inflammatory (*Faecalibacterium prausnitzii*) bacteria. Subsequent studies also demonstrated that the ocular surface microbiomes (using conjunctival swabs and corneal scrapings) also showed dysbiosis in individuals with keratitis. These studies implied that dysbiosis in both gut and ocular microbiomes influence ocular diseases. But it is not clear whether dysbiosis in the microbiomes is the cause or effect of the disease? So also, it is not known whether ocular microbiome dysbiosis is modulated by the gut microbiome dysbiosis? Microbiome studies could form the basis to mitigate inflammatory diseases of the eye by probiotic therapy or fecal microbiota transplantation.

Keywords: Microbiome dysbiosis, Ocular diseases

I6: Life at the Edge: Innovative, Evolutionary and Biotechnological Survey of Extreme Microbes from Saudi Arabia

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ABSTRACT

Microbial life represents most of Earth's biodiversity and regulates the primary biogeochemical cycles on our planet. Microbiome science aims to advance the understanding of microbial communities (microbiomes) for health applications, food production, and environmental restoration to benefit individuals, communities, and the planet. Among all the different applications of microbiome science, the study of extremophilic microorganisms allows us to understand the limits of life on our planet and, within the multidisciplinary field of Astrobiology, can provide clues about the origin, evolution, distribution, and future of life on planet Earth and possibly in other parts of the universe. In nature, over billions of years, highly specialized microbes have developed strategies to live in extreme conditions and to catalyze almost all known renewal processes. These corresponding bioproducts could form the basis of modern biotechnology. In this lecture, I will share my experience studying some extreme ecosystems in Saudi Arabia (hydrothermal vents, extreme Red Sea mangroves, hot springs, deserts, and volcanoes), with a focus on interdisciplinary research using cutting-edge techniques to apply extremophiles in Ecology, Biotechnology, and Astrobiology.

Keywords: Extremophilic microorganisms, Saudi Arabia

I7: Diversity and global change vulnerability of the Earth soil mycobiome

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ABSTRACT

Fungi play pivotal roles in ecosystem functioning, but little is known about their global patterns of diversity, endemicity, vulnerability to global change drivers and conservation priority areas. We applied the high-resolution PacBio sequencing technique to identify fungi based on a long DNA marker that revealed a high proportion of hitherto unknown fungal taxa. We used a Global Soil Mycobiome consortium dataset to test relative performance of various sequencing depth standardization methods (calculation of residuals, exclusion of singletons, traditional and SRS rarefaction, use of Shannon index of diversity) to find optimal protocols for statistical analyses. Altogether, we used six global surveys to infer these patterns for soil-inhabiting fungi and their functional groups. We found that residuals of log-transformed richness (including singletons) against log-transformed sequencing depth yields significantly better model estimates compared with most other standardization methods. With respect to global patterns, fungal functional groups differed in the patterns of diversity, endemicity and vulnerability to main global change predictors. Unlike α-diversity, endemicity and global-change vulnerability of fungi and most functional groups were greatest in the tropics. Fungi are vulnerable mostly to drought, heat, and land cover change. Fungal conservation areas of highest priority include wetlands and moist tropical ecosystems.

Keywords: Soil-inhabiting fungi, Fungal conservation

I8: Microbes in Space: Lessons Learned

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ABSTRACT

In the coming years, expansion of crewed space exploration beyond low Earth orbit, to the Moon and on to Mars are planned by the National Aeronautics and Space Administration (NASA), along with other international space agencies and commercial partners. This involves designing new space habitats for both interplanetary travel and surface habitation. In this new era of human expansion in the universe, thorough examination of microbiome of the closed habitats is necessary to understand how they accumulate, persist, survive, and their molecular mechanisms to impact on human health and spacecraft infrastructure (biocorrosion). Such basic understanding will also enable development of novel technologies to contain or eradicate these problematic microorganisms.

Safety and success of the future human missions rely on reducing and monitoring the number of pathogenic microorganisms associated with the crew habitats. Since contribution of the microbial contamination is primarily by the inhabitants, contamination of these facilities is unavoidable. It has been well documented that number of microbes is exceedingly more than human cells and human host them since we live on and need them. In general, these microorganisms are benign and their presence is necessary; majority of them are beneficial to the metabolism/digestion/conversion of nutrients; even protect human from pathogens. On the contrary, problematic microbes (pathogens and metal eating members) are harbored by human, transported, and dispersed in the living quarters. It is virtually not practical and unrealistic to eradicate these contaminants and will pose a direct threat to the closed habitat and the crew. However, to be successful for the future crewed mission, novel engineering mechanisms are needed for the habitat construction to manage microbial ecology as that are the recent trends in hospital and medical instrument design. Subsequently, continuous monitoring of the remaining microbial populations will be critical.

Studies on the microbiome of homes, offices, classrooms, museums, and hospitals revealed an assemblage of bacteria, fungi, viruses, and protozoa which are distinctive to these indoor environments. These assemblages are influenced by a variety of factors such as building design, ventilation, humidity, air pressure and flow, occupant numbers or activities performed. In addition to the habitat types and maintenance, susceptibility to allergies, infectious diseases, or sick building syndrome will impact human health. Hence, minimizing and monitoring closed cabin microbiome is more important for astronauts for their long space travel since their immune system is altered due to spaceflight conditions.

In this talk, microbial communities associated with analogue space habitats (underwater aquatic and terrestrial), crew resupply vehicle that transport materials from Earth to ISS, environmental surfaces and air particulates of ISS, crew surfaces and saliva, as well as spacesuit microbiomes are presented. Presence of microorganisms isolated from these closed habitats that possess potential virulence, enhanced antimicrobial resistance, and their persistence in the closed habitats as well as their significance are discussed.

The work described in this publication was carried out at JPL under a contract with NASA.

Keywords: Space exploration, Microbial ecology, Space habitats, Pathogens, Biocorrosion

I9: The role of the microbiome in coral adaptation to climate change

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ABSTRACT

Corals live in a complex, multipartite symbiosis with diverse microbes across kingdoms, some of which are implicated in vital functions that are critical for coral survival, such as those related to resilience against climate change. However, knowledge gaps and technical challenges limit our understanding of the nature and functional significance of complex symbiotic relationships within corals. In this talk, I will provide an overview of the complexity of the coral microbiome focusing on the bacterial microbiome. In specific, the genus *Endozoicomonas* has received significant attention lately as coral symbionts though their true symbiotic role for the coral is mostly unknown. Using shotgun metagenomics and metabolomics, I will show how *Endozoicomonas* symbiotic with the coral *Acropora tenuis* manipulates coral holobiont steroid hormones, akin to *Mycobacterium* spp. in the human microbiome. These steroid transformations are believed to enable the coral to withstand thermal stress in the Arabian Gulf.

Keywords: Coral microbiome, Symbiosis, Endozoicomonas, Thermal stress

O1: Deciphering salivary microbiome signature in Crohn's disease patients with different factors contributing to dysbiosis

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ABSTRACT

Crohn's disease (CD) is a chronic inflammatory disorder of the gut. An imbalanced microbiome can predispose to many diseases including CD. The role of oral dysbiosis in CD is poorly understood, with limited reports on species alterations. We aimed to explore factors contributing to dysbiosis of the salivary microbiome in CD, and correlate microbiota alterations to the level of inflammation. Saliva samples were collected from 40 CD patients and 40 healthy controls (HC). Microbiome was analyzed by sequencing the entire 16S rRNA gene using Oxford nanopore technology. Inflammatory biomarkers were measured by enzyme-linked immunosorbent assay. Five dominant species were significantly enriched in CD and depleted in HC, namely Veillonella dispar, Megasphaera stantonii, Prevotella jejuni, Dolosigranulum pigrum and Lactobacillus backii. Oral health was confirmed to have a significant impact on the microbiome. Furthermore, disease activity, duration and frequency of relapses impacted the oral microbiota with distinct species alterations. Treatment with biologicals led to the emergence of a unique species called Simonsiella muelleri. Combination of immunomodulatory agents with biologicals significantly increased multiple pathogenic species such as Salmonella enterica, Escherichia coli, Klebsiella pneumoniae and Pseudomonas aeruginosa. A significant loss of diversity in CD was shown by multiple diversity indices. A significant negative correlation was found between gut inflammatory biomarkers (particularly calprotectin) and α-diversity, suggesting more inflammation associated with diversity loss in CD. Dysbiosis was evident in CD patients, with unique microbiota signatures and perturbed species that can serve as disease biomarkers, or potential targets for microbiota modulation. The interplay of various factors collectively contributed to dysbiosis, although each factor had a unique impact on the microbiome. The emergence of pathogenic bacteria in the oral cavity of CD patients is alarming since they can disturb gut homeostasis by various mechanisms such as swallowing, or hematogenous spread of microbiota, their metabolites or generated inflammatory mediators.

Keywords: Crohn's disease, salivary microbiome, dysbiosis, oral

O2: Metagenomic Analysis of Oral Microbiome during pregnancy

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ABSTRACT

Normal pregnancy represents a unique, transient, and dynamic state of altered physiology and immune function. Recent evidence highlight the significant role of gut microbiota on maternal metabolism supporting fetal growth and preparing the body for lactation. Changes in the composition of gut microbiota over the course of pregnancy are well documented. The oral cavity houses the second largest and diverse microbiota after the gut harboring over 700 species of bacteria. Oral microbiome play a crucial role to health as it can cause both oral and systemic diseases. Dysbiosis in oral microbiome have been associated with dental and periodontal diseases as well as diabetes, Hypertension and cancer. Little is known about the composition and role of the oral microbiota during pregnancy. In this study, we collected saliva samples from second and third trimester pregnant women participating at Qatar Birth Cohort study at Qatar BioBank. Genomic DNA was extracted from saliva samples and subjected to 16S rRNA amplification using ONT 16S barcoding kit and libraries sequenced using a flongel on a GridION. We found no difference in alpha and beta diversity between the trimesters. There was decrease in abundance in *Streptococcus mitis*, *Streptococcus sanguinis* and *Catonella morbi* species and an increase in *Campylobacter concisus* between the two trimesters. These changes in bacterial species may reflect the physiological nature of pregnancy throughout the second and third semester.

Keywords: pregnancy, microbiome, Qatar Biobank.

O3: Investigating the Microbial Community Contaminating Mobile Phones: A Metagenomic Sequencing and Microbial Genotyping Study from the United Arab Emirates

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ABSTRACT

Mobile phones (MPs) of health care workers (HCWs) are high touch surfaces which can act as fomites contributing to the dissemination of microbes. To address the lack of data from the United Arab Emirates (UAE), this point prevalence study was conducted at the Emergency care unit of a tertiary care facility in Dubai to investigate the microbial community present on HCWs' MPs and environmental sites (Env) in the unit. Microbial culture (for MP and Env swab samples), Shotgun metagenomic analysis (pooled Env swab samples and for each swabbed MP) and DNA microarray (for Staphylococcus aureus isolates only) were carried out. Bacterial positive culture was detected in 33 (94.2%) MPs with a preponderance of *Staphylococcus epidermidis* (n/N=18/35), *Staphylococcus hominis* (n/N=13/35) and *Staphylococcus haemolyticus* (n/N=7/35). Two methicillin sensitive and three methicillin resistant *S. aureus* (MSSA/MRSA) isolates were detected while DNA microarray characterized these as CC15-MSSA, CC361-MSSA, CC1-MRSA-[V/VT+fusC+ccrAB1] and CC1-MRSA-[V+fusC+ccrAB1] (n=2). Of note, there was a single pan-drug resistant carbapenemase producing *Acinetobacter baumanii*. Shotgun metagenomic analysis revealed a highly dominant presence of *Pseudomonas aeruginosa* in all MPs and environmental samples. The sequencing data revealed an important *P. aeruginosa* antimicrobial specific resistome and virulome with genes encoding for antibiotic efflux pump systems and virulent motility, adherence, aggregation and biofilm formation respectively. *P. aeruginosa* bacteriophages were found across all MPs and Env samples. *Malassezia* and *Aspergillus* spp were the predominant fungi detected and 14/35 MPs and one environmental sample harbored protists. In conclusion, the MPs of HCWs were found to be important fomites for potentially pathogenic and highly drug resistant microbes. The potential risk of transference of these pathogens to patients is a concern and the introduction of highly efficient phone sanitization methods is recommended to enhance global infection control in health care settings.

Keywords: Shotgun metagenomics, Environmental microbiome, Mobile phones, Healthcare workers, United Arab Emirates

O4: Multiomics reveals distinct oral microbial functions and metabolic profiles contributing to host phenotypes

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ABSTRACT

The UAE Healthy Future Study is a large population-based study designed for investigating disease factors of high public health relevance. The prevalence of obesity in the UAE and the region rapidly increased since its shift to a more urbanized society, posing significant health challenges. Emerging evidence links the oral microbiome to several metabolic disorders, including obesity. In this study, we employed a multi-omics approach to identify the biological mechanisms by which oral microbiota contribute to obesity in the Emirati population. Strain-level microbial community profiling based on metagenomics revealed 26 differentially abundant bacterial species between the obese and non-obese groups. Among ~1500 metagenomically assembled genomes, 74 had an unknown species-level taxonomy and no clustered representatives, potentially representing novel species. Functional profiling highlighted several differentially depleted health-promoting pathways in the obese group, such as vitamin biosynthesis pathways and nitrate reduction, while diseasepromoting pathways such as pyruvate fermentation and pyrimidine degradation were enriched in the obese group. In addition, we detected metabolites such as lactate and uracil which corroborate the enrichment of fermentation and degradation pathways in the obese group. Remarkably, gene enrichment analysis showed gene functions associated with vitamin B12 and other co-factor biosynthesis pathways, exclusively enriched in non-obese Proteobacteria MAGs. Next, we correlated functional pathways and abundant taxa with ~60 blood and urine biomarkers and found glycemic and lipid markers such as HbA1c, triglyceride, and the atherogenic index of plasma negatively associated with healthpromoting pathways and positively associated with BMI. Interestingly, these clinical markers, along with glucose and BMI were strongly associated with a Streptococcus salivarius strain, which was concurrently negatively associated with health-promoting pathways. Our findings hint to the potential role of specific taxa and metabolites as biomarkers for obesity and lay the foundation for utilizing the oral microbiome as a diagnostic tool, presenting a promising avenue for personalized healthcare.

Keywords: oral microbiome, metagenomics, obesity, metabolomics, microbial pathways

O5: Gut Microbiota Profile among Advanced Colorectal Cancer

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ABSTRACT

The prevalence of colorectal cancer (CRC) is worldwide health concern. Studies on the intestinal microbiota have demonstrated the significant role of gut bacteria in many types of cancer, especially CRC. The objective of this study is to evaluate the risk factors for CRC, with an emphasis on diet quality and fat intake. It also investigates the role of dysbiosis in the gut microbiota and its association to the development of CRC. A cohort of 25 advanced CRC patients and 25 healthy volunteers were included in the study. A modified version of the short-form food frequency questionnaire (SFFFQ) and a modified version of a previously used food frequency questionnaire (FFQ) were used, respectively, to evaluate the quality of the participants' diets and their intake of fat. Using 16S ribosomal RNA gene sequencing and clustering analysis, the diversity of fecal bacteria was studied. To evaluate the relationship between diet quality and fat intake and the most prevalent bacteria in CRC, simple linear regression was performed. According to genera abundance, CRC was found to have enriched populations of Streptococcus, Lactobacillus, Klebsiella, Intestinibacter, Ralstonia, Alistipes, Pseudomonas, and Veillonella ($p<0.05$). In CRC patients, only Alistipes sp. was found to be positively associated with a poor diet ($p=0.029$; R-square=0.47). These findings suggested that the development of advanced CRC tumors may be influenced by the imbalance of intestinal bacteria. To clarify the exact involvement of the gut microbiota in CRC and its possible implications for diagnostic, preventive, and treatment techniques, more study is required. Keyword: Colorectal cancer (CRC), Microbiota, 16s rRNA, Genome, Dysbiosis, Bacteria, Operational taxonomic unit.

O6: Dissecting and understanding the seed microbiome differences between cultivated groundnut and wild germplasm accessions.

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ABSTRACT

A comprehensive understanding of the differences between the microbiomes of wild and cultivated germplasm accessions is crucial for both conservation initiatives and agricultural practices. Wild relatives that grow in their native habitats are exposed to a variety of environmental factors. These habitats generally exhibit microbial communities that are distinguished by higher levels of variability and complexity. We attempted to study the microbiome variation among wild relatives of groundnut germplasm vis-à-vis cultivated ones. The wild relatives (32) originated from Bolivia, Argentina, Brazil, and Paraguay were included. In addition, we included landraces (10) from Egypt, Zimbabwe, USA, and India. Further indigenous varieties and released cultivars were also included. Metagenomic DNA from seeds was amplified for bacteria (16s), and sequenced using MiseqIllumina platform for specific V3-V4 region. A comprehensive analysis of sequences for both wild and domesticated ones revealed a distinct microbial community. In terms of species composition and geographic origin, the study reveals a higher level of beta diversity in cultivars, but a lower level of alpha diversity (measured by Chao1 index). These results indicate that agricultural practices have a discernible effect on the seed microbiome. LEFSe analysis revealed the indicator species and observed that a diverse bacterial community are present in wild relatives, landraces, and modern cultivars regardless of their origins. Further, ANOSIM analysis reveals that the seed microbiomes of all native species are more variable than those of their respective cultivars, indicating that modern breeding techniques and agricultural practices have significantly influenced the seed microbiome composition of contemporary cultivars. This is the first microbiome study on wild relatives of groundnut, which highlights the loss of indigenous microbiota in present day cultivars.

Keywords: Wild relatives, Groundnut, Seed microbiome

O7: Unraveling Antarctic Soil Microbial Communities and Environmental Shifts

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ABSTRACT

Antarctic soils host highly adapted communities composed of bacteria, fungi and few metazoans. These organisms endure multiple combined stresses resulting in the development of simplified ecosystems that are optimal models for defying the mechanisms of soil communities assembly and diversification. The effect of climate change in the continent is still not fully evident, but it is expected to threaten these unique, highly adapted ecosystems. In this light, we implemented studies aimed at describing the relationships between the diversity and composition of soil microbial communities and the properties of their environments, in order to track possible shifts in environmental conditions related with changes in the communities. All our experiments resulted in strong correlations between the communities and the abiotic environmental conditions. Additionally, given the geographic isolation of the continent, we aimed to clarify the differential selection on microbial communities of the two substrata supporting life in the continent, namely rocks and soils. We found that the different microclimatic conditions of both substrata select highly differentiated fungal and bacterial communities, even if bacterial communities share a larger proportion of taxa between the two substrata. These differences were linked to the differential distribution of few genera, with rocks being mainly dominated by lichenized fungi and soils by yeasts. Additionally, due to the possible effect of extracellular DNA on the diversity estimations through DNA-based approaches, we performed a depletion of extracellular DNA through Propidium Mono-Azide (PMA). Comparing the results of PMA treated and native samples, we did not find significant differences in the total diversity and in the distribution of dominant taxa. However, extracellular DNA strongly inflated the analyses of correlations with environmental parameters, with a higher number of parameters and correlations resulting significant in extracellular DNA depleted samples.

Keywords: continental Antarctica, soil communities, environmental filtering, extracellular DNA, extreme environments.

O8: Extremophilic Microbiome in the Arabian Deserts: Novel Diversity, Metabolic Processes And A Great Potential For Biotechnology

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ABSTRACT

The subtropical Arabian Desert covers almost the entire Arabian Peninsula and is considered as the fourth largest desert (ca. 2.3 million km^2) in the world. The diversity, activity and adaptation of microorganisms in these deserts are understudied. We studied the diversity of extremophilic microorganisms in the deserts of Oman, nitrogen cycle and their surface color change to green and hydrotaxis following addition of water. The Arabian deserts harbor unique bacterial and fungal communities that are diffrenet that what has been reported earlier for other deserts around the world. Denitrification was the major nitrogen loss process in the desert soils of Oman. Strikingly, N_2O gas was emitted at very high potential rates. Microsensor measurements revealed that N_2O was produced in the anoxic layer. So far dentification has never been reported in any studied deserts around the world, highlighting the novelty of of this process in the Arabian desert. The desert soils of Oman turned green in less than 5 minutes following water addition. Hyperspectral imaging showed that, in both wet and dehydrated crusts, cyanobacteria formed a layer at a depth of 0.2-0.4 mm and this layer did not move upward after wetting. 13C labeling experiments and MALDI TOF analysis showed that Chl a was already present in the desiccated crusts and *de novo* synthesis of this molecule started only after 2 days of wetting due to growth of cyanobacteria. We concluded that the color change of soil crusts to green upon water addition was not due to hydrotaxis but rather to the quick recovery and reassembly of pigments. Microorganisms from desert soils were isolated and screened for the production of different biotechnologically relevant compounds. While some bacterial strains could produce antifouling and antimicrobial compounds, some cyanobacteria and algae showed a great potential for biofuel production. The relevance of desert microbes for biotechnology will be presented.

O9: Ecological Engineers Of The Thar Desert: A Long-Read Metagenomics Perspective

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ABSTRACT

Biological soil crusts (biocrusts) are key components of arid zone ecosystems around the world. Formed through the coordinated activity of microbial communities, biocrusts drive various ecosystem functions. Such functions include stabilization of the soils, carbon and nitrogen fixation, dust trapping, erosion prevention and biogeochemical cycling. Naturally, this unique community of ecosystem engineers have been studied extensively in the several deserts of the world. However, not much is known about the microbial communities that reside in biocrusts of the great Indian Thar desert. In a pilot shotgun metagenomics study using Oxford Nanopore sequencing, we profiled the microbial communities from biocrusts recovered from distinct ecoregions of the Thar desert including the less arid central region to the highly arid western frontiers. We highlight variations in the biocrust microbial community and subtle, yet key differences in the function potential of the microbes inhabiting the biocrusts of these ecoregions. A thorough understanding of the microbial communities and their functions in the Thar desert biocrusts will provide key insights into their development and functioning, which will pave the way for the conservation and/or restoration of these critical desert resources.

Keywords: biological soil crusts, microbial community, shot-gun metagenomics, nanopore, function potential

O10: Exploring the Potential of Organic Waste-derived Biochar for Soil Bioremediation in Diesel-contaminated Environments

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ABSTRACT

Soil and water contamination due to globalization and anthropogenic discharge of volatile hydrocarbons is a major threat to the environment. The goal of this research is to generate biochar from organic waste and sewage runoff and then evaluate its potential in the biological remediation of diesel-contaminated soil. A standard curve, FTIR, and gas chromatography were used to assess diesel deterioration. Furthermore, physicochemical parameters were also measured. Moreover, CFU count and dehydrogenase enzyme activity were used for microbiological investigation, while Illumina 16S RNA sequencing was used to evaluate the diversity of the soil's microorganisms. The results showed that introducing biochar to soil not only improved the soil physicochemical parameters but also hydrocarbon removal by up to 72.27%±0.50 for organic waste biochar and 75.63%±0.351 for sewage biochar. In naturally polluted soil, the SDN treatment exhibited the highest reduction efficacy, with a removal percentage of 82.86%±0.60, accompanied by the VDN method, which showed a removal efficacy of 78.51%±0.38. Furthermore, wheat growth parameters and biomass yield were shown to be greatest at a 0.5% biochar concentration, whereas the maximum microbial population was detected with 1% sewage biochar. Finally, optimal biochar amelioration to soil enhances soil characteristics and activates soil microorganisms, thereby enhancing soil agricultural activity and crop production.

Keywords: Biochar, Soil Microbiota, Diesel-Contaminated Soil, Dehydrogenase Enzyme Activity, Bioremediation

O11: Halotolerant Plant Growth-Promoting Bacteria Isolated From *Avicennia Marina* Alleviate Saline Stress In Radish (*Raphanus Sativus L.*)

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ABSTRACT

Salinity is a major abiotic stressor that negatively impacts crop growth and productivity worldwide. However, certain halotolerant plant-growth-promoting bacteria (PGPB) can alleviate salt stress's adverse effects and promote better plant growth. This study assessed the influence of two PGPB strains, *Bacillus licheniformis* (S1) and *Bacillus paralicheniformis* (S2), and their mix on radish plants grown under salinity stress. These selected PGPB strains were isolated from the roots and sediments of mangroves in the United Arab Emirates, and their effectiveness was assessed through germination tests and pot experiments under four levels of salinity (0, 25, 75, and 100 mM NaCl). In the germination test, radish seeds were directly inoculated with PGPB and grown on filter papers in Petri dishes to assess their germination. For the pot experiment, self-watering pots containing a mixture of vermiculite and peat were used, and radish seeds were sown in a sterilized substrate. The PGPBs were inoculated seven days after sowing to evaluate their growth. The results showed that the inoculation with *Bacillus paralicheniformis* (S2) significantly increased plantlet height and seedling vigor index at lower salinity levels. In contrast, inoculation with *Bacillus licheniformis* (S1) led to statistically significant reductions in all studied parameters related to seed germination, including complete inhibition at the highest salinity level. However, no statistically significant effect was observed for any inoculation treatments on the germination percentage compared to the control. After four weeks of data analysis using the PlantEye instrument for the pot experiment, halotolerant PGPB, particularly strain 2, mitigated the adverse effects of salinity stress on radish plant growth. This was evidenced by improved morphological and spectral plant growth indices compared to the uninoculated control. These findings suggest that PGPBs from UAE mangroves have the potential to enhance plant growth and tolerance to salinity stress.

Keywords: Bacillus, Mangrove, PlantEye, Plant growth-promoting bacteria, Radish plant, Salt stress

O12: Unlocking Nature's Blueprint: The Saudi Soil BioAtlas and its Transformative Impact on Ecosystems towards a Greener Saudi Arabia

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ABSTRACT

Saudi Arabia's ecosystem is characterized by vast deserts, coastal areas, and mountain ranges. The country's diverse ecosystems provide habitats for various species (flora and fauna) adapted to arid conditions and play a crucial role in preserving natural resources, water conservation, and maintaining ecological balance. Within these ecosystems, the soil serves as a crucial medium for plant growth and sustains a diverse range of organisms collectively known as soil biota, including fungi, bacteria, insects, and worms, which fulfill essential functions such as nutrient cycling, decomposition, and maintenance of soil health. The Saudi Soil BioAtlas project aims to map and characterize the chemical and biological components of Saudi-soil, by analyzing the genetic diversity and composition of soil microbiota, identifying indicator species, and studying their interactions. The impact of the Saudi Soil BioAtlas project encompasses several key areas. Through the identification and mapping of soil biodiversity, it can help identify areas of high ecological value or those in need of restoration, guiding conservation efforts and informing land management practices. Understanding the soil biota also enables the development of sustainable agricultural practices that promote beneficial soil organisms, reduce reliance on chemical fertilizers and pesticides, and enhance soil fertility and crop productivity. Moreover, soil biota and their role in carbon sequestration have implications for climate change mitigation. By studying soil biodiversity, strategies for mitigating climate change and developing carbon-offset programs can be reached by 2060. Additionally, assessing soil biota facilitates the identification of indicators of soil health and guides soil management practices that prevent degradation, erosion, and loss of productivity. In summary, the Saudi Soil BioAtlas project would contribute significantly to our understanding of soil biodiversity, distribution, and ecological functions. This knowledge, in turn, would have far-reaching implications for ecosystem functioning, sustainable agriculture, climate change mitigation, and environmental sustainability in Saudi Arabia.

Keywords: Saudi Arabia, Soilbiota, Carbone sequestration, Soil health, Ecological restoration

O13: Harnessing Plant-Microbiome Interactions for Abiotic stress mitigation in Date Palm

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ABSTRACT

Date palm (*Phoenix dactylifera L.*) is a vital crop in arid and semi-arid regions, where it faces significant challenges due to various abiotic stresses, such as salinity, drought, and high temperatures. To enhance the resilience of date palms to abiotic stresses, we explored the potential of harnessing plant-microbe interactions and the role of beneficial microbes, including fungi and rhizobacteria. Our findings revealed that the endophytic fungus *Piriformospora indica* established symbiotic relationships with date palm roots, promoting nutrient uptake and water retention, thereby improving drought and salt tolerance. Molecular analyses have highlighted the upregulation of stress-related genes in plants colonized by beneficial microbes, shedding light on the intricate interplay between plant hosts and their microbial partners. Transcriptome sequencing using RNA-seq of date palm roots grown under salt stress (250 mM), with or without *P. indica* inoculation, revealed that more than 90% of the reads were mapped to protein-coding genes. More than 3,187 unigenes displayed significant differentially expressed genes (DEGs) in both control and salt-stressed colonized plants with up regulated DEGs accounting for 994 unigenes and 2193 downregulated DEGs. Using KEGG pathways, DEGs were specifically involved in metabolic pathways, photosynthesis, plant hormone signal transduction, and plant pathogen interaction. In addition, using 16s metabarcoding, we assessed the effects of irrigation sources (freshwater vs. saline groundwater) on root-associated bacterial dynamics in response to irrigation practices. Multivariate analyses revealed strong structuring of bacterial communities according to irrigation sources, and both soil electrical conductivity and irrigation water pH were the major factors affecting bacterial communities. The genera *Bacillus*, *Micromonospora*, and *Mycobacterium* were dominant when saline water irrigation was used, whereas contrasting patterns were observed for *Rhizobium*, *Streptomyces*, and *Acidibacter*. In conclusion, our study indicates that beneficial microbes can be a powerful tool to enhance the thermotolerance and salinity tolerance of date palms in a sustainable manner.

Keywords: Date palm, endophytes, RNAseq, DEGs, 16sRDNA

O14: Microorganisms Activity for Degrading Chemical Contaminants Displayed in Recycled Water Used for Managed Aquifer Recharged

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ABSTRACT

Microbial degradation of chemical contaminants, namely benzotriazole (BTri) and its derivative 5-methyl benzotriazole (5-MeBT), was investigated to mimic conditions displayed in a typical full-scale groundwater recharge system, as part of a managed aquifer recharge (MAR) project. Samples from large-scale laboratory columns at the Commonwealth Scientific and Industrial Research Organisation (CSIRO) in Perth, Western Australia were collected and analysed monthly over approximately one year. Degradation indicated first order biodegradation of the BTri and 5-MeBT under anaerobic aquifer conditions after a biological lag-time of approximately 30 to 60 days. Biodegradation half-lives of 29 ± 2 and 26 ± 1 days for BTri and 5-MeBT were respectively observed, with no threshold effect to biodegradation observed at the 200 ng L-1 . Moreover, biodegradation products of each of the compounds were analysed and identified using an optimised liquid chromatography mass spectrometry (LC-MS) method. The LC-MS methodology was successfully developed for detecting the occurrence of ultra-low (ng L-1) concentrations of both contaminants in various Western Australian environmental water samples. The detection of degradation products provided further evidence of BTri and 5-MeBT biodegradation. Overall, these results suggested that if BTri and 5-MeBT were present in recycled water recharged to the Western Australia aquifer, biodegradation during aquifer passage is likely given sufficient aquifer residence times or travel distances between recycled water injection and groundwater extraction.

Keywords: Date palm, endophytes, RNAseq, DEGs, 16sRDNA

F1: MBECS: Microbiome Batch Effects Correction Suite

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ABSTRACT

The emergence of unwanted variation introduced by batch processing is a well-researched challenge in next-generation sequencing data. While appropriate measures during the planning and execution of an experiment can limit the emergence and magnitude of batch effects, they are only partially preventable and thus need to be accounted for before statistical analyses. Despite the availability of batch effect correcting algorithms (BECA), no comprehensive tool that combines batch correction and evaluation of the results exists for microbiome datasets. This work outlines the utility of the Microbiome Batch Effects Correction Suite (MBECS), which integrates several BECAs and evaluation metrics into a software package for the R statistical computation framework.

Keywords: Microbiome, Batch effects, R-package, phyloseq, Bioconductor

F2: Impact of trace metal deposition on marine microbial communities.

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ABSTRACT

The dissolution of metals from atmospheric aerosol deposition into oceans plays a crucial role in enhancing and inhibiting phytoplankton growth rates. It also modifies bacterial community structures, significantly impacting marine biogeochemistry. In this study, we examined variations in the structure and abundance of microbial communities as a response to elevated concentrations of trace metals. We performed microcosm experiments and used next-generation sequencing techniques, targeting the V3-V4 region of 16S rRNA gene. This approach helped elucidate the phylogenetic response of microbial communities to varying concentrations (10nM, 100nM) of iron, copper, manganese, and zinc. We sourced the water from the chlorophyll maxima region of the Indian Ocean. The dominant phylum across all the experiments was Proteobacteria, followed by Bacteroidata. At higher trace metal concentration (100nM), the phylum Marinimicrobia (SAR 406 Clade) replaced members of the candidatus group Dependentiae as the 7th major phylum. Marinimicrobia bacteria, which are widespread in the oceans, are believed to play roles in carbon cycling and the dissimilatory processes of inorganic nitrogen and sulfur. At the species level, the hydrocarbonoclastic bacterium, Alcanivorax, was stimulated in microcosms with trace metals. However, their abundance decreased in experiments where multiple metals were combined. The abundance of hydrocarbon-degrading bacteria increased at higher trace metal concentration. A similar trend was seen in the case of Cyanobacteria. The abundance of Prochlorococcus species increased in all experiments with the trace metals, except for zinc. Furthermore, the abundance positively correlated with the metal concentration. However, in the combination treatment, a higher concentration negatively affected the cyanobacterial population. Marine Synechococcus and Prochlorococcus species are together thought to be responsible for at least 20% of global carbon fixation. They play a significant role in the carbon cycle and thus it is essential to understand their susceptibility and response to various environmental stressors.

Keywords: Atmospheric deposition; Chlorophyll maxima; Next-generation sequencing; Microcosm; Trace metals.

F3: Influence of Environment and Diet on Gut Microbiota Variation in Two Subspecies of *Macaca fascicularis*

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ABSTRACT

The intricate interplay between the environment, diet, and gut microbiota plays a pivotal role in shaping the health and well-being of hosts. This study delves into the comparative analysis of gut microbiota between two subspecies of *Macaca fascicularis* (*M. f. fascicularis* and *M. f. aurea*) inhabiting mangrove and island populations. Employing 16S rRNA gene sequencing on a nanopore platform, the study investigates the potential impact of environmental factors and dietary patterns on the composition of the gut microbiota. The findings shed light on compelling differences in gut microbiota richness and evenness between the two subspecies. Notably, populations of *M. f. fascicularis* that were exposed to anthropogenic food sources exhibited higher bacterial diversity in their gut microbiota compared to their *M. f. aurea* counterparts inhabiting distinct habitats. While Firmicutes and Bacteroidetes emerged as the predominant bacterial phyla within the gut microbiota of both subspecies, their relative abundances displayed significant differences. *M. f. aurea* displayed notably higher levels of these phyla compared to *M. f. fascicularis*. These variations in gut microbiota were primarily attributed to the differing dietary patterns of the two subspecies. Furthermore, the distinct adaptation of *M. f. aurea* to varied environments, each characterized by differing food availability, exerted a marked influence on their microbial composition. In conclusion, this study underscores the intricate relationship between environment, diet, and gut microbiota in *M. f. fascicularis* and *M. f. aurea* in different habitats. The observed differences in microbial diversity and composition between the two subspecies highlight the nuanced interplay of ecological factors. The study contributes to a broader understanding of how host-environment interactions modulate gut microbiota, emphasizing the role of dietary habits in shaping these microbial communities.

Keywords: *Macaca fascicularis*, Gut microbiota, Environment, Diet, 16S rRNA sequencing

F4: Decoding Microbiome and Their Antibiotic Resistance Patterns in a UAE Wastewater Treatment Plant: A Wake-Up Call for Effective Measures

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ABSTRACT

Antibiotic resistance genes (ARGs) from wastewater plants (WWTPs) pose global health and economic threats. The different treatment stages namely, primary effluent (PE), activated sludge (AS) and returned activated sludge (RAS) in WWTPs may potentially serve as a platform for the exchange and transfer of ARGs among complex microbial communities due to stage specific environmental changes. We collected samples from these three different stages of a WWTP in UAE and investigated the bacterial communities and associated ARGs using culture dependent, VITEK2 analysis, and metagenomic analyses, respectively. The culturomics results revealed a higher abundance of ESBL bacteria in RAS, particularly *E. coli*, *Aeromonas sobria*, and *Vibrio cholerae*, and they displayed resistance against ESBL, Ampicillin and Fosfomycin etc. Metagenome analyses showed significantly higher bacterial richness in the PE compared to AS and RAS. At phyla level, *Pseudomonadota* dominated across all three treatment stages, while *Bacteriodota* and *Bacillota* were enriched in PE, whereas *Actinomycetota* and *Pseudomonadota* were common in AS and RAS. PE bacterial communities were distinct compared to AS and RAS communities, wherein electrical conductivity, pH and turbidity were the most important factors in PE, while dissolved oxygen was the most significant factor in AS and RAS. Bacterial taxa showed highest percentage of co-exclusion relationship with ARG abundances across all treatment stages. The network complexity (higher number of nodes, links, and average degree) and connectivity (density) of bacterial taxa in bipartite networks were higher in PE and RAS compared to AS. *Acidovorax* sp. showed maximum links with ARG abundances of beta-lactam, tetracycline, aminoglycoside, and lincosamide in both PE and RAS, while *Delftia acidovorans* exhibited highest number of links with trimethoprim, phenicol, beta-lactam, and tetracycline in AS. Overall, the study emphasizes treatment stages' role in shaping resistant bacterial patterns and their interaction with ARGs. Additionally, it underscores the importance of RAS in antibiotic-resistant bacteria evolution.

Keywords: Antimicrobial resistance, Activated sludge, Metagenomics, Microbial communities, Wastewater treatment plant

F5: In Vitro Detoxification of Aflatoxin B1 By Bacterial Isolates from The Gut of The Rice Weevil (*Sitophilus oryzae* L.) (Coleoptera: Curculionidae)

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ABSTRACT

Aflatoxin contamination in food and feed products represents a significant global concern due to its well-documented carcinogenic, mutagenic and immunosuppressive effects on human health. Among the various types of aflatoxins, aflatoxin B1 (AFB1) is the most threatening foodborne mycotoxin to humans. In order to minimize AFB1's harmful effects, a variety of degradation procedures are performed. Several strains of fungi and bacteria are known to detoxify AFB1. In general, the insects feeding on AFB1-contaminated cereal grains are unaffected. We hypothesized that bacteria residing in the gut of such insects may possess the capacity to degrade/bind AFB1 and reduce its toxic effects. In the present study, bacteria dwelling in the gut of the rice weevil (*Sitophilus oryzae* L.) (Coleoptera: Curculionidae) feeding on AFB1-contaminated corn kernels were isolated and tested for their ability to detoxify/decontaminate AFB1. A total of four morphologically distinct bacterial isolates were isolated and identified as *Bacillus subtilis* (MWGB1), *Cytobacillus oceanisediminis* (MWGB2 and MWGB3) and *Pseudomonas aeruginosa* MWGB4 based on MALDI Biotyper analysis. These bacterial isolates were highly effective and exhibited more than 80% degradation of AFB1. In addition, these bacterial isolates showed direct antagonism against *Aspergillus flavus* and inhibited its growth in an in vitro dual culture assay and induced morphological abnormalities in the hyphae as evidenced by scanning electron microscopy. The bacterial isolates *B. subtilis* MWGB1, *C. oceanisediminis* MWGB2 and *P. aeruginosa* MWGB4 were capable of producing volatile organic compounds that inhibited the growth of *A. flavus*. *Cytobacillus oceanisediminis* MWGB2 produced Butanoic acid, 2-methyl-, ethyl ester, while *Pseudomonas aeruginosa* MWBG4 produced 1-Decanol as major components. These findings suggest that the bacterial isolates derived from the gut of rice weevil have the potential to detoxify AFB1. Further exploration on application of these bacterial isolates in food and feed industries could contribute to safer food and feed production.

Keywords: Aflatoxin contamination, Aflatoxin degradation, Human health, Safer food, Safer feed

F6: Dynamics of The Vaginal Microbiome and Cytokines Levels In Women With Gestational Diabetes

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ABSTRACT

According to the World Health Organization (WHO) and the International Federation of Gynaecology and Obstetrics (FIGO), Gestational diabetes mellitus (GDM) or diabetes in pregnancy (DIP) is defined as the carbohydrate intolerance during pregnancy leading to hyperglycemia with variable severity. Women with GDM are more predisposed to have pregnancy associated complications such as pre-eclampsia, premature rupture of membranes, cesarean section, and preterm delivery. GDM is also known to increase the rate of vaginal infections during pregnancy suggesting microbial dysbiosis. In this study, we aim to study the dynamics of the vaginal microbiome and cytokines levels in Karen and Burman pregnant women with GDM compared to controls. A total of 92 pregnant women enrolled in the MSP (Molecular Signature of Pregnancy) cohort were included, 46 women with GDM and 46 matching controls. All subjects delivered at term. Women were followed-up each trimester and vaginal swab samples were collected at six different time points including T1 (6-14 weeks), T2 (20-24 weeks), T3 (32-35 weeks), during delivery and two times postpartum. Vaginal swab samples were collected from the posterior formix by a trained midwife using the Copan Eswab™ collection system. DNA was isolated from the vaginal swabs using the modified MoBio Powersoil as previously reported. Microbial composition was analyzed by sequencing of 16S rDNA. The sequencing data were demultiplexed and analyzed using QIIME 2 pipeline. Vaginal Cytokines levels including IL 1B, IL2, Il 4, IL6, IL8, IL 10 in addition to INF-g and TNF-a and GM-CSF were measured using Bio-Rad Bio-Plex Pro human cytokine 8-Plex assay kit (Bio-Rad Laboratories, Inc., USA) with a Luminex 3D system. The Nugent score was calculated by assessing for the presence of large Gram-positive rods (0 to 4), small Gram-variable rods (0 to 4), and curved Gram-variable rods (0 to 2). A score of 7 to 10 indicates bacterial vaginosis. Lower vaginal alpha diversity was observed in the GDM group compared to the control group. Also, Beta diversity showed similarity in microbiome richness within all trimesters in both groups. Comparable cytokines and Nugent scoring levels were observed in both groups during all trimesters. Also, we found higher levels of IL 1B, IL2, Il 4, IL6, IL8, and TNF-a in vaginal swabs samples from both groups during the delivery time point, however, these results were not statistically significant. GDM is associated with lower alpha diversity and comparable cytokines and Nugent scoring levels in Karen and Burman pregnant women. This highlights the importance of ethnicity-specific microbiome studies to assess the vaginal microbiome signature in women with GDM.

Keywords: Microbiome, Diabetes, Pregnancy, Vaginal microbiome, Gestational diabetes mellitus

F7: Unveiling the Diversity and Specificity of Orchid Mycorrhizal Fungi Associations: Insights from Geographic Regions and Methodological Comparisons

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ABSTRACT

Orchids are threatened due of their great ornamental and medicinal values, and seed germination entirely dependent on compatible orchid mycorrhizal fungi (OMF). However, understanding the diversity and specificity of orchid-fungus associations is crucial for understanding ecology of these symbiotic relationships and for orchid conservation purposes. Here, we present preliminary results demonstrating the diversity of OMF isolates obtained from four orchid species, *Anacamptis morio*, *Dactylorrhiza sambucina*, *Orchis mascula* and *Platanthera bifolia* growing in Czechia, Sweden and Italy. These orchids are known to associate with Ceratobasidiaceae and Tulasnellaceae fungi, showing variation in the specificity of orchid- fungus associations. The orchid roots were screened for OMF using culture-dependent (isolation from pelotons) and culture-independent (Next Generation Sequencing of root sections) techniques. The poster presents a comparison of the diversity and specificity of orchid-fungal associations across different geographic regions and orchid taxa obtained by these two methodologies and compares their efficiency for OMF detection. The scientific outcomes can provide deeper insights into the functional implications and evolutionary dynamics of these symbiotic relationships.

Keywords: Orchid mycorrhizal fungi, Fungal diversity, Terrestrial orchids, Mycorrhizal specificity, Orchid conservation

F8: Unveiling the Microbial Tapestry: Global Diversity and Biogeographic Patterns of Mangrove Microbiomes

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ABSTRACT

Mangroves are ecologically important coastal ecosystems distributed worldwide including in UAE, which serve as a global carbon sink. This nutrient-rich mangrove ecosystem harbour a complex and diverse microbiome community, which play a critical role in ecosystem functioning. There is a limited understanding pertaining to the bacterial diversity and composition of mangrove ecosystem and their distribution pattern across the globe. We performed a meta-analysis using ~270 millions of 16S rDNA amplicon sequences pooled from 78 different studies to investigate the global distribution and the influence of salinity, temperature, pH, organic matter on mangrove plant-associated and sediments microbiomes. The biogeographic distribution of bacterial richness and diversity exhibited considerable variation across the globe and salinity was the most important structuring factor. Additonally, we also found organic matter and pH as other critical environmental factors affecting the bacterial communities of dominant mangrove plants namely, *Avicennia* and *Rhizophora*. We found distinct bacterial communities among different compartments (root, rhizosphere, soil and sediments) of mangrove ecosystem. Moreover, significant differences in bacterial communities between riverine vs non-riverine mangrove ecosystems and natural vs transplanted mangrove plants were also observed. The detected dominant phyla across the compartments included Proteobacteria, Chloroflexi, Acidobacteria, Bacteroidetes, Firmicutes and Planctomycetes. Taken together, we demonstrated that salinity is an important global predictor for bacterial richness, diversity and communities; bacterial communities were distinct between riverine vs non-riverine and natural vs transplanted, mainly driven by a multitude of local factors such as salinity, organic matter and pH.

Keywords: Biogeographic distribution, Environmental factors, Mangrove microbiome, meta-analysis, pH, Salinity

F9: Wheat Microbiome Promotes the Defense Responses Against *Fusarium Culmorum* Colonization

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ABSTRACT

Soil-borne diseases have a global impact on agricultural productivity and quality. The current study aims to investigate the interaction of rhizosphere microbiomes with the plant and the pathogen, as well as how these microbiomes impact the results of pathogen infection, gaining an insight into how these microbiomes react to disease exposures to develop strategies to control diseases. Crown rot disease is a serve disease that causes wheat crop damage caused by *Fusarium culmorum* (Fc). We collected healthy and infected wheat plants, in order to investigate the microbiome content in different plant parts, immunological responses of plants, and interactions with Fc to increase our understanding of microbiome-mediated modulation of plant pathogen responses. The results indicated that Fc-colonized plants increased the fungal population in the rhizosphere and endosphere by 15.7% and 72.3%. However, low communities (1.6 %) in leaves. Therefore, the infection caused a considerable fluctuation in the rhizosphere and root endospheric microbiome and little changes in leaf microbiomes. Using structural equation modeling, we found that wheat defense signaling pathways, wheat microbiomes, and the pathogen are closely related. We also found ecological groupings that accounted for wheat defensive signaling pathways variations. Lastly, the complexity of the microbial co-occurrence network was greater in Fc-infected plants than in healthy plants, indicating that Fc infection may have produced an increase in microbial interactions in plants. In conclusion, soil-borne pathogens dramatically alter the subterranean plant microbiomes, altering plants' immune responses to pathogens.

Keywords: Diseases, Rhizosphere, Wheat microbiomes, Plant pathogen response, Pathogens

F10: Mangrove (*Avicennia Marina*) Growth and Development Are Further Enhanced by The Use of Halotolerant Plant Growth-Promoting Actinobacteria In Conjunction With Fish Emulsion

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ABSTRACT

The use of commercial fish emulsion (FE) mixed with plant growth-promoting actinobacteria able to produce plant growth regulators (PGRs) as a biofertilizer to stimulate the expansion and maturation of grey mangroves (*Avicennia marina*) was investigated in the United Arab Emirates. It has been demonstrated that *Streptomyces griseorubens* UAE1 (Sg) was rhizosphere-competent and was able to produce auxins, cytokinins, gibberellic acid, polyamines, and 1-aminocyclopropylic acid (ACC) deaminase. Additionally, Sg was capable of solubilizing phosphorus and creating several other plant growth factors. In vivo analyses were carried out to investigate growth promotion, nutritional content, and PGR levels in the tissues of mangrove plants that had been treated with FE and/or Sg. It was discovered that sediments altered with FE only (+FE/-Sg) supported the growth promotion of mangrove trees more successfully than those inoculated with Sg (-FE/+Sg) exclusively, both in a greenhouse and in a natural open-field nursery environment. Plant growth promotion by Sg was more pronounced in the presence of FE (+FE/+Sg) than in any of the individual applications. According to the findings of our research, Sg, which was responsible for the production of PGRs, appeared to utilize the biostimulant FE as a source of nutrients and precursors for the encouragement of plant growth. Thus, in planta PGR levels following the combined +FE/+Sg were significantly ($P<0.05$) induced over other treatments. This was made abundantly clear when compared to the control group, the maximum velocity of rubisco carboxylation (Vcmax) and triose phosphate utilization rate (TPU) increased by a factor of three in plants that had been treated with +FE/+Sg. To the best of our knowledge, this is the first study of its sort on the use of the biostimulant FE as a nutrient-base for soil microorganisms, including the bioinoculant Sg, in order to stimulate mangrove development in an agricultural context that is located near the shore.

Keywords: Agriculture, Biostimulant, Mangrove, Plant growth regulators, Rhizosphere

F11: The Mangrove-Associated Bacteria for Crop Plant Sustainability

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ABSTRACT

A major challenge for global food security is the lack of fresh water, making up for 60% of yield losses. A smart solution to the above challenge would be to use abundantly available saline water. Since most crops lack the ability to cope with salinity, major plant breeding efforts are underway to enhance crop tolerance to salt stress. However, these costly and long-term approaches have not provided the expected breakthrough results so far. In contrast, we show here that root-associated microbes from mangroves can enable plants to grow using saline irrigation. Firstly, the microbiome of the mangrove of *Avicennia marina* was analyzed and then candidates were chosen depending on the functional analysis of the genetic markers. Secondly, a collection of bacterial strains were tested to enhance rice (*Oryza sativa*) growth and salt stress resistance using a hydroponic greenhouse system. Rice plants inoculated with either of two strains or their consortium showed enhanced growth and development compared to control non-inoculated plants. Under salinity stress conditions, non-inoculated rice was strongly growth inhibited and showed very poor yield. In contrast, microbial consortium inoculated rice showed massive salt tolerance, continued growth, and produced a high yield. These results show that a plant-microbial symbiosis is a tool for enhancing rice agricultural sustainability providing an important means for human food safety.

Keywords: Mangroves, Salinity, Microbiome, PGPB, *Oryza sativa*

F12: Responses of Soil Microbial Communities to The Spread of Invasive Alien Species In Coastal Sand Dunes

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ABSTRACT

Species of the genus *Carpobrotus*, introduced to stabilize coastal dunes or for ornamental purposes, have spread and naturalized along the coasts of both northern Europe and the Mediterranean basin. Their diffusion led to the disappearance of native vegetation and the associated biodiversity, also due to the short- to medium-term allelopathic effect exerted by *Carpobrotus* litter. Despite that, the impact of the *Carpobrotus* diffusion and the release of allelopathic compounds on soil communities have not been clearly determined. Additionally, fungal strains native to *Carpobrotus*-invaded soils may have evolved the ability to cope with the toxic compounds released by the plant. In this regard, soil samples have been collected in three localities of central Italy, in association with different species, selected in both natural and *Carpobrotus*-invaded areas. Fungal strains have been isolated from the samples and the most frequent ones have been selected to test their resistance to the *Carpobrotus* allelopathic effect, in terms of ability to grow in the presence of water-extracts of *C. edulis* and *C. acinaciformis* leaves. Strains with enhanced growth in the presence of the extracts have been tested to improve the growth of native plant species. Seed germination and plantlet growth were significantly reduced in the presence of both *Carpobrotus* extracts, but they were significantly increased when fungal inocula were added. Additionally, total soil bacterial and fungal diversity has been characterized by a DNA metabarcoding approach. We found few differences in the diversity of communities associated with the native vegetation and *Carporbotus*-invaded plots. However, we found strong differences in the composition of the communities, that were even stronger when considering the effect of *Carpobrotus* invasion on the single species of the native vegetation. The differences were linked to the enrichment of a few bacterial and fungal genera in *Carpobrotus* plots.

Keywords: Alien species, Bioremediation, Coastal dunes, *Carpobrotus*, Bioaugmentation

F13: Characterization of Plant Growth Promoting Rhizobacteria (PGPR) for Enhancing Drought Tolerance in Mung Bean Under Variable Moisture Regimes

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ABSTRACT

With the climate change scenario and looming world population predicted upto 8 billion people by 2050 is a huge challenge for the agriculture sector to sustain and ensure the food security according to the demand. In a study conducted during 2018-19 at the National Agriculture Research Centre (NARC) in Islamabad, the characterization and potential application of Plant Growth Promoting Rhizobacteria (PGPR) isolates for improving drought tolerance in mung bean (Vigna radiata) were investigated under different moisture conditions. Soil samples from districts Layyah and Bhakkar in Punjab, Pakistan, were collected and subjected to isolation and characterization of bacterial strains exhibiting crucial traits such as Rhizobium association, indole acetic acid (IAA) production, and phosphate solubilization, within the Soil Biology Laboratory at NARC. Subsequently, a pot experiment was conducted to assess the efficacy of these bacterial strains when applied to mung bean plants experiencing varying soil moisture levels. The study yielded significant insights: PGPR inoculation resulted in a marked enhancement in multiple parameters of plant growth, including root and shoot length, pod and flower production, plant dry and fresh weight, overall biomass, 1000-grain weight, and the uptake of nitrogen (N) and phosphorus (P) in comparison to control groups without PGPR inoculation. Under conditions of limited soil moisture, all four PGPR inoculation treatments demonstrated significant improvements in plant growth relative to the control group. However, Treatment-1 (Rhizobium spp. + PSB-1 + IAA-1) and Treatment-2 (Rhizobium spp. + PSB-1 + IAA-2) exhibited the most promising results in terms of plant growth enhancement. These findings suggest that the isolated PGPR strains have the potential to be employed for seed inoculation in mung bean crops, particularly in regions prone to water scarcity. This research contributes to the development of sustainable agricultural practices and highlights the valuable role of beneficial rhizobacteria in mitigating the adverse effects of drought stress on crop yields.

F14: Chemical and Biological testing of potable water in AL AIN City

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ABSTRACT

The highest amount of purified water is produced in the Arabian Gulf region, where some countries are 90% dependent on desalinated water for home use. There are over 100 desalination plants in the Arabian Gulf Region, 30 plants are in the Kingdom of Saudi Arabia and 70 plants are in the UAE. Potable water in the city of Al Ain was sampled. Water samples were submitted for biological analysis and chemical analysis. All samples were filtered, filter paper was incubated on a Plate Count Agar (PCA). PCA is a culture medium used for aerobic and anaerobic bacteria. It is a universal versatile, non-selective medium that provides sufficient nutrients to allow the growth of a wide variety of microorganisms. All plates were incubated overnight at temperatures 30^{o} C to 37^{o} C. Results indicated that 100 % of water samples contained a variety of pathogenic bacterial species such as *Enterococcus*, *Staphylococcus*, *Sphingomonas*, *Rhizobium,* and *Klebsiella*.

The filtered samples were chemically analyzed using US EPA, Test Method (300.1), EPA, 1993 utilizing the Dionex DX500 and the Columns: Dionex AG9-HC and AS9-HC, 2 mm. Water samples were all checked for Phosphates(PO4) Detection limit(DL)* 0.009, Fluoride (F) (DL) 0.05 mg/l, Bromate (BrO3) (DL)0.0003 mg/l, Chloride (Cl) (DL)* 0.0001 mg/l, Chlorate (ClO3) (DL) 0.0017 mg/l, Bromide (Br) (DL)* 1.0 mg/l, Nitrate (NO3) (DL) 1.00 mg/l, Sulphate (SO4) (DL) 15 to 321 mg/l, Total dissolved solids (T.D.S.), and Carbonate. Results indicated that Bromate levels are higher than the allowable limits of the UAE as per the Regulation and Supervision Bureau (RSB) standard. Further studies are underway to test for organic compounds and Eukaryotic species contents.

Keywords: Bacteria, Pathogens, Drinking water, United Arab Emirates

P1: Microbiome Magic: Illuminating the Path to Healthy Brain And Overall Development In Children

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Abstract

The human microbiome, a bustling community of tiny creatures living within us, is like a hidden treasure chest of health secrets. In this literature review, we are going to look at the intriguing connection between this bustling microbial world and the healthy growth of young minds and bodies. Our mission? To uncover the mysterious ways in which these microbiomes influence the development of sharp young brains and overall well-being in kids.

So, here's how we went about it: We searched through multiple literature's, touching fields like microbiology, neurology, and pediatrics. What we found out is that the microbiome has a huge role to play in how kids think and behave by involving neural pathways and regulating brain chemicals, shaping young minds in profound ways. It also breaks down complex carbohydrates and fibers, producing vital nutrients and contributing to the digestive system in growing children. Furthermore, it also acts as guardians of the immune system, teaching it how to distinguish between friend from foe. The microbiome maintains balance in our system and when dysbiosis occurs it can lead to consequences affecting not only digestion and immunity but also increases risk of allergies and autoimmune diseases in developing children.

To sum up, our journey uncovers microbiomes effect on the development of smart and healthy kids. By understanding the microbiome's power, we're not just illuminating the path to healthier brains in children; we're rewriting the story of lifelong well-being.

Keywords: microbiome, health, kids, Immune system

P2: Lactobacillus Reuteri Attenuates the Intestinal Barrier Damage Induced by Porphyromonas Gingivalis Via Promoting M2 Macrophage Polarization

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Abstract

Porphyromonas gingivalis, a potential oral pathogen, is evident to be associated with inflammatory bowel disease marked with intestinal barrier damage. Despite the protective effects of Lactobacillus on maintaining intestinal epithelial regeneration and homeostasis, the mechanisms involved are not yet understood. Macrophages play key roles in tissue homeostasis, defense, disease and repair by exhibiting distinct functional phenotypes based on micro-environmental stimuli. However, the contribution of intestinal macrophages in Lactobacillus promoted epithelial barrier repair is still unknown. Therefore, in the current study, the role of microbiota driven macrophages in attenuating the P. gingivalis induced intestinal epithelial damage is evaluated. Our data demonstrated a reduced intestinal leakage and increased tight junction proteins (Tjp) when L. reuteri co-stimulated with P. gingivalis lysates in an ex-vivo murine intestinal culture, suggesting an intestinal barrier protective role of L. reuteri. In addition, human intestinal epithelial cells (IEC) exhibited a reduced apoptosis and increased Tjp's mRNA expression levels when L. reuteri co-stimulated with P. gingivalis lysates and when co-cultured with human macrophages in vitro. Moreover, in vitro L. reuteri promotes M2-like macrophage phenotypes with significantly elevated mRNA expression levels of pro-tissue repair mediators, suggesting that secreted L. reuteri products play a role in skewing macrophages to pro-repair M2-like phenotype and orchestrate the resolution of inflammation in vitro. Thus, our findings first time demonstrate the role of probiotic bacteria driven macrophages in resolving oral pathogen induced intestinal barrier damage.

Keywords: oral pathogen, intestinal macrophages, mRNA, M2-like, probiotic bacteria

P3: Molecular Landscapes Associated with Gut Microbiome Dysbiosis in Colorectal Cancer Progression - A Meta Data Analysis.

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Abstract

Colorectal cancer often originates in the colon or rectum, which are parts of the digestive system, and is the second most common type of cancer worldwide.The relationship between the gut microbiome and colon cancer is a complex and multifaceted one. According to the previous studies gut microbiome dysbiosis, can influence the risk, development, and progression of colon cancer.In this study we are going to figure out how gut microbiome-colon cancer -host pathogenicity axis being associated with colon cancer progression.The electronic database pubmed was searched for all recent studies from 2018 to 2023 and categorized them according to different molecular aspects.We further analyzed the involvement of microbial community for the enhancement of colon cancer in different domains of pathogenicity .We observed that there is a direct correlation between microbiome derived metabolites and metabolic remodeling in colon cancer development. F.nucleatum and Bacteriods fragilis predominantly found in colon cancer patients which raise inflammatory response, immuno modulatory actions and metabolic dysregulation.F.nucleatum promotes cellular inflammations through IL-8,TNF-NF-KB pathway.It also enrich immunosuppressive myeloid cells in colorectal cancer cells .Bacteroides fragilis triggers inflammatory responses through IL-17R-NF-κB-Stat3 axis which mediates distal colon tumorigenesis.Bacteroides fragilis produced toxin promotes cleaves E-cadherin ,release of β-catenin and c-myc expression leads to cellular proliferation.Bacterial toxins along with proinflammatory cytokines alter mitochondria and leads to the loss of colon epithelial barrier integrity to cause IBD. Gut microbiome also associated in immuno modulatory actions by dysregulating NF-KB,TLR and Treg signalling.It is important to elucidate the background of these microbial -host interactions in pathogenicity to proceed with a personalized therapy ,where each individual acquire unique gut microbial ecosystem

Key words: gut microbiome, colon cancer, microbes, metabolism

P4: Exploring the Role of Microbiome in Lung Cancer: A Systematic Review

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Abstract

The lung and gut microbiomes have emerged as pivotal factors in comprehending the intricate landscape of lung cancer's tumor microenvironment. Dysbiosis, immunomodulation, and metabolite production constitute primary mechanisms through which these microbiomes exert influence on lung cancer progression and therapeutic outcomes. We conducted a systematic literature review, adhering to PRISMA standards, with the primary goal of delineating the associations between lung cancer and microbiome composition. Among the initial pool of 2079 articles identified, 86 articles were included in our review. Although the articles were heterogeneous, we categorized microbiome taxa that exhibited enrichment or depletion patterns in lung cancer patients. Furthermore, we reported the relative abundance percentages of bacterial species, highlighting substantial differences in composition and diversity within the lung cancer patient cohort. Of particular significance, our analysis unveiled distinct microbiome taxa that were enriched in patients responding favorably to immunotherapy, in comparison with non-responders. We found that the Firmicutes phyla in the gut exhibited a decreased relative abundance, and Actinobacteria phyla in the BALF exhibited an increased relative abundance in lung cancer patients compared to healthy individuals. These findings underscore the potential implications of microbial signatures in influencing disease progression and therapeutic outcomes in the context of lung cancer. Consequently, our data elucidate the integral role of the gut microbiome in the carcinogenesis process and its ability to modulate the efficacy and safety of immunotherapy. The findings demonstrate that lung cancer harbors distinctive microbial communities. These revelations not only provide novel mechanistic insights into the biology of lung cancer but also illuminate promising avenues for the identification of new therapeutic targets and the development of innovative strategies for the prevention and treatment of lung cancer.

Keywords: Lung Cancer, Microbiome, Therapeutics

P5: In-Silico Approches to Identify Structural and Functional Annotation Of Hypothetical Proteins From Klebsiella Pneumoniae Strain, NUBRI-K.

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Abstract

The opportunistic pathogen Klebsiella pneumoniae is a causative agent of several hospital-acquired infections. It has developed resistance to a wide spectrum of antibiotics now accessible, resulting in substantial patient fatality rates. Many proteins in this organism, however, have yet to be annotated and are classified as hypothetical proteins, implying that in-vivo functions remain unknown. These putative proteins could be important in the infectious process and used as a therapeutic target. The primary objective of this research was to use whole genome and bioinformatics technologies to annotate hypothetical proteins (HPs) in Klebsiella pneumoniae strain, NUBRI-k. Method: In present study, different bioinformatics tools were used on the basis of protein family comparison, identifying conserved domains , physiochemical properties and sub cellular localization to assign the possible functions for the HPs Results: The results have shown that 13 HPs out of the 837 were annotated and were categorized into different functional classes comprising enzymes, regulatory proteins, transporters, binding protein, lipoprotein and lipopolysaccharide. Moreover, we have found these new proteins have a role in cellular, metabolism and information. Conclusion: Bioinformatics methods were found to be a suitable approach for assigning putative proteins from Klebsiella pneumoniae in this investigation. The findings could aid in a better understanding of pathogenesis, drug resistance, host adaptability, epidemic causes, and drug discovery in Sudan.

Keywords: Hypothetical Proteins, Klebsiella pneumoniae strain, NUBRI-K

P6: The Use of Portable Sequencers to Facilitate the Characterization of Microbiota Alterations in Inflammatory Bowel Disease

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ABSTRACT:

Inflammatory bowel disease (IBD) is a complex inflammatory gut disorder with unclear aetiology. The human microbiome is a dynamic ecosystem with diverse microbial species whose varied compositions are linked to many diseases. Next-generation sequencing (NGS) technologies producing long reads are helpful for exploring the microbiome in depth down to the species level. Utilizing NGS in studying the human microbiome can aid in identifying potential biomarkers of disease, develop targeted therapeutic interventions, and improve overall health outcomes. NGS also offers a universal platform for studying diseases using complex samples such as saliva and formalin-fixed paraffin-embedded samples (FFPE). The study aims to explore the applications of nanopore technology with a portable sequencer to characterize human microbiota alterations in inflammatory bowel disease (IBD). DNA was extracted from samples of patients with IBD and compared to healthy controls. For FFPE, optimization was required for the protocol of DNA extraction and sequencing of the 16s rRNA gene. This is related to the complexity of these samples and the difficulty of obtaining intact DNA with high concentration. After sequencing, appropriate bioinformatic tools were used for analyses. 16s rRNA sequencing uncovered the microbiota down to the genus and species levels, with microbial signatures unique for IBD patients. Linear discriminant analysis revealed multiple microbiota that can be used as disease biomarkers. In conclusion, advanced next-generation sequencing technologies and bioinformatics analysis tools have significantly advanced our ability to characterize and understand the human microbiome. The NGS allows us to explore the microbiome in depth, providing valuable insights into its composition and function. The portable sequencing platform occupies a relatively small benchtop area, with integrated computing capacity and analysis software, making it suitable for users with basic bioinformatics skills. Furthermore, a combination of machine learning algorithms and lab testing can aid in identifying disease biomarkers, which ultimately can improve healthcare.

Keywords: inflammatory bowel disease; gut microbiome; portable sequencers; nanopore technology

P7: Characterization of Exopolysaccharides Produced by Lactobacillus delbrueckii and Lacticaseibacillus rhamnosus: Biological Activities, Prebiotic Potentials, and Effect on Gut Microbiome

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ABSTRACT

Exopolysaccharides (EPS) are complex polysaccharides that are produced by probiotic bacteria and have a broad range of applications in food, pharmaceuticals, and other industries. However, the characteristics, biological activities, prebiotic potentials, and effect on the gut microbiome and the skimmed bovine milk of EPS produced by different probiotic strains are still not fully understood. This study aimed to investigate the characteristics, biological activities, prebiotic potentials, and effect on the gut microbiome of EPS produced by Lactobacillus delbrueckii MW725385 (LB3) and Lacticaseibacillus rhamnosus MW725389 (MLB3). The average molecular weight of the extracted EPS was 3762.43kDa and 1272.19kDa with the monosaccharide's compositions Glu: Rib: Man: Xyl (6.5:16.4:6.61.0) and Rib: Man: Xyl: GA: Ara (7.1:1.6:4.8:1.0:9.0) for EPS_LB3 and EPS_MLB, respectively. EPS_LB3 and EPS_MLB3 at 250 mg/L showed scavenging rates for 2,2-diphenyl-1-picrylhydrazyl (34.0±1.7, 37.5±1.1), 2,2′-azino-bis-(3-ethylbenzothiazoline-6-sulfonic) acid (47.3±0.8, 56.6±0.7), superoxide dismutase (38.3±0.5, 43.5±0.6), superoxide anion scavenging (53.9±0.1, 54.7±0.1), hydrogen peroxide scavenging (10.6±0.1, 10.7±0.2), hydroxyl radical scavenging (88.8±0.1, 84.8±0.5), metal chelation (80.0±1.4, 84.5±0.8) and lipid peroxidation (60.6±1.7, 58.1±0.9) respectively, suggesting good antioxidant properties. It also exhibited antimicrobial, anti-biofilm and antiproliferative activities on several food-borne pathogens and cancer cell lines. Additionally, the utilization of EPS by several probiotics provided evidence for the prebiotic nature of EPS. The effect of both the EPSs on the gut microbiome by fecal fermentation revealed that these EPSs are promoting selective bacteria like Faecalibacterium prausnitzii and Ruminococcus bromii in the gut which are responsible for carbohydrate metabolism and short-chain fatty acids production which can be used as steppingstones for the in vivo studies. Gelation time and other rheological properties were also improved when the EPS-producing bacteria were added together with the starter culture for the bovine skimmed milk fermentation, which can be used in the dairy industry.

Keywords: Probiotics, Prebiotics, Exopolysaccharides, Bioacitivites, Gut Microbiome

P8: Molecular Crosstalk Between Polyphenols and Gut Microbiota in the Prevention and Treatment of Cancer

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ABSTRACT

Cancer remains a significant global health challenge, necessitating the development of novel therapeutic approaches. In recent years, the molecular crosstalk between polyphenols and the gut microbiota has emerged as a promising avenue for cancer prevention and treatment. Polyphenols, abundant in many plant-based foods, possess diverse bioactive properties, including antioxidant, anti-inflammatory and anticancer activities. The gut microbiota, a complex microbial community residing in the gastrointestinal tract, plays a crucial role in host health and disease. This review highlights cancer suppressive and oncogenic mechanisms of gut microbiota, the crosstalk between gut microbiota modulation and polyphenol biotransformation, and the potential therapeutic implications of this interplay in cancer prevention and treatment. Furthermore, the authors delve into the molecular mechanisms underlying the synergistic effects of polyphenols and the gut microbiota, such as modulation of signaling pathways, immune response, and epigenetic modifications in cancer. The current review also explored the challenges and future directions in this field, including the development of personalized approaches that consider inter-individual variations in gut microbiota composition and function. Understanding this molecular crosstalk offers new perspectives for the development of personalized cancer therapies targeting the polyphenol-gut microbiota axis. Future research should focus on elucidating the precise mechanisms and conducting clinical trials to validate the potential of polyphenols and gut microbiota as innovative therapeutic strategies for cancer treatment.

Keywords: Cancer treatment, Polyphenols, Gut Microbiota, Molecular mechanisms, Metabolites

P9: From Normal Composition to Transplantation: Unlocking the Secrets of Vaginal Microbiota

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ABSTRACT

Globally, over 175 million women are diagnosed with gynecological conditions annually, contributing significantly to morbidity and mortality rates. Understanding the composition and variations of the vaginal microbiome is a pressing health challenge, pivotal for enhancing therapeutic approaches. This review traces the historical obscurity surrounding the vaginal microbiome and delves into recent breakthroughs in this ecosystem.

This review has a twofold objective: Firstly, to provide an exhaustive examination of the vaginal microbiome that extends beyond conventional bacterial analysis. Secondly, to investigate the intricate connections between these microorganisms and human health, along with recent advancements in microbiota transplantation. Our approach commenced with an extensive literature survey encompassing diverse databases such as Google Scholar, PubMed, and Web of Science. The search utilized specific keywords, including "vaginal microbiota/microbiome, "Microbiota transplantation", This was carried out to present the most recent insights into the vaginal microbiome and the emerging field of microbiota transplantation.

Research into the intricate interplay among these diverse microorganisms is nascent and not yet fully comprehended. Initial findings suggest that these microbial communities collectively serve as the body's initial defense against infections. Conversely, even minor disturbances in this microbiome can lead to diseases. Therefore, a deeper understanding of these associations is crucial for identifying predispositions to specific illnesses, potentially opening novel therapeutic avenues. Presently, our comprehension of this ecosystem remains limited, with ongoing research revolutionizing our understanding of human health and disease.

Keywords: Vaginal Microbiota, Microbiota transplantation, Next Generation Sequencing, Vaginal Infections

P10: Curcumin Loaded Cellulose Aerogels Mitigates Biofilm and Virulence Of Food-Borne Pathogens

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Abstract

Biofilm formation is a common strategy employed by various foodborne pathogens to survive and thrive in food processing environments, leading to contamination of food products and increasing the risk of foodborne illnesses. Cellulose has been studied for biomedical applications due to its biocompatibility, biodegradability, lower antigenicity, and renewability. The functional and structural characteristics of this biopolymer can be dramatically improved by their transformation into fibrous bioaerogels due to their outstanding characteristics such as low density, high porosity, and large specific surface area. Aerogels demonstrate enhanced mechanical properties, stiffness, and shapeability. Cellulose aerogels were synthesized using super critical (CO2) drying. Further, the synthesized cellulose aerogel was loaded with curcumin. Characterization of the bioaerogel loaded with curcumin was done using XRD, FTIR, TGA, SEM, TEM and BET to determine morphology, textural properties, thermal stability, mechanical properties. Curcumin loaded cellulose aerogels were assessed for their antimicrobial, antibiofilm and antivirulence potential against food-borne pathogens. Bioaerogels were observed to possess broad-spectrum bactericidal action against all test pathogens. Synthesized aerogels demonstrated significant inhibition of biofilm formation against S. aureus, P. aeruginosa, S. marcescens, E. coli and L. monocytogenes. Reduced production of virulence factors such as EPS, cell surface hydrophobicity and motility was also observed. Enhanced production of intracellular ROS was observed to be the plausible mechanism for the biofilm inhibitory action of aerogels. Thus, the current work provides a novel perspective on the development of aerogels a therapeutic option. Since, Curcumin loaded cellulose aerogels exhibited anti-biofilm properties, it could further be exploited in treatment of biofilm based persistent food-borne infections.

Keywords: Biofilm, environment, foodborne illnesses, biopolymer, cellulose, bioaerogels, therapeutic

P11: Nex Generation Sequencing Based Viral, Bacterial and Fungal Microbiome Analysis Of Mucormycosis Co-Infected Covid-19 Patients From Gujarat, India

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Abstract

Mucormycosis (MCM) is a rare fungal infection that has recently become more common in tandem with novel COVID-19 infection. MCM combined with COVID-19 is extremely lethal, especially in immunocompromised patients. During the second COVID-19 wave, India experienced a rapid and unexpected increase in not only COVID19-delta variant cases, but also mucormycosis, making the infection even more lethal. Metagenome was isolated from five post-operative tissue samples obtained from Covid -19 ward patients suffering from mucurmycosis at a hospital in Surat, Gujarat, India, during the second wave of Covid19. Ion torrent, a next-generation sequencing technology, was used for the sequencing. The sequence data was analysed using Kraken and One Codex to detect the presence of viruses, bacteria, and fungi. Virome analysis revealed the presence of 36 virus families, with Poxvirida being the most abundant, followed by Siphoviridae and Myoviridae. At the species level, BeAn 58058 virus predominated, followed by Pseudomonas phage JBD25 and Pseudomonas virus phi3. The dominant family in the bacterial microbiome was Pseudomonadaceae, followed by Enterobacteriaceae and Thermoascaceae. The presence of Candida albicans predominated in ITS targeted metagenomics, followed by Aspergillus fumigatus and Rhizopus microspores. A significant challenge in treating this patient's infection was highlighted by the current study: the formation of a complex microbiome as a result of the infection.

Keyword: Mucormycosis, virome, mycome, microbiome

P12: Exploring the Probiotic, Antagonistic and Immunomodulatory Properties of Staphylococcus Warneri MN336185 Isolated from Fermented Rice Water

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ABSTRACT

Our diet modulates gut microbiome diversity and the intervention with fermented foods has shown significant effects. Fermented rice water, a staple traditional drink, has been employed as rehydration solution for ages to treat diarrhea in extreme cases of malnutrition. In the current study, a prospective strain was isolated from fermented rice water and identified by 16srRNA typing as Staphylococcus warneri MN336185. Further, the probiotic properties and cell surface properties of the strain were performed. Adhesion ability of the strains to HT-29 cell lines and inhibition of pathogen adherence was performed by competition and replacement assays. We further checked the ability of the strains to produce potential metabolites by LC-MS analysis. Bacteriocin like inhibitory substance (BLIS) from the strains were partially purified and their inhibitory effects were studied in C. elegans infection model. In attempts to confirm their gut lumen colonisation ability and protective effects, we used C. elegans as in vivo model. Cytokine and intestinal tight junction protein expression profiles with supplementation of the strains was also determined. S. warneri demonstrated acid, bile, phenol and gastric juice tolerance, produced exopolysaccharides and exhibited significant binding affinity with gelatin and heparin in in vitro experiments. Strain demonstrated adhesion potential to cell lines in the range of 63% which was confirmed by SEM analysis and modulated expression of cytokines and tight junction proteins. Prot ection assays conducted in C. elegans demonstrated an increased survival rate of the worms infected with Klebsiella (86%). The strains significantly prolonged the worm lifespan and S. warneri fed worms showed higher resistance to pathogens, high pharyngeal pumping rate and active locomotion. We could qualitatively determine the presence of antimicrobial metabolite phenyllactic acid (PLA) from cell-free supernatant of strains. These observations could be a major factor enhancing the protective effects of the strains in future food applications.

Keywords: Fermented rice water, probiotics, food safety, C. elegans, PLA

P13: Evaluation of The Alterations To The Gut Microbiome In Obese Patients After Bariatric Surgery

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Abstract

Obesity is a major problem for public health worldwide and is contributory to metabolic disorders, including type II diabetes. Bariatric Surgery, such as Roux-en-Y (RYGB) is presently the most successful treatment for chronically obese individuals, as it prompts a sustained weight loss and a significant improvement in glucose metabolism and insulin sensitivity. Thus, we hypothesise that changes in gut microbial communities, post-surgery, contribute to this recovery. Therefore, the aims of this study were to evaluate gut faecal microbiota in obese patients at 2- and 13-weeks after RYGB surgery compared to 4 weeks pre-surgery. Methods: Six obese patients were treated for weight-related health problems by RYGB at Crosshouse University Hospital Ayr, Scotland, UK. Faecal samples were collected from patients at three-time points, and bacterial identity and metabolic capacity established by QIIME2 and PICRUSt2 analysis of Illumina MiSeq sequences of the variable region (V3-V5) of the 16S rRNA gene. Results: Although each patient had a unique set of gut bacteria before and after the surgery, the composition and community structure underwent changes after surgery that were observed in all patients. The trends for relative abundance of organisms in the phylum Proteobacteria was increased after surgery at W2, and W13 while the phylum Firmicutes was decreased. In contrast, after the surgery at 2 weeks, there was a reduction in organisms belonging to the Bacteroidetes phylum and an increase in Actinobacteria while these patterns were reversed at Week 13. The α-diversity of bacterial communities of the entire patient group showed significant differences in some metrics. Conclusion: Alterations in the gut microbiome were linked to the development of a more uniform community structure as a result of surgery. Observed reductions in body weight alongside shifts in microbial communities with associated biochemical profile, indicate a complex interaction between host homeostatic metabolic control and the microbiome.

Keywords: obesity, type II diabetes, gut microbial, body weight, Bacteroidetes phylum, Actinobacteria

P14: Microbiota of Endodontic Infections: Metagenomic And Culture-Dependent Analysis

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Abstract

The microbiome of endodontic infections is polymicrobial and its composition determines pathogenesis and associated host responses. Whilst studies from different regions of the world have previously investigated the microbiota of endodontic infections, these have not employed shotgun metagenomic sequencing nor have they been done for patients in the Arabian Gulf region. This study therefore addressed these research gaps, and further sought to detect genes associated with resistance and virulence and compare the microbiomes of symptomatic and asymptomatic cases. Such investigations would potentially identify biomolecular signatures associated with endodontic infections. Samples from root canals (n=32) of patients attending the Dental Hospital at Sharjah were collected over a 5-month period. The collected samples were analysed by shotgun metagenomic sequencing and by culture-dependent methods. In total, 28 bacterial species were identified by culture, with Lactobacillus species isolated from 40.6% of the samples. Ten species (71.4%) had resistance to at least one of the tested antibiotics. Metagenomic analyses revealed a total of 366 bacterial species in the samples, with Actinomyces species being most prevalent. Alpha and beta diversity analysis showed no differences between symptomatic and asymptomatic cohorts. However, LEfse analysis showed discriminative features between the two cohorts. Prevotella marshii and Peptoamaerobacter stomatis were more prevalent and with higher abundance in symptomatic patients. Virulence and resistance genes (59 AMR genes identified including polymyxin-colistin) were found in 81.3% and 84.4% of the samples, respectively. Functional profiling detected pathways related to core cellular metabolism. Interestingly, terpenoid biosynthesis-associated pathways were detected in 96.9% of the samples. No difference in the functional profile was found between the patient cohorts. In conclusion, this study is the first to use shotgun metagenomics along with culture-dependent techniques in analysing the microbiota of endodontic infections. The results highlighted high bacterial diversity in root canals of patients with endodontic infections in the Gulf region.

Keywords: microbiome, microbiota, Gulf region, endodontic, root canals, bacterial species, biosynthesis-associated pathways.

P15: Cultivating Change: Exploring Fecal Microbiota Transplants in the Realm of Ulcerative Colitis

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Abstract

Fecal microbiota transplantation (FMT) is a procedure that delivers healthy, eubiotic human donor stool via colonoscopy, enema, nasogastric (NG) tube, or in capsule form into another individual to normalize the gut microbiota composition for gaining therapeutic benefit. Use of FMT till date has been approved by FDA only for recurrent Clostridium difficile infections. However, there are many ongoing promising studies for the treatment of gastrointestinal diseases, type 2 diabetes, AIDS, obesity, neuro-cognitive disorders, and even peanut allergy; where gut dysbiosis is a common root cause.The objective of this study was to assess the efficacy and safety of FMT as a potential therapeutic intervention for Ulcerative Colitis (UC) and to evaluate its impact on gut microbiota composition. To achieve the goal of our study, we conducted a comprehensive search of the literature on the internet and read relevant articles, clinical trials, systematic reviews, literature reviews and meta-analyses from authentic databases such as PubMed, Google scholar, clinicaltrials.gov, fda.gov, and ProQuest. We analyzed the articles and summarized the information. Our research focused on exploring the viability of fecal microbiota transplantation (FMT) as a potential intervention for UC. By meticulously analyzing 22 clinical trials (9 randomized controlled trials, 10 cohort studies, and 3 case studies) involving a total of 506 patients, we have gathered substantial evidence. On an average we found the clinical response rate to be 65.5% following FMT, alongside a clinical remission rate of 45.4%. These results indicate promising prospects for FMT in UC treatment. This study sheds light on the potential benefits of FMT in addressing these complex conditions, offering new avenues for further investigation and therapeutic development. In summary, our investigation underscores FMT's encouraging role in UC treatment, warranting continued research for potential therapeutic breakthroughs and advancements.

Keywords: Fecal microbiota transplantation (FMT), therapeutic, Ulcerative Colitis (UC), gut microbiota

P16: Unraveling the Impact of Gut and Oral Microbiome on Gut Health in Inflammatory Bowel Diseases

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ABSTRACT

Inflammatory bowel disease (IBD) is a complex disorder characterized by chronic inflammation of the gastrointestinal tract (GIT). IBD mainly includes two distinct diseases, namely Crohn's disease and ulcerative colitis. To date, the precise etiology of these conditions is not fully elucidated. This study aims to investigate the connection between the oral and gut microbiome in the context of IBD, exploring the intricate interplay between these microbial communities and their impact on overall gut health. A comprehensive literature search was conducted to identify relevant studies and resources. Electronic databases and relevant medical databases were systematically searched. A standardized data extraction form was developed to extract relevant information from the selected articles. The following data points were extracted: IBD type, sample type, sample size, age range of participants, sex, geographical region, methods for assessing the oral and gut microbiome, key findings related to the oral and gut microbiome's association with IBD. Recent research has shed light on the significant role of the oral and gut microbiome in the development and progression of IBD and its collective influence on gut health. Recent advances in microbiome research have revealed a compelling link between the oral and gut microbiome, highlighting their pivotal role in maintaining overall health. Reduction in diversity and abundance of beneficial bacterial species with the colonization of opportunistic pathogens can induce gut inflammation. Some of these pathogens can arise from oral origin, especially in patients with oral diseases such as periodontitis. It is essential to discern the mechanisms of microbial transmission, the impact of oral health on the gut microbiome, and the potential role of dysbiosis in disease development to enhance our understanding of IBD pathogenesis and identify potential therapeutic avenues. Furthermore, innovative strategies for modulating the oral and gut microbiome can promote health and prevent disease occurrence and progression.

Keywords: inflammatory bowel disease; Crohn's disease; ulcerative colitis; gut microbiome; oral microbiome

P17: Survey of The Human Gut Fungi in Health And Disease

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Abstract

Human gut fungi, mycobiome, are an essential part of the gastrointestinal microbiome and play an important role in host immunity and inflammation. Substantial evidence linking fungal taxa, Candida and Malassezia, with IBD disease biology has emerged.(1) In another study, 14 fungal species enabled the distinction of colorectal cancer patients from controls.(2) Fungal diversity can be altered due to host geographical location, dietary habits, and medication use.(3) Recent advances have provided tools for studying human gut mycobiome; however, DNA preparation methods and primers can affect the results of culture-independent sequencing of mycobiota, impacting clustering and taxonomic identification.(4)

The study aims to identify gut fungal communities in cancer patients and cancer-free participants, targeting three sequence regions within the ribosomal DNA gene complex; ITS1, ITS2, and 18S rRNA hypervariable region V4.

The study cohort comprised two groups; cancer patients (n=8) from the Oncology Services Tawam Hospital in Al-Ain, and cancer-free participants (n=8). Stool samples were collected and examined phenotypically via microscopy. After genomic DNA extraction, ITS1, ITS2, and 18S rRNA-V4 amplicon sequencing will be executed with the DNBSEQ™ sequencing system. Findings will be presented comparing fungal (ITS1, ITS2, and 18S rRNA-V4) amplicon sequencing between cancer patients vs. cancer-free controls using alpha diversity estimates and differential abundance analysis. Thus, characterizing the fungal species present in the gut microbiome and understanding their potential roles in health and disease.

The results will offer valuable insights into the composition and dynamics of gut fungi, contributing to a deeper understanding of their roles in gut homeostasis. Thus, exploring therapeutic strategies focused on modulating gut mycobiome.

This study was approved by the Tawam Hospital Ethics Board (MF2058-2020-748), and funded by the United Arab Emirates University SURE program (G00004442).

Keywords: gastrointestinal microbiome, fungal, gut mycobiome, cancer, ITS1, ITS2, 18S rRNA

P18: Metabolic Effect of Prebiotic Supplements on Commercial Probiotic Strains

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Abstract

Consumption of prebiotics or non-digestible dietary fibers nowadays has been prescribed, encouraged, and recommended by physicians, doctors, and dietary specialists to maintain health. These fibers are fermented selectively and generate specific changes in the composition and/or activity of the gut microbiota, providing health benefit(s) for humans. Various pharmaceutical companies are using a combination of numerous fibers from different sources in commercial prebiotic supplements available in the market. However, their effect on gut microorganisms has never been evaluated. We aimed to analyze the effect of commercial prebiotic supplements on the growth of probiotics (beneficial gut microorganisms) and their respective metabolites to evaluate their effectiveness in human health care. Nine different prebiotic brands selected for this study showed 100 % (completely soluble; prebiotic 4)- 0% (non-soluble; prebiotic 5) water solubility. A commercial probiotic strain isolated from yogurt (strain Y) showed higher growth in the presence of prebiotics as compared to the control, except in prebiotic numbers 4 and 8. On the other hand, prebiotic samples didn't support the growth of another commercial probiotic strain isolated from a sachet (S-strain) except prebiotics 1 and 7. Very interestingly, thin layer chromatography (TLC) analysis of the media before and after microbial growth showed the absence of mono/oligosaccharides and the production of a new type of polysaccharides by both strains which look different than the parent prebiotic supplement. Importantly, the Y-strain produced different exopolysaccharides than the S-strain indicating a distinct mechanism of action of different probiotics to metabolize different fibers. Moreover, differences in secondary metabolite production by both strains, extracted with ethyl acetate, in the presence of a water-soluble prebiotic number 2 will be presented here.

Keywords: gut microbiota, fibers, commercial prebiotic supplements, probiotics

P19: Expression and Characterization of a Halophilic Fructosyltransferase from Haloarcula Marismortui for the Synthesis of Novel Fructooligosaccharides

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Abstract

Fructooligosaccharides (FOS), short fructose chains, have gained significant attention as prebiotic compounds with the potential to enhance gut microbial health in recent years. Prebiotics are non-digestible fibers that selectively stimulate the growth and activity of beneficial microorganisms in the gut, thereby conferring health benefits to the host. The human gut is the richest microbiome ecosystem in the human body, with an estimated 1013 microbial cells [1]. These microorganisms preferentially ferment prebiotics to grow and generate essential metabolites for health. Thus, a variety of fibers must be consumed in order to maintain the diversity of human gut microbiota. The frequent use of junk food and less fiber consumption by the young generation nowadays leads to gut dysbiosis which results in several health issues including mental disorders [2]. Few prebiotics added in juices and baby formulas show the capability to support the growth of limited gut microbial species. Thus, provoking the need for new prebiotics able to stimulate the growth of diverse gut microbial communities. Therefore, the current study aims to use recently identified fructosyltransferase (FTF) enzymes from halophilic microorganisms for the production of novel FOS. We have cloned an ftf gene from an extremely halophilic archaeon, Haloarcula marismortui, into a pET15b vector. A soluble and active recombinant FTF enzyme with reasonable expression was obtained when E.coli Rosetta cells were transformed with pET-15bftf vector and induced with 1mM IPTG. Ni-NTA affinity purification method provided ~90% pure protein. The recombinant enzyme showed the highest activity at pH 7.0 in the presence of 2.5 M NaCl. Thermal stability and activity studies indicated that this enzyme was soluble but inactive when heated at 50℃ for 5 minutes however it retained 100% activity at 40℃ for several days. Stabilizing effect of some metals on this enzyme and its product will also be reported.

Keywords: fructosyltransferase (FTF), Prebiotics, gut microbial, fructosyltransferase (FTF) enzymes

P20: Development and Evaluation of MDRO Risk Assessment Tool in ICU Setting in the United Arab Emirates Hospitals

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ABSTRACT

The overuse of antibiotics in healthcare has increased due to the high rate of multi-drug resistant organisms (MDRO) related infections. Identifying the causative organism at the earliest can be achieved using a predictive tool to identify patients at high risk of developing MDRO infection, hence; initiating an appropriate antimicrobial therapy while waiting culture results. The aim of this study is to develop a tool to determine the predictors for developing an MDRO infection in patients admitted to the intensive care unit (ICU), in UAE based population, and validate this tool for its accuracy. A total of 384 patient data will be collected retrospectively in this observational, cohort study from two tertiary hospitals in UAE, using simple random sampling method. Data includes patient demographics, infection type, culture results, history of antibiotics and others. Univariate analysis will be used to identify the independent predictors of MDRO infection, and those with a P value less than 0.05 will be retained to be used in the prediction model. Then, the model will be transformed into a point-based rule with weighted scores assigned to each variable. Predictive analysis will be used to determine the accuracy of the tool. The prevalence of gram-negative MDRO in the ICU is expected to be approximately 40%, of which ESBL E.coli and Klebsiella pneumonia will have higher percentage among other bacteria. The most commonly identified predictors for developing MDRO infection would be history of antibiotic use in the last 3 months, recent hospitalization, and invasive procedures such as mechanical ventilation or hemodialysis. The accuracy of the developed model is expected to be more than 80% in order to identify high-risk patients.

Identifying patients with high-risk of developing MDRO infection at the early stage of disease helps in the selection of the appropriate antibiotic. Since the tool is built using local epidemiology data, it will provide accurate detection of those patient in UAE population.

Keywords: MDRO, Predictive tool, Risk Assessment, ICU

P21: In-silico Analysis of the Microbiome Associated with Colon Adenocarcinoma in Low Vs. High Hypoxia

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Abstract

Colon adenocarcinoma (COAD) is a major cause of morbidity and mortality worldwide. Although a growing body of evidence supports the pivotal role of intestinal microbiota in the development of COAD, the influence of tumour oxygen level in shaping the gut microbiome remains unclear. Using an in-silico approach, we investigated the microbiome associated with COAD in hypoxic compared to normoxic tumour environments. The Cancer Genome Atlas (TCGA) PanCancer Atlas study was explored using cBioPortal online tool to extract hypoxia score, tumor stage and genetic alterations of COAD patients. 54 patients with COAD who had the same ethnicity and genetic mutations profile in APC, TP53, TTN, KRAS, PIK3CA genes were included in the analysis. Analysis of some microbiome signatures showed a significantly higher predominance of Coprobacillus and Emaravirus genera in the low hypoxic score group compared to those with high hypoxic score ($p < 0.01$). Syntrophomonas genus was found to be predominant and significantly higher in the high hypoxic score group ($p<0.05$). These findings were validated using the Kraken-Derived Normalized Microbial Abundances in TCGA. DISP3 genomic alteration was enriched in the low hypoxic score group ($p<0.05$). Differential gene expression (DEG) profile revealed higher CA9 gene expression in the high hypoxic score group, whereas EDNRB, COL4A3, CXCR2, FUT7 gene expression was higher in the low hypoxic score group ($p<0.05$). Our findings show that COAD patients with different hypoxic scores showed differences in their microbiome signatures and DEGs. This suggests the potential of using these as biomarkers to distinguish between low and high hypoxia COAD.

Keywords: Colon Adenocarcinoma, Hypoxia, Microbiome, Differential Gene Expression (DEG), in-silico

P22: Anti-Multidrug Resistant Pseudomonas aeruginosa of Glycerhiza glabra

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Abstract

Pseudomonas aeruginosa, especially multi-drug resistance, is pathogenic bacterium responsible for many infections threatened public health of human beings, so, there is an urgent need to search for medicinal plants that have anti pseudomonal activity.

This research aims to study anti-multidrug resistant Pseudomonas aeruginosa of leaves and fruit of Glycerhiza glabra, as a natural source of effective antibacterial ingredients. Antibacterial susceptibility of P. aeruginosa was determined to 15 antibiotics belonging to 10 Antibiotic groups, by using disc diffusion method. Isolates Multi drug resistance (MDR), extensively drug-resistant (XDR), and Pan drug-resistant (PDR) were identified. Anti-multidrug resistant Pseudomonas aeruginosa of Glycyrrhiza glabra extracts (20%) was studied, using Agar well diffusion method. Minimal Inhibitory Concentration (MIC) was determined using Microdilution method in microtetration plates.

P.aeruginosa isolates were susceptible to Colistin by 74.1%, and to Fosfomycin by 37%, while they were resistant to Chloramphenicol by 89.9%, Gentamicin by 77.8%, and Cefepime by 74.1%. 96.3% of isolates were MDR, and 74.1% were XDR, while none of tested isolates were PDR. Glycyrrhiza glabra, Methanol and hexane extracts of leaves showed antipseudomonal activity more than chloroformic one with inhibition zone of 13.67 mm. chloroform extract of fruits was more active than methanol and hexane extracts, with inhibition zone of 21.67 mm. Conclusions: The best MIC value was 0.19 mg/ml for methanol extract of Glycyrrhiza glabra leaves and chloroform and hexane extract of Glycyrrhiza glabra fruits.

KeyWords: Pseudomonas aeruginosa, infections, Glycerhiza glabra, MDR, XDR

P23: Role of The Gut Microbiome in Inflammatory Bowel Disease and Impact Of Selected Regimes On The Gut Microbiota Composition And Balance

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ABSTRACT

Inflammatory bowel disease (IBD), which includes ulcerative colitis and Crohn's disease, is a chronic condition characterized by inflammation of the gastrointestinal tract. While the exact cause of IBD is not fully understood, it is believed to result from a complex interplay of genetic, environmental, immune-mediated, and microbial factors. This review provides a concise overview of the existing research concerning the gut microbiome's involvement in the development of Inflammatory Bowel Disease (IBD) and the role of different selected regimes (such as Crohn’s Disease Exclusion Diet, Immunoglobulin Exclusion Diet, Specific Carbohydrate Diet, LOFFLEX Diet, Low FODMAPs Diet, Mediterranean Diet) in the IBD management, and their effects on the gut microbiota (GM) composition and balance. The most used method is fecal samples to depict the gut microbiome by 16S rRNA sequencing. Moreover, machine learning (ML) methods target specific microbiome signatures either the bacteria genes or species for disease classification. Over the past few decades, an increasing number of animal and human studies have shown consistent alterations in gut microbiome composition that contributes to IBD pathogenesis, Moreover, an individualized nutritional treatment is more appropriate for IBD patients affected by such a chronic and heterogeneous condition. In summary, research shows that changes in the gut microbiome are linked to inflammatory bowel disease (IBD). Different types of microbes, like bacteria and fungi, may be involved. This suggests that microbiome markers could be used for diagnosing and predicting IBD. Advances in technology may lead to better understanding and potential treatments. The diet also affects IBD through the gut microbiome. A healthy diet can help manage the condition, but specific dietary guidelines for IBD are still lacking. Individualized nutrition plans supervised by professionals are best for IBD patients due to the disease's complexity.

Keywords: IBD, Gut microbiome, Diet

P24: Exploring the Potential Pandemic Threat Of The Andes Virus Through Computational And Experimental Analysis

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ABSTRACT

Viruses make up an important part of the human microbiome. This microbiome is dominated by an everlasting battle between the host's immune system and viral proteins. Changes to proteins associated with attachment of the virus to the host receptors are potentially associated with transmissibility. Towards conducting the increasingly compelling task of surveilling the ability of viruses to “jump species barrier” or become more infectious, one could examine how changes to viral genomes are manifested as phenotypes relating to transmissibility. Furthermore, these changes could be implicated in immune system evasion. We opted to use the case of Andes virus to demonstrate our approach. Computational methods were applied to elucidate how the recent changes to the amino acid sequences of Andes virus' glycoproteins affect the viral entry mechanism, as well as detection by known antibodies. Our methods included Monte-Carlo calculations to sample electrostatic and conformational states, in addition to Molecular Dynamics to examine protein-protein binding changes. The results were captivating as they showed that the recent mutations associated with the super-spreader event are manifested at the molecular level as changes to the interaction between the two glycoproteins. These changes could effectuate easier viral entry. Furthermore, the changes associated with the super-spreader event might cause weakening of the binding of known antibodies to the glycoprotein complex. Motivated by these computational results, we pursued the construction of pseudoviruses corresponding to the mutations so that we may examine the effect of mutations on both viral entry and antibody neutralization. We were able to designate the regions of the glycoprotein complex most likely to affect immune system detection. Consequently, these results present a very attractive path to the development of future therapeutic antibodies. The results are also particularly timely as Andes virus is implicated in potential Bioterrorism attacks and is designated as a potential pandemic agent.

Keywords: Andes virus, Protein-Protein interactions, Virology, Viral Evolution, Immunology

P25: The Mystery of Tomato Flu in India

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Abstract

While the globe fights against monkeypox and the coronavirus, a new virus known as "Tomato flu" threatens. This virus's recognized target is children. In May 2022, the virus was found for the first time in Kerala, India. Due to its principal symptom, tomato-shaped blisters all over the body, the ailment was given the term "Tomato Flu." Recent reports described it as type of hand, foot and mouth disease (HFMD). It is easily diagnosed by a history and physical examination. It is an infectious condition, but there are still a lot of unanswered questions. To shed light on this topic, we decided to collect and summarize the information on this novel viral pathogen. To accomplish this, we undertook a thorough literature assessment of the Tomato Flu research that has already been done. We analyzed data from various sources such as medical journals, government reports and news articles to gain a better understanding of this emerging disease. In addition, we conducted interviews with healthcare professionals who have treated patients with Tomato Flu to gain insights into their experiences. Survey of literature showed that Tomato Flu is a self-limiting disease. Children under the age of 5 and immunocompromised individuals are more susceptible to this disease. There is no diagnostic test for the disease, differential diagnosis involves typical symptoms and the absence of other known viral agents. There is no treatment, supportive care brings relief. Conclusion: Overall, this review provides a better understanding of Tomato Flu and its potential impact on public health. By shedding light on this emerging virus, we hope to contribute to ongoing efforts to prevent and treat of this infectious disease.

Keywords: Tomato flu, HFMD, infectious disease.

P26: The Mystery of Tomato Flu in India

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Abstract

Introduction:

While the globe fights against monkeypox and the coronavirus, a new virus known as "Tomato flu" threatens. This virus's recognized target is children. In May 2022, the virus was found for the first time in Kerala, India. Due to its principal symptom, tomato-shaped blisters all over the body, the ailment was given the term "Tomato Flu." Recent reports described it as type of hand, foot and mouth disease (HFMD). It is easily diagnosed by a history and physical examination. It is an infectious condition, but there are still a lot of unanswered questions. To shed light on this topic, we decided to collect and summarize the information on this novel viral pathogen.

Material And Methods:

To accomplish this, we undertook a thorough literature assessment of the Tomato Flu research that has already been done. We analyzed data from various sources such as medical journals, government reports and news articles to gain a better understanding of this emerging disease. In addition, we conducted interviews with healthcare professionals who have treated patients with Tomato Flu to gain insights into their experiences.

Results:

Survey of literature showed that Tomato Flu is a self-limiting disease. Children under the age of 5 and immunocompromised individuals are more susceptible to this disease. There is no diagnostic test for the disease, differential diagnosis involves typical symptoms and the absence of other known viral agents. There is no treatment, supportive care brings relief.

Conclusion:

Overall, this review provides a better understanding of Tomato Flu and its potential impact on public health. By shedding light on this emerging virus, we hope to contribute to ongoing efforts to prevent and treat of this infectious disease.

Keywords: Tomato flu, HFMD, infectious disease.

P27: Controlled Release of Benzanthrone derivative Using Polymeric Coated ZIF-8 Metal-Organic Framework

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Abstract

Controlled drug delivery systems have developed as a feasible alternative to traditional methods for increasing bioavailability, extending drug release, and keeping medication plasma levels within the therapeutic window while minimizing adverse effects. Metal–organic frameworks (MOFs) as a drug delivery system have received interest because of their unique properties, such as coordinately unsaturated centers, large surface area, and ease of synthesis. In this context, ZIF-8@alginate was synthesized as a carrier. Benzanthrone (6A) was synthesized, as an oral antihyperglycemic agent for the treatment of type II diabetes and trapped inside the alginate-coated ZIF-8 pores. The goal of this study is to examine the use of polymeric coated ZIF-8 as drug carriers to improve the control release rate of 6A. The findings showed that the problem of rapid ZIF-8 degradation in acidic pH is resolved and its stability is improved by utilizing sodium alginate, a biocompatible polymer. In addition, the regular porosity of the MOF, as well as the presence of metal ions, could help to increase the effectiveness and controlled release of the 6A compound improving the drug's bioavailability. The Benzanthrone (6A) and 6A-ZIF-8@Alginate formulation are characterized by powder X-ray diffraction (XRD), thermogravimetric analysis (TGA), Fourier transform infrared spectroscopy (FT-IR), NMR, scanning electron microscopy (SEM) and Brunauer–Emmett–Teller surface area analysis (BET).

Keyword: drug, Metal–organic frameworks (MOFs), ZIF-8@alginate, Benzanthrone (6A)

P28: Metaproteomics Profiling of Gut Microbiota in Pediatric Acute Lymphoblastic Leukemia Patients

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ABSTRACT

The gut microbiota is the collection of microorganisms that harbor the human gastrointestinal tract. The relationship between gut microbiota and cancer is an emerging field, as several recent studies have pinpointed a potential link. Such findings opened the door to a new era of research aiming to reveal the underlying mechanism of gut microbiota alterations, or dysbiosis, in cancer. Although several metagenomics studies have provided insights into the gut microbial composition in healthy and diseased states, the microbial functional characteristics are still poorly understood. With the current advances in mass spectrometry, a comprehensive understanding of the microbiota proteome profile became possible. In this vein, the objective of this study was to explore the gut microbial composition in patients with acute lymphoblastic leukemia (ALL), one of the most common pediatric cancers, compared to healthy individuals. Additionally, the study aimed to identify the microbial-secreted proteins and their potential functions in the human host. Collected stool samples from newly diagnosed pediatric ALL patients and controls were subjected to metagenomics and metaproteomics analyses. The gut microbial composition of the ALL patients was notably denoted by some differentially abundant genera, such as Bacteroides, Prevotella, and Streptococcus, in addition to other less abundant taxa, including Blautia, Dialister, and Lachnospira. Furthermore, the metaproteomics results inferred the functional characteristics of the microbiota in ALL patients, with remarkably high iron demand and oxidative stress compared to healthy individuals. On the other hand, functions related to amino acid, carbohydrate, and butyrate metabolism were downregulated in ALL patients. This study provided insights into the differences between the healthy and ALL-diseased microbial functional profiles. These promising results are a preliminary step towards a deeper understanding of the underlying role of gut microbiota in cancer.

Keywords: Microbiota; Metagenomics; Metaproteomics; Cancer; Leukemia. Theme: Human Microbiome

P29: Microbiome and metabolome of the Entero-Mammary Pathway

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ABSTRACT

The entero-mammary pathway is a specialized route that facilitates the transfer of immune components from the intestine to the mammary gland. This pathway has been hypothesized to selectively translocate bacteria, leading to their ingestion by the newborn, potentially playing a crucial role in neonatal development. Previous studies have successfully identified common bacterial and archaeal taxa shared between human milk and the neonatal intestine. However, the functional implications of this process in neonatal development are still not fully understood due to limited evidence. Therefore, this study aims to identify and characterize these features by assessing the microbiota diversity and the metabolome profile of colostrum, mother, and neonate stool samples using high-throughput DNA sequencing and FT-ICR MS methodology, respectively. Preliminary results from our study have shown promising findings. Spearman's correlation analysis has revealed features that may be associated with distinct metabolic pathways. Discriminatory analysis (LIM-LRT) demonstrated differential expression of metabolites across sample types. Our comprehensive analysis of the microbiota revealed unique microbial communities in each sample type, interestingly, we also identified several bacterial taxa consistently shared between human milk and neonate intestine, supporting the notion of bacterial transfer through the entero-mammary pathway and vertical transmission. In conclusion, these findings contribute to a broader understanding of the role played by the early acquisition of microbiota from human milk in neonatal development. Our study highlights the importance of considering the microbiota composition and its implications for neonatal health. Based on the current evidence, these results suggest implications for developing targeted interventions or recommendations aimed at optimizing infant health and well-being. This work was supported by CONACyT 163235 INFR-2011-01 and CONACyT FORDECYT-PRONACES/6669/2020_Programa Presupuestario F003-Ciencia de Frontera 2019.

Keywords: metabolome, microbiome, 16S RNA gene, Mass spectrometry, Entero-mammary pathway.

P30: Effect of Heavy Metal Arsenic, Cadmium and Metal Mixture on gut microflora of mice: A comparative account

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ABSTRACT

Heavy metal pollutants stemming from various industrial processes pose a significant environmental threat, impacting ecosystems and human health. The Gastrointestinal (GI) tract is the primary site that gets exposed to xenobiotics. Thus, there is a possibility that exposure to environmental pollutants can lead to alteration in gut microflora (dysbiosis). We investigate the impact of arsenic (As) and cadmium (Cd) alone and in combination on gut microbiota through Illumina NextSeq high-throughput sequencing. Analysis of 506 OTUs (23% of total OTUs) shared among As, Cd, As/Cd treated, and untreated control groups demonstrate this effect. The Shannon diversity index, calculated for V3/V6 regions, yielded an average diversity index of 6.01/4.95 for the untreated control group. In contrast, the Arsenic-treated group displayed a diversity index of 6.54/5.75, while the Cadmium-treated group showed a lower index of 5.32/4.25. The lowest diversity index was observed in the As/Cd mixture group, measuring 5.16/3.89. These findings suggest that As exposure increases microbial diversity, while Cd or the As/Cd mixture significantly reduces it. Furthermore, the major bacterial phyla composition analysis shows differential abundance between the untreated control and heavy metal-treated groups. For instance, Arsenic exposure led to increased Firmicutes (23%) and Proteobacteria (8%), whereas Bacteroidetes decreased (67%). Conversely, Cadmium exposure sharply decreased Firmicutes, while Actinobacteria increased. These changes indicate dysbiosis in the gut microflora. At lower taxonomic ranks, specific clades, such as Prevotellaceae, Lactobacillaceae, Ruminococcaceae, and Succinivibrionaceae, were significantly enriched in response to different heavy metals. The presence of hydrogen sulfide-producing desulphovibrionaceae was notable across all heavy metal-exposed groups, while butyric acid-producing Lachnospiraceae were reduced. Our study underscores how heavy metal exposure alters gut microbiota dynamics. Understanding these interactions is essential for assessing the health risks associated with heavy metal pollution.

Keywords: Gut microbial diversity, Dysbiosis, Gastrointestinal impact, Environmental pollutants, Xenobiotics.

P31: Identification of Gut Microbiota Derived Metabolites In Cardiovascular And Skeletal Muscle Deconditioning In Stimulated Microgravity

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Abstract:

The role of gut microbiota and their metabolites in cardiovascular and musculoskeletal health is significant. Microgravity's impact on cardiovascular, skeletal muscle, and gut microbiota is evident, but the precise mechanisms and consequences remain unclear. We used a hindlimb unloading (HU) mouse model to simulate space conditions and assessed cardiovascular and skeletal muscle function and structure through proteomics and metabolomics analyses. In C57/Bl6 mice, three weeks of unloading led to significant changes in cardiovascular and skeletal muscle parameters. These changes included decreased mean arterial pressure, reduced heart weight, increased aortic collagen content, and thicker tunica media. Grip strength and skeletal muscle mass also decreased, indicating muscle atrophy. Importantly, a two-week recovery period partially reversed these changes, underscoring the importance of recovery. Proteomics analysis identified dysregulation in 12 proteins related to atherosclerosis, oxidative stress, vascular permeability, and muscular atrophy diseases. Metabolomics analysis revealed alterations in 12 metabolites. Notably, HU mice had lower levels of inosine, a cardioprotective metabolite produced by Akkermansia muciniphila, while HUR mice had elevated inosine levels. These findings suggest that various proteins and metabolites contribute to cardiovascular and skeletal muscle changes in microgravity. Furthermore, gut microbiota-secreted metabolites may play a role in muscle and cardiovascular deconditioning in space, warranting further research into their effects on health in such environments.

Keywords: gut microbiota, hindlimb unloading (HU), proteins

P32: Synchronizing the Gut Microbiome: Dioscorea-Infused Synbiotic Approaches in Ulcerative Colitis Management

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ABSTRACT

The chronic inflammatory disorder known as ulcerative colitis (UC) can potentially arise from various factors. The integration of probiotics and prebiotics, known as synbiotics, is considered a practical strategy for addressing inflammation in UC. Bacillus coagulans has garnered recognition as a promising probiotic agent for the treatment of intestinal diseases due to its advantageous industrial and probiotic characteristics, such as sporulation and lactic acid synthesis. Although, most of the species of the genus Dioscorea have shown potential as a prebiotic, but till date less studies have been made to explore its potential as a component of a synbiotic combination in gut health. This study aimed to investigate the efficacy of prebiotics from Dioscorea spp. and probiotic Bacillus coagulans spores in ameliorating colitis induced by TNBS in a rat model. The treatment effects of probiotic were assessed in the presence or absence of the prebiotic. The administration of probiotic, prebiotics, and synbiotics demonstrated a notable beneficial impact on TNBS-induced UC. Following the administration of these supplements, there was a notable decrease in both the disease activity index and histological damage score. In comparison to the TNBS group, the aforementioned supplementations exhibited significant modulation of cytokines and C-reactive protein (CRP) levels. Furthermore, they significantly preserved the expressions of tight junction proteins and facilitated the restoration of the intestinal barrier. Moreover, these dietary supplements exert regulatory effects on the composition of the gastrointestinal microbiota and enhance the synthesis of short-chain fatty acids (SCFAs). In brief, the synbiotic intervention demonstrated a notable improvement in the inflammatory condition of the experimental model of UC, surpassing the therapeutic efficacy of probiotic or the standalone administration of the prebiotic. In summary, this study underscores the potential efficacy of synbiotic therapy as a promising modality for the management of ulcerative colitis, as it addresses various pathological mechanisms concurrently.

Keywords: Gut-Microbiome, Probiotic, Prebiotic, Synbiotic and Ulcerative colitis.

P33: Potential Probiotic Bacilli Isolated from Broiler Chicken Intestines: Characterization and Antimicrobial Activity

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Abstract

The intestinal microbiota of broiler chickens harbors a diverse array of microorganisms with potential implications for both animal health, and food safety. This study focuses on the isolation, and characterization of Bacillus strains from the intestinal tract of broiler chickens, and their antimicrobial properties against some pathogenic microorganisms. The results highlight the potential of these isolates as probiotic candidates for improving animal health and food safety.

A group of bacilli bacteria as Bacillus cereus, Lysinibacillus sphericus, Bacillus amyloliquifaciens, and Bacillus subtilis were successfully isolated from the intestinal contents of broiler chickens. These isolates were identified biochemically with different techniques, genetically using PCR, sequencing of tested gene, as well as phylogeny of the sequence results demonstrating their taxonomic diversity within the Bacillus genus.

Notably, the isolated Bacillus strains exhibited remarkable antimicrobial activity against a spectrum of pathogenic microorganisms including Staphylococcus aureus, Escherichia coli, Listeria monocytogenes, Candida albicans, Klebsiella pneumoniae, and Pseudomonas aeruginosa. The antimicrobial activity was assessed through multiple methods using the whole bacteria, and the bacterial products. These findings highlight the potential of these Bacillus isolates as valuable sources of antimicrobial agents.

The implications of these results extend beyond their potential use as probiotics. The antimicrobial properties of the isolated Bacillus strains suggest their applicability in food preservation and disease prevention. As antibiotic resistance becomes an increasing concern, the identification of naturally occurring antimicrobial agents holds promise for addressing this challenge.

In conclusion, this study presents a comprehensive analysis of Bacillus isolates from the intestinal tract of broiler chickens, showcasing their taxonomic diversity and antimicrobial potential. The findings underscore the importance of exploring the microbial diversity within agricultural systems for applications in both animal health and food safety.

Keywords: Antimicrobial activity, Bacillus isolates, Broiler chicken intestines, Food safety, Microbial diversity, Probiotics

P34: Role of B Cell Mediated Immune Responses During Skin 'Atopic Dermatitis' Disease

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ABSTRACT

The increase in prevalence of allergic diseases and the lack of a cure for these conditions have made it important for researchers to understand allergies, especially from the immunological perspective, for discovering potential new therapeutic targets. Atopic dermatitis (AD) is the most common of skin allergies characterized by pruritus and eczematous lesions that effects a person's health, social and economic wellbeing. The complex pathophysiology of AD involves several factors, one of which is

the disruption of the epidermal barrier hence disturbing the microbiota of the skin that helps in various functions such as preventing the colonization of pathogens. An altered skin microbiome with a dominant colonization of S. aures is a significant characteristics of AD. Recently AD was also recognized as a systemic disease rather than just atopic due to the robust adaptive Th2 response to secondary infections due to defects in innate immunity. This study will help in enlightenment of some basic questions to understand the immune system (especially B cells) at the molecular level during allergic responses in the skin using mouse models for atopic dermatitis as allergic model. In this study, vitamin D3 analogue Calcipotriol (MC903) was used as an allergen to investigate how it modulates the B and T cell subsets during skin allergic responses. In-vitro and in-vivo experiments were performed to study the underlying the molecular mechanisms and immune-profiling during these allergic reactions respectively. A reduction in the capacity of B cells to produce anti-inflammatory cytokines and modulation of T cells towards producing more IL-2 and INF-y was observed when challenged invitro with Calcipotriol as an allergen. Furthermore, the skin microbiome being an ecosystem in itself, the future directions of this study will focus on dissecting the changes in the skin microbiota at molecular level during such allergic responses.

Keywords: Calcipotriol, Allergy, B cells, Skin microbiome

P35: Microbiome Diversity of Hyalomma anatolicum Ticks Associated with Livestock in the United Arab Emirates

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Abstract

Hyalomma anatolicum acts as a vector transmitting tick-borne pathogens (TBPs) in livestock. TBPs affect the health of livestock and consequently reduce their productivity. This study was conducted to quantify microbial diversity in H. anatolicum. Hyalomma anatolicum ticks were collected from livestock (cattle, sheep, and goat) in three emirates, Abu Dhabi, Dubai and Sharjah in the United Arab Emirates during 2019. DNA was extracted from 175 male ticks sampled from livestock (n = 78) and subjected to next-generation sequencing. The 16S rRNA gene was analyzed using the Illumina MiSeq platform to determine the microbial communities. Principal coordinate analysis (PCoA) was performed to identify patterns of diversity in the microbial communities. Twenty-six bacterial families with high relative abundance were identified, of which the most common were Staphylococcaceae, Francisellaceae, Corynebacteriaceae, Enterobacteriaceae, Moraxellaceae, Bacillaceae, Halomonadaceae, Xanthomonadaceae, Pseudomonadaceae, Enterococcaceae, Actinomycetaceae and Streptococcaceae. The diversity of the microbial communities in terms of richness and evenness was different at the three study locations, with the PCoA showing clear clusters separating the microbial communities in ticks collected at Abu Dhabi, Dubai, and Sharjah. In the microbiome of H. anatolicum, the relative abundance of genera was highly variable among all hosts. Staphylococcus and Corynebacterium were the two most common genera reported from all locations, with high relative abundance detected in sheep (57.6% and 41.5%, respectively). Francisella had a relative abundance of 72% in ticks collected from goats, followed by Proteus (57.9%) from cows and Carnimonas (31.7%) and Bacillus (23.6%) from sheep. The presence of bacterial families harboring pathogenic genera showed that H. anatolicum could pose a potential threat to livestock and food security in the UAE. This study represents the inaugural exploration of the microbiome of H. anatolicum in the UAE. This newfound knowledge enhances our understanding of microbial distribution in livestock ticks within the UAE, illuminating microbe relationships and contributing to the formulation of more effective management strategies.

Keywords: Hyalomma anatolicum, 16S rRNA gene, Microbial communities, Pathogens, Livestock

P36: Antimicrobial Agents Induced Disruption of Gut Microbiome Leads to Depression and Behavioral Changes in Mice

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Abstract

Gut microbiome regulates important intestinal function and immunity. Thus, it has a significant influence over health and disease. The gut microbiome is able to communicate with other organs, such as the brain. This is known as “Gut-brain-axis”, a bidirectional communication between the gut and the brain. Alternations in the microbiota leads to neurological and behavioral changes. This has been shown in our experiment, in which we divided mice into control and experimental groups. Experimental group received a cocktail of oral antibiotics consisting of Vancomycin, Muropenem, Neomycin, and Metronidazole for 7 days. Afterwards, the microbiota was monitored using 16S rRNA sequencing. Data showed a significant decrease in Bacteroidetes with an increase in Firmicutes, indicating a shift into a dysbiotic state. As for the behavioral changes, elevated plus maze system was used. Control group roamed around both the light and dark tunnels. Whereas the experimental group spent more time in the dark tunnel. Results showed that antimicrobial agents affect the microbiota negatively resulting in depression and stress in mice.

Keywords: Antibiotics, Microbiome, Mice, Depression, Dysbiosis

P37: Electrophoretic Analysis of Rotavirus Isolated From Diarrhoeic Poultry Using RNA-PAGE

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ABSTRACT

Rotavirus is a significant cause of acute gastroenteritis in mammals and birds. Economic losses are associated with diarrhoeal syndrome in birds, making this a major concern to poultry industry. Like mammalian rotaviruses they contain 11 segments of double stranded (ds) RNA genome. Rota viruses isolated from different species can be distinguished by the electrophoretic migration patterns (electropherotypes) of their ds RNA upon polyacrylamide gel electrophoresis (PAGE). The goal of the current study was to determine the prevalence of rotavirus infection in poultry birds affected by diarrhoea using RNA polyacrylamide gel electrophoresis (RNA-PAGE). A total of 143 faecal samples were collected from different parts of Kerala, India and screened for the presence of rotavirus using RNA polyacrylamide gel electrophoresis (RNA-PAGE). Out of 143 samples, 5 (3.49%) were found to be positive in RNA-PAGE with a migration pattern 4:2:3:2 of a mammalian-like electrophero group A rotavirus. The study records the first evidence of rota virus detection from avian species in Kerala, India.

Keywords: Rotavirus, Poultry, RNA-PAGE

P38: Curative Effects of Natural Products on Human Cancer Cells

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Abstract:

The purpose of this study is to investigate selected natural product that have antioxidant, anti-inflammation, and anti-apoptotic properties. Natural antioxidant products are explored for therapeutic purposes because such perceived safety against normal healthy cells. Piperine (P) that is found in black pepper (Piper nigrum L.) and coenzyme Q10 (Q10) is a naturally occurring compounds that have positive biological properties and act to minimize the adverse effects of toxic agents and its metabolite. Hepatocellular carcinoma cell line (HuH-7) cytotoxicity was triggered by exposing to cyclophosphamide (CP). Several biological markers such as; intracellular ROS generation, inflammatory responses, anti-oxidant enzymes activities, and NFκβ pathway were investigated in the hepatocellular carcinoma cell line (HuH-7). The findings illustrated Q10 and/or P inhabited both basal and CP-induced ROS generation without upsetting the balance in activities of antioxidants levels. Analysis of proinflammatory cytokine gene expression showed that CP treatment alone only induced expression of IL-6β. However, co-exposure of the cells to both Q10 and CP caused significant suppression of basal Cox-2 and TNF-α gene expression, while co-exposure of the cells to CP and P with Co-Q10 suppressed basal IL-1β gene expression. Both Q10 and P seem to be inhibiting NFκβ pathway to suppress CP-mediated inflammation. In conclusion, current outcome shows that Q10 and/or P induced inhibition of ROS generation mediated by CP. We also found that Q10 and P suppressed CP-induced inflammation by inhibiting gene expression-specific inflammatory cytokine. This anti-inflammatory role of Q10 and P is likely linked to their anti-oxidant mechanism. Current results showed that PIP and CoQ10 have anti-cancerous properties and may be a useful resource for effective remedies in the treatment of liver cancer.

Keywords: Antioxidant, Piperine, coenzyme Q10, Apoptosis, Cancer.

P39: Understanding How Metabolic Regulation Constrain Metabolism

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Abstract:

Metabolism is a vital process in which an organism creates energy molecules and cellular building blocks for survival. It involves numerous interconnected chemical reactions. These reactions are regulated by various intracellular metabolite-enzyme interactions, either enhancing or reducing enzyme efficiency. Any unnecessary metabolic control can lead to significant consequences, including growth disadvantages and complex metabolic diseases like cancer and diabetes in humans. In this study, we aim to analyze the impact of overproducing regulatory compounds on metabolism by reconstructing the enzyme-metabolite regulatory network and the network of co-differentially expressed genes. To do this, we used comprehensive gene expression data for Saccharomyces cerevisiae from various conditions available in public databases like ArrayExpress. In our study, LIMMA package of R language (http://bioconductor.org/biocLite.R) is used to detect differentially expressed gene considering one as a reference conditions. We collected raw microarray gene expression data from 132 and 207 different studies using YGS98 and Genome2 chips, comprising 1365 and 1733 samples, and 495 and 513 unique experimental conditions, respectively. We processed the raw CEL files and calculated the average normalized gene expression data for each unique condition. After that log-fold changes were calculated for each condition pair using R and calculate adjusted P values using the Benjamini-Hochberg multiple testing procedure with the p.adjust function. Genes with an Log2 fold change value > 2 and an adjusted P value < 0.005 were considered co-expressed. We examined the co-expression patterns of genes to understand how they co-evolved and how highly differentially expressed genes across conditions are distributed across the genomes. In conclusion this confirmation of co-expression in multiple datasets plays a vital role in demonstrating the impact of overproducing regulator compounds on metabolism.

Keywords: Metabolism, Regulatory compounds, Gene expression, Co-evolution, Saccharomyces cerevisiae

P40: Identify Microbial Markers for Gut Microbial Associated Diseases Using Systems Biology Approaches

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Abstract

One of the leading causes of death in the United Arab Emirates and worldwide is due to complex diseases such as diabetes and inflammatory bowl diseases, Cancer and obesity. There is a significant variation in the structure of human gut microbiota among these diseases states. Consequently, exploring these structure variation among human gut microbiota is a crucial area of investigation. While certain studies have reported linkage of microbial interaction with microbiome structure, a critical aspect that is shrouded in mystery how structure variation plays a role in health condition. In the context of our research, we have investigated cooperative interactions between genetically deficient strains, known as auxotrophs, and the wild-type prototrophic strain. Our findings indicate that such communal interactions enhance the exometabolome of the community, ultimately conferring tolerance to various antimicrobial drugs. Furthermore, auxotrophs appears to be highly prevalent in host linked microbiomes, constituting over 99.9% of the microbiome population, including those within the human gut. Given the specific nutritional requirements of auxotrophic species, their presence in the microbiome can drive distinct interactions that may, in turn, influence the overall community structure, potentially leading to the formation of disease related communities. The proposed study seeks to identify specific auxotrophic markers within the gut microbiome, particularly in the context of complex diseases, through a combination of mathematical modelling and analysis of microbiome data. Through the application of metabolic models, our approach involves the prediction of auxotrophic genes spanning various species. Subsequently, we will conduct a comprehensive re-analysis of gut microbiome data sourced from different disease states, through computational and mathematical modelling, with a focus on identifying sets of auxotrophic genes. Finally, we'll validate our predictions with metagenomic experiments from IBD and cancer patients. This research aims to develop therapies for restoring gut microbiota health in diseases and enhance our understanding of gut microbiota structure.

Keywords: Auxotrophic and Prototrophic bacteria, exometabolome, metagenomic, Cancer, Inflammatory bowl disease(IBD)

P41: Lactic Acid Bacterial Growth and Behavior In Camel And Bovine Milk

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Abstract

We have investigated the growth performance of three different lactic acid bacteria, i.e. Lactobacillus bulgaricus, L. helveticus, and Streptococcus thermophillus, and the fermentation of pasteurized camel and bovine milks. The milk samples were fermented at 28°C and 42° using 1% of activated milk cultures over a duration of 96 hours. Key parameters such as pH levels, titrable acidity, and microbial counts were evaluated during fermentation. The titrable acidity increased and the pH decreased in both milk samples. The microbial counts were higher for bovine than for camel milk and were higher at 42°C than at 28°C for both milks. This research illustrates the intricate interplay between specific lactic acid bacteria strains, different milk types, and varying temperatures during the fermentation process. The acquired insights may well enable an enhanced production process of fermented dairy products and facilitate deeper comprehension of microbial behavior in food-related applications.

Keywords: Fermentation, Camel milk, Bovine milk, Lactic acid bacteria, Fermented dairy products.

P42: Pseudomonas in Triple Negative Breast Cancer is associated with increased tumour-infiltrating neutrophils.

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Abstract

Breast cancer (BC) accounts for most cancer-related deaths in women. Among the non-hereditary factors, infectious agents are the third most important factor contributing to 15-20% of cancer incidence. The microbiota of human breast tissue is diverse and distinct from other areas of the organism regardless of the sample site within the breast, age, geographical location and pregnancy history. Local dysbiosis is observed in BC tissue compared to non-BC tissue. On the other end, the role of neutrophils in breast cancer shows that the N1 pro-inflammatory subtype can suppress and attack the tumour. Recently, more focus has been directed to the role of innate myeloid cells, specifically neutrophils, in regulating the responses of lymphoid populations both in the progression of cancer and in response to therapy. Identifying what microbiome-predominant neutrophil-rich BC can shed light on the exact correlation between the microbiome, immune cells and cancer prognosis. We did Immune deconvolution using bulk RNA-seq data to identify immune cell fractions and classify patients into molecular subtypes according to their immune cell profiles. Bacteria in neutrophil-rich TNBC versus neutrophil-poor TNBC were compared using Cancer (BIC) database. Furthermore, the bacterial-associated biological function was identified for select bacteria from the top 10 relative species. Our results showed that different bacterial species elicit different infiltration of neutrophils. Pseudomonas showed the highest correlation with increased neutrophils in contrast to Bacteroides, which was associated with a decreasing population of neutrophils. In conclusion, our results showed an increased correlation between Pseudomonas and neutrophils, which can be part of the related functions of Pseudomonas. While Bacteroides, which have a negative correlation with neutrophils, have been found to induce several oncogenic pathways and are linked to the promotion of breast cancer in mammary ducts.

Keywords: Breast cancer, microbiota, BC tissue, Pseudomonas, Bacteroides, neutrophils

P43: Title: Metagenomics Analysis of the Effects of Biochar Enriched Compost Application on the Diversity of Soil Microorganisms

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Abstract

To feed the ever increasing human population, agriculture production per unit land should be increased sustainably without disturbing natural harmony between soil microbiota. Results of the study of the effect of addition of Biochar enriched compost on soil microbial community structure has been presented here. Soil microbial analysis has been carried out with 16S rRNA gene amplicon sequencing using Illumina MiSeq platform. The raw read were imported to QIIME2 platform. Statistical analysis was performed on QIIME2 Import plugin. Soil bacterial Cho1, ACE, Shannon and Simpson diversity were measured. A total of 20369 and 25162 amplicon sequence variants were obtained from each sample. The results revealed that unfertile, nutrient-less soil become a rich in variety of microorganisms.

Keywords: Compost, Soil-Microbial Diversity, Community Structure, Diversity index, 16S rRNA sequencing

P44: Structural and Functional Diversity of The Willow Rhizosphere Microbiome In Petroleum Hydrocarbon-Contaminated Soils

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Abstract

Phytoremediation is an attractive approach to remediate petroleum hydrocarbons (PHCs) contaminated soils. Certain plants, such as willow, can directly bioremediate by sequestrating and/or transforming pollutants, but plants might also improve phytoremediation by promoting contaminant-degrading bacteria in soils. In this study, a combination of culture-dependent and culture-independent approaches [high-throughput sequencing of bacterial 16S rRNA genes and the alkane 1-monooxygenase (alkB) genes, isolation on selective and non-selective media, screening bacterial isolates for several plant growth-promoting (PGP) traits, complemented with the genetic characterization of genes involved in alkane degradation] were used to characterize the structural and functional diversity of bacterial communities in the rhizosphere of different willow cultivars growing PHC-contaminated soils. Additionally, selected bacterial isolates were subjected to plant growth promotion tests using a gnotobiotic approach under normal and stressed conditions and the most promising isolate was genome sequenced to reveal its PHC-degradation and PGP potential. Results indicated that the alkane-degrading bacterial communities in willow rhizosphere mainly consisted of Rhodococcus, Nocardia, Pseudomonas, and unknown alkB-harboring bacteria. Results also showed that bacterial families Enterobacteriaceae, Micrococcaceae, Nocardioidaceae, Nocardiaceae and Bacillaceae dominated the cultivable fraction of the willow rhizosphere microbiome. Our results indicated that several bacterial isolates possessed at least four PGP traits. Additionally, catabolic genes related to alkane degradation were detected in many bacterial isolates with the alkane monooxygenase (alkB) gene found in 34 isolates, the cytochrome P450 hydroxylase (CYP153) gene found in 24 isolates. Our results showed that Nocardia sp. (WB46), Pseudomonas plecoglossicida (ET27), Stenotrophomonas pavanii (EB31), and Gordonia amicalis (WT12) significantly increased the root length of canola grown in 3% n-hexadecane compared with the control treatment. Genome sequencing of Nocardia sp. (WB46) revealed that its genome contains many genes responsible for petroleum hydrocarbon degradation such as (alkB) and naphthalene dioxygenase (ndo) as well as other genes related to its PGP potentials. This work provides new insight toward the understanding of the relationships between alkB-harboring bacteria and plants selected for phytoremediation management which could lead to the development of innovative bacterial inoculants for plants to remediate PHC-contaminated soils.

Keywords: Phytoremediation; alkane 1-monooxygenase (alkB); willow, plant growth-promoting (PGP) traits; rhizosphere microbiome; petroleum hydrocarbons (PHCs) contaminated soils; degradation

P45: The Effects of Climate Warming: A Meta-Analysis on The Distribution and Determinants of Nutrient Cycling Microorganisms in The Arctic Environment

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ABSTRACT

The Arctic region features permafrost, frozen soil lasting at least two consecutive years, and an active layer of seasonally thawed soil above it. Human activity and climate change are causing more frequent permafrost thaw, leading to increased concentrations of organic carbon, nitrogen, methane, and other substances in the active layer. This alters microbial communities, enhancing organic material and nutrient cycling. This leads to higher microbial activity, resulting in greater greenhouse gas emissions, ultimately affecting the climate system. As permafrost thaws, it also opens up the soil to plant colonization. This study, we performed a meta-analysis using 16S rDNA amplicon sequence pooled from 40 different studies aimed to determine important physico-chemical parameters that influence the microbial communities in sub-arctic and high-arctic regions, and their distribution. We found a higher abundance and diversity of methane and nitrogen cycling microorganisms in sub-arctic soil which are considerably influenced by the factors like soil pH, temperature, vegetation presence, and latitude differences. We found difference in bacterial community and abundance among high-arctic and sub-artic soil. Also, we found that soil pH and vegetation are significant factors in shaping the nitrogen cycling bacterial community in both upper and lower sub-arctic tundra soil. Factors like pH and organic carbon were important in determining the Cyanobacterial community structure.

Keywords: Arctic microbiome, methane cycle, meta-analysis, nitrogen cycle, soil microbiome.

P46: Customized Biochar for Soil Applications in Arid Land: Effect of Feedstock Type and Pyrolysis Temperature on Soil Microbial Enumeration and Respiration

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Abstract

Biochar amendments are gaining globally for improving soil health and carbon storage. This study investigated the physicochemical properties and impact on soil microbes of biochar amendments derived from two feedstock sources: date palm leaves (D), and mesquite plants (M); pyrolyzed at 450, 600, and 750 ℃. SEM images revealed that the pore size increased with increasing pyrolysis temperature. According to the Fourier transform infrared spectroscopy results, the increase in pyrolysis temperatures reduced the O-H and C-O bonds while increasing the proportion of C-C bonds. The dynamic thermal gravimetric analysis evidence that the thermostability was greatest at a pyrolysis temperature of 750 °C, and was also significantly different for the two feedstock materials used. The M feedstock produced biochar with the highest surface area (600 m2 g -1) and carbon content based on loss on ignition (95%); moreover, this biochar reduced soil microbial enumeration and respiration, and this effect was more pronounced for biochar pyrolyzed at 750 °C. As a result, M biochar feedstocks are not recommended for improving soil health, but they may be useful as microbial inhibitors when soil-borne plant pathogens are present. Based on the physicochemical properties and the biochar impact on soil properties, D at 600 °C was chosen as the best-performing biochar in our study for improving soil health in arid lands and was selected for further research as a soil amendment. The large differences in biochar physicochemical properties and their observed effect on soil properties confirmed that the feedstock type and pyrolysis temperatures must be considered during biochar production for soil health applications in arid-land agroecosystems.

Keywords: Biochar amendments, soil microbes, temperatures

P47: Taxonomic Diversity of Halophilic Sulfur-Oxidizing Bacteria In Omani Soils

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Abstract

Soil elemental sulfur (S0) amendment plays a crucial role in saline and alkaline lands including soil pH reduction, and soil-water uptake amelioration, therefore, improving nutrient availability. This research aimed to study the taxonomic diversity of prokaryotes in five different soils under increasing S0 doses, ranging from 200 ppm to 1000 ppm, incubated for eight weeks. The results from the 16S rRNA V4 gene sequencing analysis showed that Proteobacteria, Firmicutes, and Actinobacteria, are the most dominant phylum for both samples (without the addition of sulfur and with 1000 ppm S0). Whereas, in the taxonomic analysis for the control treatment (without the addition of sulfur S0), the most dominant bacterial phyla were Proteobacteria (34%), Firmicutes (23%), and Actinobacteria (14%). In addition, the most dominant archaea phylum was also Thaumarcheotal (10%). For the treatment of 1000 ppm elemental sulfur (S0), the taxonomic abundance showed 90% for bacterial taxa and 10% for archaea. Whereas, the bacterial phyla were Proteobacteria (41%), Firmicutes (20%), and Actinobacteria (12%) (the Proteobacteria percentage was most dominant in the treatment of soil with 1000 ppm S0). However, the abundance of archaea diversity was negligible in the 1000 ppm S0, and Thaumarcheotal was its most dominant phyla. From the taxonomic analysis results, the main finding highlighted that even though S0 caused small changes in bacteria diversity indices it changed dramatically their community structure. In fact, in some samples, there was a considerable increase in the relative abundance of sulfur-oxidizing chemolithotrophic and autotrophic denitrifying sulfur-oxidizing bacteria after elemental sulfur addition. Further research is needed to clarify the individual role and relative ecological importance of the individual halophilic sulphur oxidising bacteria.

Keywords: Soil elemental sulfur (S0), taxonomic, bacterial

P48: Response of Soil Salinity Change to Bacterial Diversity And Ability To Metabolize Low Molecular Weight Organic Acids

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Abstract

This study dealt with the effect of soil salinity in soil bacteria diversity, enumeration of Soil Microbial Biomass (SMB), soil microbial respiration and Substrate-Induced Respiration (SIR) by low molecular weight organic acids, assessed in four Omani date palm farm soils. Eight increasing NaCl doses were used, ranging from no added salt (ECe 2.1 dS m-1) to a maximum (ECe 36.8 dS m-1), generated by adjusting moisture to 25% (v/v) with 0 to 10 % NaCl saline solutions concentration. The carbon sources used in the SIR analysis were glucose, citric, oxalic, malic, and succinic acids added at 30 μg/g of dry soil. Enumeration of aerobic microbes was determined through agar plates and microbial respiration was investigated by MicroResp™ assays. Soil bacteria and archaea diversity were assessed through 16S rRNA gene sequencing. The results showed 83% decrease in culturable heterotrophic bacterial and actinomycetes enumeration at maximum salinity, whereas fungi were decreased by 73%. Soil salinity increased the proportion of actinomycetes only at below EC levels 10 dS m-1 . At maximum salinity, respiration was increased by 27% and the Microbial Metabolic Quotient (MMQ) was increased by 631%. Moreover, the 16S rRNA gene sequence analysis indicated a steep increase in a relative abundance of salt tolerance bacterial genera e.g., Cytophaga, Ohataekwangia, Salinimicrobium, Bacillus, Clostridium and Methanobacterium. The Firmicutes, Bacteroidetes, and Thaumarchaeota phyla increased their relative abundance in response to salinity. Significant interaction between soil ECe, SIR and MMQ was observed. Increasing SMR correlated with MQ strongly contribute diversity of Bacteroidetes, Actinobacteria, Cyanobacteria, Candidatus tectomicrobia, Bacilli, firmicutes, and acidobacteria. In conclusion, this study demonstrates soil salinity decreases bacteria abundance and diversity within increases microbial activity and their ability to metabolise fresh carbon sources. The stimulation of soil halophiles was strongly observed between 9.34 and 26.62 dS m-1 . This study unravels the intricate interplay between soil salinity, and microbial communities, highlighting its transformative effect on both the composition and function of the ground microbial ecosystems, which are vital for agricultural production.

Keywords: soil, SIR, bacterial, microbial activity, salinity

P49: Soil Stabilization of Biochar-Carbon Amendments by Using Natural and Synthetic Colloidal Clay Sized Mineral Additives.

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Abstract

Biochar is a carbon-rich material used to increase the fertility of the soil and improve its properties. It is produced through a process called pyrolysis which determines its stability. Biochar produced at low temperatures is known to have a lower half-life compared to those produced at higher temperatures. In this study, we investigated the effect of different clay co-amendments on biochar stability as measured through microbial respiration (cumulative CO2 production during the first month of incubation in soils). The effect on microbial enumeration, activity, and diversity was also assayed. We hypothesized that a) the biochar treated with inorganic clays increases biochar stability and reduces its degradation rate in calcareous sandy soils of Oman, and b) based on the available literature, allophane clays would be the most effective biochar additive for this purpose. Local clays were also tested as a sustainable alternative to Allophane and Ferrihydrite synthetic clays and were separated from the Al Khaoud dam sediment after flocculation with Fe, Mg, Ca and HCl. Biochar clay homogenous mixtures were achieved in stirred suspensions at different doses (0, 0.032, 0.064, 0.128, 0.256, and 0.512) % by mass. Biochar that was obtained from date palm leaves was pyrolyzed at 450 °C and applied to the soil at 2.5% by weight. The results showed that biochar increased the soil microbial respiration rate, and the addition of different clays to biochar showed a stabilization effect bringing respiration rates closer to unamended soils. In general, the clays significantly reduced the average respiration rate except for SB-cCa and SB-cHCl treatments. Moreover, ferrihydrite (Fh) at the maximum tested dosage (0.5%) was the most effective treatment to achieve this effect. The reduction in respiration rate was not reflected in a reduction in bacterial enumeration. The 16S rRNA prokaryotic community taxonomic diversity characterization showed more diversity in control soil compared with treated soils with 2.5% biochar and 0.512% clays and revealed a decreased abundance of archaea in samples amended with biochar and clays, with an increase in the dominance of firmicutes, especially in SB-cHCl treated samples. The differences in Shannon and Evenness diversity indexes for total operational taxonomic units (OTUs) between control soil and soil amended with biochar and clays were small, while the number of bacteria classes was significantly reduced compared with control soil. The addition of both locally sourced natural clays and synthetic clays caused a strong increase in the flavobacteriia class. The pH of biochar amendments appears to be driving the abundance of actinomycetia and betaproteobacteria. These findings highlight the potential of biochar and clays as effective soil management strategies for enhancing biochar stability and the long-term effect on carbon sequestration and other soil features offering a sustainable solution for agriculture and ecosystem restoration in arid regions.

Keywords: Biochar; Biochar Pyrolysis; Allophane; Ferrihydrite; Stabilization; Clay amendment; Clay synthesis

P50: Bacillota Abundance and Seasonal Dynamics in Salt Flat Soil Ecosystems

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ABSTRACT

Salt flats, known as "Sabkha" in Arabic, are expansive mud flats with extraordinarily high sodium chloride concentrations, making them hyper-saline environments. Within these distinctive ecosystems, specialized bacterial members have evolved to endure challenging conditions, including intense salt levels and drought stress. To delve into how seasonal shifts influence bacterial communities and diversity, we gathered salt-flat samples from Abu Dhabi (UAE) during late winter, early summer, and late summer. Employing a culturomics approach with a variety of microbiological media tailored for halophilic/halotolerant bacteria, we isolated and examined 158 diverse bacterial isolates from the samples. Out of these, after removing duplicates, 41 displayed unique sequences and were identified at 99% similarity in existing databases. Across the seasons, the Bacillota phylum, particularly the Bacillales order, emerged as the dominant presence in the salt flats. Bacillus paralicheniformis and B. licheniformis were notably prevalent, showcasing pathways linked to salt (amino acid, fatty acid) and oxidative stress tolerance (polyamine). Bacterial richness exhibited noteworthy variation throughout the seasons, peaking during the early summer season. Moreover, bacterial communities exhibited distinct patterns influenced by soil heterogeneity, particularly in terms of salinity and climatic factors like precipitation. In essence, our research underscores the consistent prevalence of Bacillota in salt flats across various seasons, highlighting the adaptability of key halophilic species such as B. paralicheniformis and B. licheniformis to extreme saline conditions. These species achieve this by modifying their salt and oxidative stress tolerance-related pathways. These insights significantly enhance our comprehension of microbial dynamics within alt-flat environments and how these microbes respond to seasonal fluctuations.

Keyword: Bacterial community, Halophiles, Hypersaline soil, SabkhaSalt-flats, Sanger sequencing,

P51: Impacts of Soil Microbial Communities on Plant Performance: Insights from Microbiome Manipulation

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ABSTRACT

Soil microbial communities derive key ecosystem functions and services, including plant productivity and nutrient cycling in agroecosystems. However, the ongoing global climate change factors directly and/or indirectly impacts the composition and functioning of soil microbial communities, with consequences for plant fitness and overall agroecosystem productivity. Therefore, it becomes crucial to understand how differential soil microbial communities (likely impacted by environmental stresses) impact plant fitness, especially in the arid regions of the United Arab Emirates (UAE). To manipulate soil microbial communities, we used 'alive' versus 'sterilized' soil as inocula. We grew alfalfa (Medicago sativa L.), an important forage crop in the UAE, in one common sterilized soil with either 'alive' or 'sterilized' inocula. Control treatment consisted of 'alive' soil + ‘alive’ inoculum. After a one-month growth period under controlled environmental conditions, microcosms were destructively harvested, total root and shoot biomass was measured and various functional root traits were measured. We found significant impacts of soil inocula on plant performance. Compared to the control, shoot biomass was greater under 'sterilized' soil inocula, whereas 'alive' soil inocula had the opposite effects. These results demonstrate that it is not the diversity per se that impacts plant fitness rather the specific microorganisms are likely contributing to these effects. Currently, analysis of functional root traits is ongoing. The overall results will be presented as a poster with specific conclusions.

Keywords: agroecosystems, microbial diversity, plant performance, soil inoculum, alfalfa, pathogens

P52: Phenotypic and Genotypic characterization of Ralstonia solanacearum infecting eggplant Solanum melongena L. from Goa and Western region of India.

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ABSTRACT

In Goa, a variety of solanaceous vegetables are cultivated throughout the year. Eggplant cultivation in Goa is severely affected due to bacterial wilt caused by a phytopathogen R. solanacearum. Agassaim is the popular local cultivar found in Goa, highly susceptible to wilt and disease incidence. For the successful infection of the host, R. solanacearum possess multiple virulence factors. Environmental and soil factors have a very important role in determining the persistence of R. solanacearum in soil. Soils with poor water drainage, high salt concentration and extreme pH and temperature ranges are not favourable for survival of R. solanacearum. An extreme adaptation of R. solanacearum towards wide range of hosts, environmental factors and its survival mechanisms makes its management very difficult and hence a number of attempts have failed to manage the disease. A systematic study was undertaken to study the genetic diversity of R. solanacearum infecting solanaceous vegetables from Western regions of India. Fifty isolates of R. solanacearum were studied for their host range and were characterized using BOX and ERIC PCR. Out of these, 33 were isolated from eggplant, chilli, tomato and others were obtained from culture collection of Plant Pathology Laboratory, ICAR Research Complex for Goa. Pathogenicity of these isolates tested on three different hosts indicated that 49 isolates were pathogenic on eggplant, 44 isolates on tomato and 11 isolates on chilli. Results indicated that all the isolates studied belonged to Phylotype I based on the ITS region and biovar 3, except one isolate which is grouped under biovar 6 as per new classification. However, BOX and ERIC fingerprinting technique showed wide genetic variation among the isolates exhibiting 15 and 14 unique fingerprint patterns and 9 and 14 clusters respectively. This indicates that though R. solanacearum from Goa are phenotypically similar, great variation exists when whole genome is analyzed by rep-PCR.

Keywords: R. solanacearum, Genetic diversity, Rep-PCR, Pathogenicity.

P53: Diversity-Dilemma: Complex Relationship Between Soil Microbial Diversity and Plant Productivity

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ABSTRACT

The functionality of many natural and semi-natural ecosystems is positively linked to the diversity of soil microbial communities. Furthermore, soil microbial diversity has been identified as a mitigating factor for the negative impacts of environmental stresses on community productivity. However, in intensively managed cropping systems, this relationship has rarely been empirically tested, despite calls to incorporate microbial diversity as a measure of soil health. To explore this underlying assumption, we conducted a microcosm experiment with barley plants under controlled environmental conditions. Our aim was to determine whether increasing soil microbial diversity and complexity would result in enhanced plant productivity and if increasing microbial diversity would buffer the negative impacts of drought stress on plant fitness. We manipulated microbial diversity using a 'dilution to extinction' approach. The barley plants were cultivated in a common sterilized soil, and varying levels of microbial dilutions were introduced to establish distinct soil microbial diversity. Surprisingly, our findings indicate that augmenting soil microbial diversity led to a reduction in plant biomass production, despite the positive effects of microbial biodiversity on plant nutrient uptake. Moreover, increasing microbial diversity did not alleviate the effects of drought stress on plant fitness. These results illustrate a discrepancy in the role of microbial diversity between intensively managed cropping systems and other ecosystems, thereby emphasizing the necessity for further investigation into the role of soil microbial diversity in cropping systems.

Keywords: Soil biodiversity, drought stress, plant productivity, ecosystem functioning

P54: A Genomic Catalogue of Soil Microbiomes Boosts Mining of Biodiversity and Genetic Resources

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Abstract

Soil harbors a vast expanse of unidentified microbes, termed as microbial dark matter, presenting an untapped reservoir of microbial biodiversity and genetic resources, but has yet to be fully explored. In this study, we conducted the first large-scale excavation of soil microbial dark matter by reconstructing 40,039 metagenome-assembled genome bins (the SMAG catalog) from 3,304 soil metagenomes. We identified 16,530 of 21,077 species-level genome bins (SGBs) as unknown SGBs (uSGBs), which greatly expand archaeal and bacterial diversity across the tree of life. We also illustrate the pivotal role of uSGBs in augmenting soil microbiome's functional landscape and intra-species genome diversity, providing large proportions of the 43,169 biosynthetic gene clusters and 8,545 CRISPR-Cas genes. Additionally, we determined that uSGBs contributed 84.6% of novel viral-host associations identified from the SMAG catalog. Our results propose the SMAG catalog, a novel and expansive genomic resource that brings the soil microbial biodiversity and novel genetic resources to light.

Keywords: Soil, microbes, SMAG, SGBs, genetic

P55: Enzymatic Profiling of Halophilic And Halotolerant Bacterial Isolates Screened From Hypersaline Soil Of UAE

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Abstract

Hypersaline soils are the unique environments for the growth of novel halophilic and halotolerant microorganisms (including bacteria and archaea). These microorganisms are of special interest since they produce a range of industrially important extremozymes. Our knowledge about these extremozymes is scarce, especially in the extremely saline sabkha of Abu Dhabi (UAE). In a previous study, we screened and identified 75 different bacterial isolates from sabkha. In this study, we aimed to explore the bacterial library for their ability to tolerate the salt level and their extremozyme production potential, particularly, cellulases, proteases, amylases, lipases, xylanase, hydrolases and transferases. To assess salt tolerance analyses we grew cultures in plates with 5-15% (w/v) NaCl concentrations. We used enzymatic plate-based analyses for most enzymes, except hydrolases and transferases where we used Thin Layer Chromatography (TLC) analyses. Salt tolerance analyses confirmed that all isolates were able to grow at 10% of salt concentration whereas four isolates Rhizobium azibense, Lysinibacillus macrolides, Bacillus tropicus and Sporosarcina globispora tolerated 15% Nacl concentration. Further, we found that of total bacterial isolates, 90% produced cellulases, 85% proteases, 22% amylase, 6% lipases and 1% produced xylanases enzymes. Using TLC analyses we also observed that 66% of isolates were able to hydrolyze the sucrose thus producing hydrolases and transferases enzymes. Overall, we show that sabkha microorganisms are mostly related to the genus Bacilli that grow at 10% salt concentrations, only four isolates, particularly Rhizobium azibense, Lysinibacillus macrolides, Bacillus tropicus and Sporosarcina globispora, grow at 15% Nacl concentration producing a range of extremozymes allowing them to grow in such a hypersaline environment. These findings highlight that sabkha can offer various biocatalysts active in extreme environmental conditions that have significant industrial applications.

Keywords: Extremozymes; Halophilic and halotolerant bacteria; Hypersaline environment; Salt tolerance, Transferases

P56: Bacillus Species from Native Mangrove Plants Promote Spinacia Oleracea (Spinach) Growth in Marginal Environments

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Abstract

Growing crops in marginal environments under arid conditions is the leading global challenge for sustainable food security amid climate change scenarios. Plant growth-promoting bacteria (PGBP) from various ecosystems have been reported to enhance the productivity of edible crops worldwide. However, PGPB applications for improving crop productivity in marginal environments have yet to be reported. In this study, we attempted to assess the effects of two plant growth-promoting bacilli isolated from Umm-al Quwain Mangrove sediments on the growth of Spinacia oleracea. After screening, over eight weeks, two bacillus species with multi-plant growth-promoting traits were selected to study their effect on Spinacia oleracea growth. 16S rRNA gene sequencing identified two PGPBs as Bacillus licheniformis and Bacillus wiedmannii. After the coating, Spinacia oleracea seeds were divided into treated and untreated groups for field trials under shade house conditions. During the early germination of Spinach, the data were recorded for germination rate and leaves number. SPAD and NDVi analysis was performed to measure the amount of chlorophyll and vegetation coverage. Among the treated and the untreated groups, the Bacillus licheniformis treated group had the fastest germination rate, the most significant average leaf quantity, and the highest data for SPAD and NDVI. This study successfully demonstrated the potential of two Bacillus species from a native mangrove ecosystem in stimulating the growth of Spinacia oleracea in marginal environments. This study indicates the possibility of further exploring PGPB from native mangrove or desert plants in the UAE and using them as biostimulants for enhancing various crops in urban agroecosystems.

Keywords: Plant growth-promoting bacteria, Spinacia oleracea, marginal environment, Mangrove ecosystem

P57: New Possible Complementary Approaches to Study The Responses Of Terrestrial Alpine Ecosystems To Climate Changes In The MICROPLANTALP Project

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ABSTRACT

Climate change (CC) is causing wide alterations in the natural balance, composition, and structure of numerous ecosystems, and alpine regions are among the most vulnerable ones. Soil microorganisms play a pivotal role in the regulation of biogeochemical cycles. A substantial gap exists in the understanding of the biological response to this change at the soil level, due to the untangled plant and microbial activity. The MICROPLANTALP project aims to overcome these limits by integrating two complementary transplantation approaches within a single study, to characterize the responses of an alpine grassland ecosystem (Mont Blanc area, Courmayeur, Italy) under possible CC scenarios. In the first approach, soil monoliths containing native plants, collected at high altitudes (2,500 m a.s.l.), were transplanted to a lower altitude (1,500 m a.s.l.). Photosynthesis and soil respiration were monitored concurrently at the two elevations by automated clear and opaque closed dynamic chambers. In the second transplantation, monoliths collected in the same high-elevation area have been exposed to two different future CC scenarios (increases in temperature and CO2) at the European Ecotron of Montpellier (France) (www.ecotron.cnrs.fr). As a next step, changes in bacterial and fungal communities' diversity and composition will be studied with a DNA metabarcoding approach. Variations in the metabolic activity of microbial communities will be evaluated through enzymatic activity assays targeting biogeochemical cycle-related enzymes. Specific taxonomic groups and genes associated with these processes will be analyzed using qPCR approaches. The data obtained will be compared and integrated considering above-ground plant growth, carbon fluxes, and soil physicochemical parameters. (Project # 20204KF4RW funded by the Italian Ministry of University and Research - Call PRIN 2020) The MICROPLANTALP project was made possible thanks to the precious collaboration of Fondazione Montagna Sicura - Courmayeur, Valle d'Aosta, Italy - https://www.fondazionemontagnasicura.org/

Keywords: soil communities, biogeochemical cycles, transplantation approaches, DNA metabarcoding.

P58: Mixed Litter Modifies the Microbial Communities To Mediate Decomposition In Mountains

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ABSTRACT

Litter decomposition is an essential ecological process that drives biogeochemical cycles, nutrient pools, and their fluxes. Decomposition close to the litter source confers home-field advantage effects which results in plant-specific patterns in nutrient release and, hence, may contribute to litter-mediated Plant Soil Feedbacks. However, limited research has been conducted on the factors that govern the impact of mixing litters from multiple species on litter decomposition and nutrient dynamics. Additionally, only a few studies have examined how the effects of litter mixing might vary across different habitats or ecosystems, and how they respond to environmental gradients. As understory vegetation typically represents the largest component of temperate forest diversity, and can impact long-term productivity and stability, we conducted a litter bag experiment using leaf litter from two native understory subshrubs, Sambucus wightiana and Viburnum grandiflorum. This experiment was carried out at four different elevations within the forests of Kashmir Himalaya. Subsequently, we analyzed the soil mycobiome associated with the litter bags using Next Generation Sequencing (NGS). Litter mixing resulted in accelerated litter mass loss, decomposition rate and an increase in microbial abundance and functional diversity. This non-additive effect can be attributed to factors like interactions between the two litter types, changes in the physical and chemical properties of the litter mixture, alterations in microbial activity and nutrient dynamics, and the creation of microenvironments that favor certain decomposer organisms. The impact of elevation on both litter decomposition and microbial diversity was found to be insignificant. These findings advance our understanding of how understory vegetation in the mountains can alter microbial communities and consequently influence the ecosystem processes they mediate.

Keywords: mycobiome, litter decomposition, Next Generation Sequencing

P59: Associated Cereal and Legumes Microbiome Networks Shaped by Olive Agroforestry In Semi-Arid Conditions

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ABSTRACT

Agroforestry has been identified as a promising land-use system for climate change mitigation. Yet, little is known about the below-ground microbial communities of associated crops with such agroecosystems. Herein, we performed a microbial holistic integrated study using soil physicochemical properties and rhizospheric microbial community datasets to outline the co-occurrence pattern of organic olive-agroforestry (AF) network compared to conventional cropping (C) network for two cereals (barley and durum wheat) and two legumes (chickpea and faba bean). We determined the most suitable annual crop species in AF under semi-arid conditions. Crops microbiomes were found to be exclusively shaped by the agroecosystem, with only marginal influence of host selection, whether cereals or legumes. Of the selected soil physicochemical properties, organic matter was the principal driver in shaping the soil microbial structure in the AF system. Additionally, agroforestry reduced cereal and legume rhizospheric microbial diversity, enhanced network complexity, and leads to more stable beneficial microbial communities mitigating consequences of soil degradation. The co-occurrence network analyses indicated that the core microbial community in AF rhizosphere is more complex and established a higher number of interactions, suggesting that this latter is more stable and functional than conventional cropping. Taxa belonging to Tomentella, Funneliformis, Archaeospora, Entoloma, and Bovista genera were identified as potentially key ecological microbes. Overall, this study helps to understand the effect of AF on cereals and legume's core microbiome, especially in organic agriculture, thus providing much more accurate predictions to preserve soil microbial diversity.

Keywords: Olive agroforestry, Rhizosphere, Microbial network keystones, Cereals, Legumes

P60: Natural Existing Arbuscular Mycorrhizal-Bacterial Biofilm Associations and Their Functional Behavior

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ABSTRACT

In symbiosis with plant, arbuscular mycorrhizal fungi (AMF) access the carbon stored in the roots in exchange for increased uptake of nutrients and water from the soil. In the mycorrhizal-plant symbiosis, AMF–associated bacteria (AAB) serve as a third partner and are tightly linked to AMF. AAB are involved in mycorrhizal activity and nutrient uptake enhancement and have impact on plant development. In order to create innovative biofertilizer for sustainable crop production, it is important to understand the function and process of this inter-kingdom natural coexistence. In our research, we used in vitro and in situ co-cultures to screen 33 different AMF species, and we characterized 231 AAB using 16S rDNA analysis. 109 selected AABs were examined for ten functional qualities that promote plant growth, and it was found that different bacterial strains had a variety of advantageous traits. The association of AAB was seen as biofilm and endobacteria using microscopic methods. Further, by using an in vitro assay system, an association recreation of 12 AAB-Rhizophagus irregularis was investigated to look at the impact on mycorrhization and functional capabilities. It was observed that AABs moved along the developing R. irregularis hyphae and spores. Different AAB had an impact on AMF development as well as its capacity to solubilize phosphate and potassium, and fix nitrogen. We discovered both the synergistic interactions and partnerships between the two cross-kingdom microbial partners. Understanding the molecular elements of these fungal-bacterial connections, which will enable their later use and modification for sustainable agriculture practices, is another area of focus.

Keywords: Arbuscular mycorrhiza fungi; Mycorrhiza associated bacteria; Symbiosis; Tripartite association; Biofilms

P61: Use of Root Endophytic Enterobacter SA187 For the Improvement of Abiotic Stress Tolerance of Tomato Grown Under Greenhouse Conditions

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Abstract

Agricultural productivity is largely affected by climate change. These climatic alterations are translated into adverse abiotic stress conditions, such as heat, drought, and salinity, which restrict the geographical distribution of plants and limit their crop yields. Extreme conditions primarily affect semi-arid and arid regions, causing severe environmental and economic repercussions. Plant growth-promoting rhizobacteria (PGPR) have been proposed as a solution to overcome these challenges. The desert plant endophytic bacterium Enterobacter sp. SA187 has shown beneficial effects on plant growth and salt stress tolerance in the model plant Arabidopsis thaliana in vitro, as well as under field conditions on different crops. In this study, we examined the effects of SA187 colonization on tomato seedling growth in greenhouses under abiotic stress conditions (salinity and heat). Our findings indicate an increase in the plant biomass, lateral root density, and chlorophyll content of SA187 colonized plants under normal, salt, and heat stress conditions. Colonization enhanced plant growth metrics, including fresh and dry plant mass, lateral root density, total chlorophyll content, and Na+ and K+ ion contents. The levels of antioxidant enzymes, such as catalase, superoxide dismutase, and peroxidase, in plants were enhanced by bacterial colonization. Transcriptome sequencing using RNA-seq of tomato roots grown under salt and drought stress revealed the upregulation of certain pathway genes related to abiotic stress. In conclusion, this study demonstrated the role played by the root endophyte in inducing abiotic stress tolerance in tomato and heralded the use of this Enterobacter as a bioinoculant to adapt agriculture to the challenges of abiotic stresses.

Keywords: Plant Growth-Promoting Rhizobacteria (PGPR), Enterobacter sp. SA187, Abiotic stress tolerance, tomato, Endophytes

P62: Isolation, Characterization and Screening of Antimicrobial Producing Lactic Acid Bacteria Isolated During Fermentation of Dried Tiger Nuts (Cyperus esculentus)

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Abstract

Lactic Acid Bacteria (LAB) are generally regarded as safe (GRAS), this is due to their ability to produce certain organic substances that helps in fermented foods and preservations. This study isolated, characterized and screened for antibacterial and antifungal producing LAB during fermentation of dried tiger nuts. Dried tiger nuts were collected from three different selected locations (kuto (K), Lafenwa (L) and Panseke (P)) in Abeokuta and were fermented for 72 hours. The pH and Total Titratable Acidity (TTA) of the fermenting medium were determined. Fermentation effluents were collected at 12 hours interval for the isolation of LAB which were characterized using cultural and phenotypical features. The LAB were screened with Escherichia coli, Salmonella spp, Vibrio spp, and Pseudomonas spp to detect their antibacterial potentials. Screening for their antifungal potentials were tested against Aspergillus niger and Aspergillus flavus. From the data obtained, the pH of the fermenting medium ranged from 2.50 - 6.40, 3.84 - 6.40 and 4.61 - 6.40 for dried tiger nuts of K, L and P respectively. TTA increased from 0.57 - 3.72, 0.57- 5.12, 0.57- 2.15 for dried tiger nuts of K, L and P respectively. The LAB count increases with fermentation period. A total of 38 LAB isolates were obtained from the dried tiger nut and were identified as different as 8 genera including Lactobacillus plantarum, Lactobacillus fermentum, Lactobacillus acidophilus, Lactobacillus caesi, Lactobacillus mesenteroides, Lactobacillus helveticus, Lactobacillus crimoris, and Lactobacillus thermophilus, with L. messenteroides and L. plantarum being the predominant LAB. A total of 35 out of the 38 LAB isolates screened had antibacterial properties indicated by inhibiting the growth of selected spoilage bacteria used at 1mm-14mm of zones of inhibition. For antifungal screening, 28 out of the 38 LAB isolates screened had antifungal properties at inhibition value greater than 8% of the plate area. The antibacterial and antifungal properties exhibited by these LAB isolates indicate the possibility of using LAB as biological agent in food preservations and in the production of antimicrobials.

Keywords: Tiger nuts, Antimicrobials, Lactic Acid Bacteria

P63: Species Identification and Whole Genome Sequencing of Bacterial Isolates from Abu Dhabi Sabkha Region

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Abstract

Sabkha regions are salt-encrusted flat surfaces found along the coastal areas around different parts of the World. These regions are home to diverse microbial populations possessing unique environmental properties. This study aimed to investigate the bacterial diversity of the Sabkha present in the Abu Dhabi region of the United Arab Emirates. Bacteria were isolated from the soil samples collected from the Sabkha region. Genus-level bacterial characterization was done using Sanger sequencing, while whole genome sequencing of respective isolates was performed utilizing Illumina and Nanopore sequencing to identify bacteria at the specie level. The bacterial isolates SD, S11, S4 and SA were identified as Altererythrobacter marensis, Bacillus subtilis, Priestia aryabhattai and Staphylococcus capitis, respectively. The S4 sample showed a genome size of ~5.0 Mb with 5085 protein-coding genes. The whole genome assembly of Altererythrobacter marensis revealed a genome size of ~2.9Mb with high GC content of 66.38% and a plasmid. Staphylococcus capitis had a genome size of ~2.47 Mb, with 2351 protein-coding genes and a plasmid whereas Bacillus subtilis had a genome size of ~4.1 Mb and 4025 protein coding genes. This study provides insights into the diverse microbial community of the Sabkha region. Future studies are needed to gain a deeper understanding of the ecological role of these bacterial species.

Keywords: Bacteria, Sequencing, Sabkha, UAE

P64: Biogenic Silver Nanoparticles Decorated with Methylene Blue Boosted the Photodynamic Eradication of Pseudomonas aeruginosa and Staphylococcus aureus.

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Abstract

The relentless emergence of multidrug resistance in microorganisms has spurred efforts to explore alternative therapeutic methods. Antimicrobial Photodynamic Therapy (aPDT) has emerged as an innovative approach to combat both biofilms and planktonic cells of pathogens. Interestingly, nanoparticles (NPs) possess intrinsic antimicrobial properties. Thus, this study focused on investigating the potential of silver nanoparticles (AgNPs) to enhance aPDT using methylene blue (MB) as a photosensitizer (PS) against Staphylococcus aureus and Pseudomonas aeruginosa. AgNPs were synthesized using bacteria isolated from sewage water in Kalapet, Puducherry, India. The isolated strain was sequenced and identified as Bacillus subtilis.This bacteria was deposited in GenBank (NCBI) as Bacillus Subtilis RY3under the accession number KY490092. The produced biogenic AgNPs, averaging 30 ± 5 nm in size, were coated with MB to create nano-conjugates (MB-AgNPs) and characterized using UV-Visible spectroscopy, FTIR, TEM, DLS, XRD, and SEM-EDX. This study evaluated aPDT against planktonic cells and biofilms of test strains using antibacterial assays, Reactive Oxygen Species detection, protein leakage assessment, biofilm inhibition tests, and confocal laser microscopy. The

results indicated that MB-AgNPs exhibited four-fold greater antibacterial activity than MB alone. Utilizing biogenic AgNPs as nanocarriers for PS, led to a decrease in the required PS concentration for achieving antimicrobial photodynamic effects. Moreover, this approach improved the permeability of PS and its loading capacity into cells.The enhanced antibacterial activity was observed in both bacterial species compared with free MB and AgNPs that contributed a greater amount of ROS production as detected in fluorescence spectroscopy. Further assays revealed that the enhanced antibiofilm activity of MB-AgNPs post light exposure resulted from the nanodye conjugate's ability to penetrate deeper biofilm layers, displaying higher phototoxicity than free MB. Therefore, present study concludes that MB-AgNPs could be considered as an excellent alternative to combat antibiotic resistant bacteria.

Keywords: multidrug resistance; antimicrobial photodynamic inactivation; silver nanoparticles; methylene blue; anti-biofilm

P65: Innovative Detection of Phytohormones In Aloe Vera

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ABSTRACT

Phytohormones are plant hormones that are found in trace concentration. Their presence is necessary to maintain plant development and maturation, control over cell division and tissue differentiation, and regulate plant behavior in response to varied stimuli. Determination of phytohormones is challenged by their extremely low concentration in plant tissues and the wide variety of their levels among various plant species. Therefore, the goal of this work was to develop a novel analytical technique for identifying and quantifying phytohormones in Aloe vera. The target phytohormones included abscisic acid (ABA), gibberellic acid (GA), indole-3-acetic acid (IAA), 6-benzylaminopurine (6BAP), isopentenyl adenine (ISA), naphthalene acetic acid (NAA), and salicylic acid (SA). For a meticulous detection of the phytohormones, a LC-MS/MS method was developed. The chromatographic separation was achieved using a Zorbax Eclipse Plus C18 column. As for the mass spectrometry, a triple quadrupole mass spectrometer detector was attached to the LC. The phytohormones were ionized using positive and negative electrospray ionization techniques and quantification was done using a multiple reaction monitoring method. Out of the seven target phytohormones, four were identified including IAA, ABA, GA, and SA. The average level of the identified phytohormones in six random aloe vera samples was in the order ABA>SA>IAA>GA. However, variations in the level of these phytohormones were not significant on a 95% confidence interval. Analysis of the cross relation between any two phytohormones in a given sample revealed no trend of an increase or a decrease.

Keywords: Phytohormones, Aloe vera, LC-MS/MS.

P66: Estimation and Validation of 8 Phytohormones in Tomato Using LC-MS/MS

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ABSTRACT

Tomato (Solanum lycopersicum) belongs to the family Solanaceae and it is one of the most important plants in the world since it has a high consumption rate. Therefore, it is essential to conduct studies about its chemical composition. Small naturally occurring organic molecules called phytohormones or plant hormones are used in different mechanisms for signaling in plants, in order to regulate organ development and growth. Quantifying multiple plant hormones simultaneously is necessary to gain a comprehensive understanding of plant physiology. In this study we investigated specifically eight important phytohormones found in tomato plant using Liquid chromatography-mass spectrometry (LC-MS/MS) which is a highly sensitive and quantitative analytical technique used for detecting plant hormones. The changes in levels of phytohormones in tomato fruits over a period of the days were measured. The results show a downtrend in the concentration of Gibberellic acid with time. Gibberellic acid is known to act along with indole-3-acetic acid in signaling pathways associated with fruit ripening. Increase in abscisic acid is associated with changes in cell wall structure leading to the softening of fruits. In addition, salicylic acid is involved in changes in the flavor and aroma of the fruit with ripening. The results demonstrate the applicability of the developed method in analytical investigations of phytohormonal crosstalk and changes in fruits, which would pave the way for further examination of the role of different hormones in the stability and storage of produce. In this study we were able to achieve an efficient methodology which was validated with high precision, accuracy, and sensitivity. The method was applied in the analysis of samples of tomato. The results show that the levels of phytohormones change over time in tomato samples, which can be correlated with the deterioration of the fruit with time.

Keywords: Tomato, chemical composition, phytohormones, Gibberellic acid

P67: Studies on The Role of Rhizopus Oligosporus For The Production Of Phytase And Degradation Of Phytic Acid In Solid-State Fermentation

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Abstract

Phytic acid (myo-inositol 1,6 hexakis phosphate) is the major storage form of phosphorus in plant seeds. It acts as an anti nutritional agent by chelating with several metal ions and insoluble form of protein complex. Therefore, it cannot be metabolized by monogastric animals due to lack of phytic acid degrading enzyme present in their intestine. These consequences contribute to mineral deficiencies and phosphorus pollution in livestock industries. Addition of phytase is the best way to degrade phytic acid phosphorus that can reduce negative nutritional effects and phosphorus pollution. Fungal phytase is one of the commercially prime enzymes for food and feed industries, and is also known to deliver desirable characteristics comparable to bacteria and yeast. Among fungi, Rhizopus species is the best phytase producing fungi that has been under intensive research for higher yield. Hence, efforts are needed to produce phytase at an affordable cost so that it can be used for hydrolyzing phytic acid with high economic potential. In this study, Mustard oilcake was used as a novel substrate for phytase production with Rhizopus oligosporus MTCC 556. A mixed substrate (wheat bran:mustard oil cake) was used to optimize different medium components under solid state fermentation at a 62% moisture content, pH 5.5, 30ºC, an inoculum level of 15%, and a ratio of the volume of a salt solution to the mass of mixed substrate 1.5 mL:10 g. Different carbon and nitrogen sources were used for production of phytase. Use of the nutritional supplements maltose and ammonium sulfate resulted in high phytase yields. The hydrolytic ability of partially purified phytase was evaluated using 5 different food grains. Wheat flour showed a 43.78% phytic acid reduction, rice flour showed 92% release of inorganic phosphorus, and corn flour showed 81 and 68% releases of soluble proteins and reducing sugars. Thus, phytase is suitable for feed applications.

Keywords: Fungal Phytase, Mixed substrate, Phytic acid, Rhizopus oligosporus and solid state fermentation.

P68: Marine Bacterial Microbiome Diversity and Spatial Distribution in Coastal Seawater and Sediments of Qatar

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ABSTRACT

The marine microbiome played a crucial role in maintaining the integrity of our oceans and had far-reaching environmental effects. Scientists had recently become more interested in studying it, using advanced tools to explore the world of small marine life. Additionally, diverse environmental factors could have varying effects on the marine microbiome, significantly influencing the occurrence of biofouling in membrane-based desalination plants. These plants were critical sources of freshwater in certain parts of the Middle East.

In our study, we had used advanced metagenomic techniques, specifically 16S rRNA sequencing, to examine the diversity of bacterial communities in coastal waters and sediments at selected sites in Qatar during two different times of the year. Our analysis, based on diversity indices and molecular phylogeny, had consistently revealed the dominance of specific bacterial phyla, particularly Proteobacteria, Bacteroidetes, and Cyanobacteria, across all sampled locations. At the family level, the most abundant operational taxonomic units (OTUs) had been associated with Flavobacteriaceae (comprising 27.07% in seawater and 4.31% in sediments) and Rhodobacteraceae (comprising 22.51% in seawater and 9.86% in sediments). Moreover, at the species level, Alphaproteobacteria (constituting 33.87% in seawater and 16.82% in sediments), Flavobacteria (comprising 30.68% in seawater and 5.84% in sediments), and Gammaproteobacteria (constituting 20.35% in seawater and 12.45% in sediments) had been abundantly represented in both seawater and sediment samples, while Clostridia (comprising 13.72%) had been prevalent exclusively in sediment samples. We had also observed that changes in environmental conditions, such as higher temperature and pH, along with lower salinity in seawater samples, had affected the levels of indicator bacteria.

In summary, our findings had suggested that sediments served as reservoirs for indicator bacteria, exhibiting higher taxonomic diversity but lower abundance compared to their counterparts in seawater.

Keywords: Marine microbiome, Environmental factors, Bacterial diversity, Metagenomics, Biofouling.

P69: Testing the panspermia theory in the microbiological space experiment "Meteorite"

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ABSTRACT

Background. The possibility of a cosmic transfer of viable biological particles and the theory of panspermia dominated the minds of scientists and philosophers for many centuries. In the 21st century, we have a unique chance to test this possibility experimentally, using the power of space technologies. Objectives and Methodologies. The biosatellite will carry a number of biological experimental systems, including the microbiological experiment "Meteorite". Samples with microorganisms placed on the outer shell of the satellite will be exposed to the hostile space environment factors (almost an absolute vacuum, hard radiation, other impacts) during 30 days of orbital flight. Then the satellite will enter the mode of a gentle parabolic incidence and its envelope will heat up to 2500°C when entering the dense layer of the atmosphere. By combining *cultivation/culturing* methods and molecular biology applications (quantitative extraction of polynucleic acids, high sensitivity cyclic amplification, Next Generation Sequencing), we will analyse whether the various microbiomes will remain viable or whether their molecular components will remain intact at the time of contact with the planet's surface. Preliminary and Expected results. Similar experiment in 2013 showed the potential survival of Bacillus subtilis during space flight. Samples containing various microbiomes of microflora and viruses, as well as samples with extremophiles will be processed for extraction and sequencing of a pool of DNA and RNA molecules. We will also detect mutational changes and genomic rearrangements caused by prolonged space flight. A comparison will be made between the data from exposed microbiological samples and control samples kept inside the satellite, as well as terrestrial controls. Conclusion. The obtained results will be important in our understanding the possibility of interplanetary transfers of life forms and the development of the theory of the origin of life on Earth, as well as for solving the practical problems of planetary quarantine.

Keywords: panspermia theory, origin of life, meteorite, biosatellite

P70: Green Approach for Indigenous Pharmaceutical Wastewater Treatment through Lab-Scale Sequential Batch Reactor

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ABSTRACT

Industrialization, globalization, and growing population results in the shortage of water and overall food reserves in the current era. To meet the global water demand, conventional wastewater treatment strategies have been employed previously, however, due to the high per capital cost and reduction in the overall land usage this technology faces certain limitations. Sludge aerobic granulation technology is a comparatively new treatment approach that is being utilized to treat different types of wastewaters, particularly pharmaceuticals. This technology is thought to be more sustainable, cost-effective, and eco-friendly. In this study, aerobic granules were prepared by an efficient Sequential Batch Reactor (SBR) with poly aluminum chloride (PAC) for the treatment of pharmaceutical wastewater. The reactor was first optimized under controlled parameters for 80 days. It was observed that PAC 50mg/L dosage accelerated the granulation process by promoting settleability, mechanical strength and denitrification rate of aerobic granules. Presumably, XRD, SEM, granule biomass and wastewater analysis showed that aerobic granules play a significant role in lowering the COD, BOD, NH_3-N and PO-P levels, respectively. The sludge granules, characterized by active microbial ecosystem dominated by Proteobacteria community, exhibited capabilities to remove organic load due to their nutrient retention, and resistance against toxic compounds. Moreover, their adaptability to fluctuating operating conditions made them suitable for treating complex pharmaceutical effluent. Results concluded that the established SBR had efficiently removed pharmaceutical burden from wastewater. This research highlights the potential of sludge aerobic granulation in the indigenous pharmaceutical wastewater sample, offering a sustainable solution with wide-ranging applicability. The future application and advance treatment mechanisms highlighted the usage of treated wastewater in cultivation of agricultural products, combat the need of water shortage by making it usable for human consumption and safe to drain in marine reservoirs. Moreover, further investigations regarding in depth analysis of aerobic granulation formation is required.

Keywords: Wastewater Treatment, Sludge Aerobic Granulation, Sustainable Approach, Green Environment

P71: Microbial Community Variation in a Pediatric Hospital environment : Implications for infection control and Patient Health

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ABSTRACT

The diversity of patients, the use of antibiotics, cleaning procedures, and ventilation systems all have an impact on the hospital microbiome, which is made up of many microbial populations that are present on surfaces, in the air, water, and among healthcare staff. These microbial communities may serve as reservoirs for prospective pathogens, hence promoting antibiotic resistance and healthcare-associated illnesses (HAIs). It is yet unclear what causes the hospital microbiome to vary and what other variables might be involved. In this investigation, we took surface samples from patient rooms in a new hospital's newborn intensive care unit (NICU), both before and after the start of inpatient procedures. Furthermore, we involved staff members in a citizen science project, gathering surface samples from six different locations throughout the hospital. A total of 197 samples underwent analysis using 16S rRNA gene amplicon sequencing, with an additional 160 samples cultured. NICU patient room samples taken before and after opening exhibited similar alpha and beta diversities, suggesting microbial community stability possibly due to restricted access. Conversely, samples taken after opening displayed wide-ranging alpha and beta diversities across different hospital areas, clustering into two distinct groups in Principal Coordinates Analysis (PCoA) based on diversity (high and low). Areas with more foot traffic were connected to high diversity samples, while areas with lower diversity samples were connected to lower foot traffic. With testing accuracy ranging from 86.37 % to 100 %, LASSO classification models found that 152 ASVs were the most useful for predicting sample origin, outperforming SVM and random forest models. The culture experiment found 138 viable species, however it did not show any changes that were noteworthy based on the type of location, reiterating the value of 16S rRNA gene amplicon sequencing in hospital microbiome research.

P72: Preterm birth significantly impacts the composition of Human Breast Milk Microbiome.

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ABSTRACT

Breastmilk (BM) provides complete nutrition for infants for the first six months of life and is essential for the development of the newborn's immature immune and digestive systems. While BM was conventionally believed to be sterile, recent advanced high throughput technologies have unveiled the presence of diverse microbial communities in BM. These insights into the BM microbiota have mainly originated from mothers who experienced uncomplicated pregnancies, possibly not reflecting the circumstances of mothers with pregnancy complications like preterm birth (PTB). In this article, we investigated the BM microbial communities in mothers with preterm deliveries (before 37 weeks of gestation). We compared these samples with BM samples from healthy term pregnancies across different lactation stages (colostrum, transitional and mature milk) using to 16S rRNA gene sequencing. Our analysis revealed that the microbial community became increasingly diverse and compositionally distinct as the BM matured. Particularly, mature BM samples were significantly enriched in Veillonella and lactobacillus (Kruskal Wallis; $p<0.001$). The comparison of term and preterm BM samples showed that the community structure was significantly different between the two groups (Bray Curtis and unweighted unifrac dissimilarity; $p<0.001$). Preterm BM samples showed increased species richness with significantly higher abundance of Staphylococcus haemolyticus, Propionibacterium acnes, Unclassified Corynebacterium species. Whereas term samples were enriched in Staphylococcus epidermidis, unclassified OD1, and unclassified Veillonella among others. Our study underscores the profound influence of pregnancy-related complications, such as preterm birth, on the composition and diversity of BM microbiota. Given the established significance of the maternal microbiome in shaping child health outcomes, this investigation paves the way for identifying modifiable factors that could optimize the composition of BM microbiota, thereby promoting maternal and infant health.

P73: Novel algorithm to reveal the unique chemistry of the human microbiome

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ABSTRACT

The human microbiome is a diverse ecosystem of microbial species that plays a crucial role in health and disease. Our understanding of the composition of the healthy human microbiome and how it is altered in human disease has advanced dramatically in recent years. We have now reached a key point in developing processes to rapidly delineate the key mediators of microbiome functions and benefits. The field must focus on defining the evolved mediators exclusive to beneficial microbiomes and understanding how their functions correlate with biological outcomes to conduct detailed testing. A mechanism to rationally infer the actions of these cryptic small molecules in an automated high-throughput manner would unlock a trove of clinical drug lead candidates. We have developed an algorithm that utilizes large- scale omics data to identify functional gene products in silico. This machine learning tool holds exciting prospects not only for harnessing beneficial microbiome products but also for applying this logic more broadly to solve significant challenges in defining the key functional products from the human microbiome using large-scale multi-omic data.

P74: CoSMIC - A hybrid approach for large-scale, high-resolution microbial profiling of novel niches

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ABSTRACT

Microbiome studies have become integral to a wide range of biological research from ecology to oncology, mainly relying on short-read sequencing of variable regions along the 16S rRNA gene. However, the comprehensiveness of 16S rRNA studies has been persistently challenged due to a lack of primer universality and primer biases, causing differences between a study's results and the underlying bacterial community. Moreover, relying on a small part of the gene often provides low phylogenetic resolution, hampering downstream taxonomy-based analysis and the ability to harmonize results from studies performed using different variable regions.

Here, we introduce a framework called 'Comprehensive Small Ribosomal Subunit Mapping and Identification of Communities' (CoSMIC), effectively addressing these challenges. CoSMIC begins with long-read full-length sequencing of the 16S rRNA gene, using Locked Nucleic Acid primers over pooled samples. This step augments the Small Subunit (SSU) reference database with novel niche-specific SSUs. Subsequently, CoSMIC optimizes a set of primer pairs targeting multiple non-consecutive variable regions along the gene, followed by standard short-read sequencing of each sample. Data from different regions are seamlessly integrated using the SMURF framework, thus alleviating primer-based biases and providing extremely high phylogenetic resolution. We evaluated CoSMIC across plant, root, soil and marine sponge samples, yielding higher profiling accuracy and unprecedented phylogenetic resolution compared to standard methods while detecting ~40,000 novel SSUs. CoSMIC provides researchers with a robust, customizable, and cost-effective framework addressing the challenges of 16S rRNA sequencing, especially in underexplored habitats, paving the way for data harmonization across microbiome studies.

Keywords: microbiome, short read, long read.

P75: Metagenomic Sequencing Unveils Diverse DNA Microbiome in Aedes Mosquitoes from Pakistan

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ABSTRACT

Mosquitoes pose a significant health threat to humans. The most prevalent and widely distributed diseases worldwide are vector-borne diseases with mosquitoes being the most common and efficient vectors for parasite transmission. Among mosquitoes *Aedes* species are good vectors due to their anthropophilic behavior and hematophagous feeding habits, preferring primates'blood. They are implicated in the potential transmission of viruses like yellow fever, chikungunya and dengue. Dengue virus has an RNA genome and four distinct serotypes rendering the development ofa vaccine against this virus a challenging endeavor. Dengue is a global issue with millions of annual infections, in both urban and rural areas. Dengue has established endemicity in Pakistan causing seasonal outbreaks that strain country's healthcare system and economy. The World Health Organization(WHO) advocates IVM (Integrated Vector Management) for controlling larvae and adults mosquito population. Research indicates the noteworthy impact of the *Aedes* microbiome of *Aedes* in hampering pathogenic viral transmission from vector to host. In this study, we employed a metagenomic sequencing approach to characterize the DNA-based microbiome of *Ae. aegypti* and *Ae. albopictus*, primary dengue vectors. Mosquito samples were collected during dengue outbreak and pooled. We sequenced two pools of each species and conducted metagenomic analysis, identifying a variety of bacteria and viruses. Common bacterial genera included *Klebsiella*, *Stenotrophomonas*, *Acinetobacter,Staphylococcus,Elizabethkingia,Pantoea,Enterobacter, Pseudomonas, Brevundimonas*, and *Lampropedia*. Additionally, we detected DNA viruses from the *Siphoviridae, Hk97virus, Myoviridae, Epsilon15virus, N15virus*, and *Retroviridae* genera." The most abundant bacterialand viral specie were *Klebsiellavariicola*, *Stenotrophomonasmaltophilia,Klebsiellapneumoniae,Acinetobacterbaylyi, Enterobacterhormaechei,Acinetobactersoli,Stenotrophomonasmaltophilia*, *Pseudomonasputida, Brevundimonasdiminuta* and *Escherichia_phage_HK639, Enterobacterial_phage_mEp390, Lactobacillus_phage_A2, Human endogenous retrovirus K* respectively. Our study highlighted first time identification of bacterial specie *Lampropedia aestuarii* and viral specie *Human endogenous retrovirus K in Ae. albopictus* by the power of next generation sequencing. The microbiota inhabiting

Aedes mosquitoes encompasses multiple facets, with the potential to exert significant influence on various critical aspects of vector biology. These include the modulation of pathogenic virus replication within the vector, the potential to impact the vector's longevity, and the alteration of its vector competence, all of which collectively contribute to the complex dynamics of mosquito-borne disease transmission.

Keywords: *Aedes*, microbiome, *Human endogenousretrovirus K*, vector biology.

P76: Environmental Remediation and Nanoparticle Synthesis: A Profound Role Played by Eco-Friendly Microbes

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ABSTRACT

The garden soil of UAE has experienced gradual heavy metal accumulation due to continuous irrigation with treated sewage water. This study focuses on isolating and characterizing metal-resistant bacteria, particularly *Stenotrophomonas maltophilia* and *Bacillus subtilis*, identified through 16S rDNA sequencing and whole genome analysis.This comprehensive study aims to investigate metal-resistant strains in soil irrigated with treated sewage water, with a primary focus on *Stenotrophomonas maltophilia*. The objectives include characterizing its metal resistance, nanoparticle synthesis capabilities, and environmental implications. Identification of metal- resistant strains involved 16S rDNA sequencing and whole genome analysis. *Stenotrophomonas maltophilia*'s metal resistance and nanoparticle synthesis abilities were examined. Characterization of synthesized nanoparticles employed advanced analytical techniques such as FTIR, XRD, EDX, SEM, TEM, and ICP-MS. *Stenotrophomonas maltophilia* exhibited exceptional metal resistance against 13 metal salts, particularly at higher metal ion concentrations. Moreover, it demonstrated the synthesis of copper oxide (CuO), zinc oxide (ZnO), tungsten trioxide (WO3), and molybdenum oxide (MoO) nanoparticles. Characterization techniques confirmed the chemical composition, crystalline phases, morphology, nanoscale visualization, and precise metal quantification of these nanoparticles.

The significance of this study lies in advancing our understanding of metal-microbe interactions and their environmental implications. These findings offer valuable insights into the potential of *Stenotrophomonas maltophilia* as a key player in bioremediation and sustainable nanoparticle synthesis within metal-contaminated environments. Moreover, the environmentally friendly approach of utilizing kitchen scraps for nanoparticle synthesis underscores the importance of sustainable practices in addressing metal pollution. This research contributes not only to the field of environmental science but also to the development of innovative and eco-friendly strategies for mitigating heavy metal contamination, which is a growing concern in urban areas worldwide.

Keywords: Heavy metal accumulation, Metal-resistant bacteria, Nanoparticle synthesis, Metal-microbe interactions, Sustainable bioremediation

P77: Abundance and Diversity Of Oil-Degrading Bacteria In Produced Water Wetland Treatment System, Rima-Oman

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ABSTRACT

Produced water is the excess water from oil production, containing hydrocarbon residues and other pollutants. One of the methods that can be used to treat produced water is by constructing artificial wetlands. The Rima Water Treatment Project (Oman) is a constructed wetland recently implemented to treat the produced water biologically. In this study, the abundance and diversity of oil-degrading bacteria across the wetland system were evaluated and compared to water quality as it progressed through 4 subsequent terraces in three parallel tracks of the wetland. The chemical properties of the sample were measured including the oil content in water, pH, EC, and the elemental the total elemental composition. Culturable bacteria enumeration was carried out using nutrient agar, Bushnell Haas mineral salt (BHMS) agar medium, and Mineral salt medium (MSM) as minimal media. Morphologically different bacteria were isolated and tested for their capability to degrade the crude oil. Moreover, the microbial diversity was assessed for 16S rRNA V4 gene sequencing. Our findings show that the EC, pH, and minerals such as Na progressively increased as they flowed through the four stages of the wetland. The bacteria enumeration was progressively decreased, being highest in the first terrace. Curiously, there was also a significant difference in bacteria enumeration between the three parallel tracks. The oil-degrading bacteria are more abundant in the first two terraces of the wetland and in the second and third tracks. The 16S rRNA diversity showed a higher bacteria diversity in the last stages of the wetland system with an overall very low number of archaea. Even though the differences in Shannon and Evenness diversity indexes between the terraces were small, the number of bacteria classes and the community structure were significantly affected by both terraces and tracks. The most abundant class observed was alphaproteobacteria in the beginning stages of the wetland, where most of the oil degradation is taking place. To increase the efficiency of the wetland system, further cross-inoculation trials can be further tested, using the identified oil-degrading bacteria isolates.

Keywords: Constructed wetland, Produced water, Oil-degrading bacteria, Crude oil, Biological treatment

P78: High School Students Discover New Microorganism Species

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ABSTRACT

In recent years, the significance of soil and plant microbiota has gained prominence due to their crucial roles in ecosystems, including plant growth stimulation and pathogen defense. However, limited research and under-sampling have resulted in inadequate understanding of plant microbiota across various terrains. Exploring this realm holds potential for uncovering valuable microorganism species akin to the untapped richness of soil, which could revolutionize biotechnological tools and methods, impacting personalized human medicine. The Plant Microbiome initiative, a collaboration between our lab and the Davidson Institute of Science Education, merges cutting-edge scientific research with 21st century skill-based learning, embedding academic and industrial scientific practices into school curricula. This innovative program empowers students to lead field sampling, data collection, and analysis in diverse ecosystems, followed by advanced sample analysis at WIS labs. Using a system developed for microbiome mapping in diverse ecological niches, we will construct an expansive open-access database housing genetic and environmental data of bacteria and fungi from plant parts and soil. The database will cater to scientists, educators, and students, fostering fundamental research and applied tool development in areas such as environment, agriculture, health, and biotechnology, while enriching contemporary learning experiences. The project targets high school students throughout Israel from the southern desert to northern mountains. Launched in 2018, the Plant Microbiome Project has garnered extensive participation, uniting students across Israeli society, including both Arab and Jewish backgrounds. Remarkably, these students have collectively unearthed 80,000 novel bacterial species, highlighting the program's transformative impact.

In summary, the study of soil and plant microbiota's pivotal roles in ecosystems has spurred our Plant Microbiome initiative, combining pioneering research and skill-based learning. By fostering experiential education, advancing scientific knowledge, and unearthing new microorganisms, this project emerges as a catalyst for interdisciplinary advancement, with far-reaching implications across scientific, educational, and technological domains.

Keywords: Citizen Science, Environmental Microbiome

P79: Physico-Chemical, Thermal and Functional Characteristics of Degraded *Phoenix dactylifera* L. Date Pits fiber via *Trichodema reesei* at Low Moisture

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ABSTRACT

Phoenix dactylifera L. date pits have been a major waste byproduct that showed to be valuable source of energy, organic and inorganic materials. Solid state degradation systems were applied to observer degraded date-pits by Trichodema reesei at various moisture content (66.67%, 39.39% and 33.33%). The main objective of this study was to degrade date-pits fibers to simple or less complicated structures by T.reesei. Chemical and thermal properties of degraded date-pits were estimated to study the effect of fungus in their physical and chemical properties. Moisture content of degraded date-pits were ranged between 1.2 and 1.6 g/100g of, protein (4.94- 8.13 g/100g), fat (2.62-0.24g/100g), ash (0.83-1.10 g/100g), water absorption (2.19-3.38 g/g) and solubility (2.72-8.69 g/L). Crud fiber was estimated to be 75.27%, 85.15%, 80.56% and 74.95% for control and treatment sample (66.67%, 39.39% and 33.33% wet sample) respectively. Proximate analysis of treated samples showed the improvement in their characteristics compared to control. It was clear increase in their crud fiber content, protein, water absorption and solubility compared to control with almost 6.58%, 46.29%, 38.97% and 144.83% respectively. While fat content was decreased with roughly 65 %. DSC analysis was showed that 39.39% and 33.33% treated sample were recorded the highest levels of amorphous properties (ΔCp: 734 J/kg oC and 758 J/kg oC respectively), while 66.67% treated sample (ΔCp: 405 J/kg oC) was showed the lowest level of amorphous. Fourier Transform Infrared spectra showed higher absorptions for the selected functional groups in the fungal treated date-pts fibers as compared to the control, which indicated to increase molecular damage in the treated sample. Overall, T.reesei has been shown to be an important biodegradable tool for degraded date-pits fiber. It has high potential to improve the physicochemical and thermal properties of date-pits fiber, therefore increase the possibility to use the product in food industry.

Keywords: Physico-chemical; thermal characteristics; Trichoderma reesei; fiber; moisture

P80: Antimicrobial Activities of Organic Solvent Extracts of Four Seaweeds from Oman

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ABSTRACT

Seaweeds are deemed one of the valuable origins of bioactive compounds in biomedicine, nutraceutical, cosmetic, cosmeceutical, pharmaceutical, and food industries. The present investigation reveals the antibacterial activities of selected red and brown seaweeds compiled from the southern coastline of Oman in an endeavor to be applied as a substitute to generally used antibiotics. The purpose of this investigation was to examine the antibacterial activities of organic solvent extracts from two red seaweeds species (*Melanothamnus somalensis & Gelidium omanense*) and two brown seaweeds species (*Jolyna laminarioides & Nizamuddinia zanardinii*) against bacterial strains of *Staphylococcus aureus* (ATCC 25923), *Pseudomonas aeruginosa* (ATCC 27853), Escherichia coli (ATCC 25922) and Klebsiella pneumonia (ATCC 1706), and fungal strain *Candida Albicans*. Five organic solvents were used sequentially to achieve extraction. The solvents were applied in the subsequent order: hexane, dichloromethane, ethyl acetate, acetone, and methanol. Only the methanol extract of *Nizamuddinia zanardinii* showed antimicrobial activity. This methanolic extract was further fractionated, and the active fraction was recognized. Stock concentration revealed the highest activity against antibacterial activities and 3h incubation was the optimal time. TEM and SEM results showed that *E. coli* had an irregular shape, rough surface, and leakage of cellular content was observed. Furthermore, ribosomes were clustered and directed toward the inner membrane of the bacteria, and the DNA clustered in the center of the cell. In conclusion, the methanol extract of *Nizamuddinia zanardinii* had good efficiency against pathogenic bacteria and fungi. Therefore, it can be a good candidate for the development of anti-pathogenic drugs in the food and pharmaceutical industries.

Keywords: Antimicrobial activity; Organic extract; Oman; Seaweeds; *Nizamuddinia zanardinii.*

P81: Streptomycete Actinobacterial Isolates as Biocontrol Agents for Royal Poinciana Stem Canker Disease Caused By The Fungus *Neoscytalidium Dimidiatum* In The United Arab Emirates

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ABSTRACT

This study involved the acquisition of 47 actinobacterial isolates from the rhizosphere soils of royal poinciana in the United Arab Emirates (UAE). Three *Streptomyces* strains displayed substantial in vitro antifungal effectiveness against *Neoscytalidium dimidiatum*, the pathogen responsible for royal poinciana stem canker disease. The primary mechanism underlying the antifungal activity of *Streptomyces rochei* UAE2 and *Streptomyces coelicoflavus* UAE1 appears to be related to antibiosis and the production of cell-wall-degrading enzymes, respectively. S*treptomyces antibiotics* UAE1, on the other hand, was found to be associated with both modes of action. The aforementioned isolates exhibited the ability to inhibit the progression of lesions on apple fruits that were inoculated with *N. dimidiatum* during the apple fruit bioassay. In a controlled greenhouse environment, it was observed that the efficacy of individual biocontrol agents (BCAs) in combating stem canker was significantly higher when they were applied prior to the introduction of *N. dimidiatum*, as compared to their application after the pathogen had been established. The therapeutic properties of Cidely® Top, a chemical fungicide, and *S. antibioticus* UAE1 exhibited similar efficacy in mitigating disease symptoms in royal poinciana. Before the inoculation of the pathogen, it was observed that *S. antibioticus* UAE1 exhibited the ability to effectively suppress disease symptoms and inhibit the spread of the pathogen. This observation suggests that *S. antibioticus* UAE1 may possess a comparative advantage over the other treatments that were tested. The results demonstrated a statistically significant ($P < 0.05$) reduction in the number of defoliated leaves and conidia counts of *N. dimidiatum* in seedlings treated with *S. antibioticus* UAE1 compared to the other two treatments involving biological control agents (BCA) or chemical treatments. In summary, the diverse range of mechanisms exhibited by *S. antibioticus* UAE1 can prove highly efficacious in generating synergistic effects against fungal pathogens. This study is the first attempt to evaluate the viability of using a combination of biocontrol agents and fungicides to develop integrated disease management strategies for stem canker in royal poinciana.

Keywords: Actinobacteria, Antibiosis, Biocontrol, Chitinase, *Neoscytalidium dimidiatum*, Stem canker.

P82: Phage-Based Mitigation of Malodour Menace Of Ammonia Through Manipulation Of Urinal Microbiome

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ABSTRACT

One of the significant barriers associated with improving sanitation is the control of malodour, especially in toilets which comes from urine that remains on the commode and cannot be drained efficiently. The predominant malodour causing compound in urinals is ammonia with a low odour threshold of 0.05ppm. The environmental and clinical effects of ammonia are both detrimental. The conventional treatment methods lead to harmful byproducts, so it is vital to consider an alternate biological treatment that uses bacteriophages. The potential of these viral entities has been gaining significant interest in the wastewater treatment system due to the increase in demand for good sanitation practice. In this study we are exploring the potential of phages to be used as an alternative approach for altering the urinal microbiome. A preliminary study revealed the predominance of gram-negative ureolytic bacterial species in public urinal settings. Isolates were delineated based on colony morphology, gram reaction, biochemical characteristics and 16S rRNA ribotyping. An assay based on ninhydrin is optimised in order to monitor the generation of ammonia. Phages were raised against the isolate and characterised based on plaque morphology, host specificity, burst size and Restriction Fragment Length Polymorphism. Phages were employed to demonstrate the reduction in biogenic ammonia. Inorder to establish the proof of concept, phage ϕPh_EQ4 was isolated from wastewater against the ureolytic bacteria Enterobacter quasiroggenkampii. ϕPh_EQ4 gave large clear plaques and showed tropism to E. coli ST155. The potential of lytic phages to reduce biogenic ammonia was quantified and there was a significant reduction of 70% which was achieved within 5hr post-treatment. In conclusion, Bacteriophages can be considered a promising, cost-effective, innovative, and safe method of targeting malodour-producing compounds in urinals

Keywords: Urinals, malodour, ammonia, ureolytic bacteria, bacteriophages

P83: Metagenomic Profiling of Sediments From Unexplored Mangroves From Palk Bay, India: An Ecological Perspective.

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ABSTRACT

Mangroves are coastal wetland ecosystems with diverse topography and assemblage of shrubs tolerating harsh environmental conditions – high tides, and soil-salinity. The metagenomics approach can provide deeper insights into soil microbiomes. This study examines the microbial ecology of three rare mangroves (Panthanendal - PN, Muthukuda - MK, and Karankadu - KK) from the Palk Bay of Rameswaram Coast, Tamil Nadu, India. The sediments were characterized by soil analysis, and the metagenomic profiling of the total microbiome was conducted using Illumina Miseq (150×2) platform. Data analysis was performed using QIIME2–MOTHUR pipeline. Sediment analysis revealed the heterogenous presence of soil nutrients, wherein PN and MK samples depicted – high electrical conductivity (8.4 and 8.3) and alkaline pH (8.4 and 8.32) as compared to KK (3.8; pH 7.6). In addition, a wide range of minerals were identified in available form, supporting growth of mangrove plants and their associated microbes. Microbiome analysis revealed the presence of 19 taxa and 128 families in PN, 26 taxa and 108 families in MK, and 21 taxa and 179 families from KK mangroves. The α-diversity estimated by Chao1 showed MK sample with high species abundance, followed by KK and PAN. Similarly, Shannon and Simpson's index states that species richness and evenness were high in KK compared to other samples. The beta diversity analysis showed the dominance of Proteobacteria, Firmicutes, and Bacteroidetes taxa among all the samples. Several rare microbes, such as Ignavibacteriae, Calditrichaeota, Balneolaeota, Kiritimatiellaeota, and Tenericutes from KK; Verrucomicrobia, Gemmatimonadetes, and Deferribacteres from MK, and Deinococcus-Thermus and Elusimicrobia phyla were identified in the PN mangroves. Study findings suggested a direct correlation between soil nutrients and microbiome availability. This ecological perspective on mangroves revealed the presence of rare and polyextremophilic microbes in the selected mangroves, which could aid in isolating the bacteria promoting plant growth.

Keywords: Mangroves, Sediment, Metagenomics, Diversity, plant growth promoting.

P84: The Role of Microbial Mat Microorganisms in the Degradation of Acrylamide in Oilfield Produced Water

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ABSTRACT

Constructed wetlands have proven effective in treating the significant amounts of produced water generated from oil extraction operations. However, with the increasing use of partially hydrolyzed polyacrylamide (HPAM) in enhancing oil recovery, and its natural degradation into its toxic acrylamide (AM) monomer, the negative impacts of AM on the biological processes of wetlands have been a topic of interest. Microbial mats in wetlands play a key role in the bioremediation of hydrocarbons present in produced water, and the effect of this AM contamination on the mats is still understudied. This project aimed to investigate the impact of AM on microbial mats, and their potential in AM degradation under aerobic and anaerobic conditions at different AM concentrations, using GC and HPLC techniques, respectively. Additionally, AM degradation by pure bacterial and algal strains has been explored. Results showed that AM generated CO2 in the treatment groups (500, 1000, and 2000 ppm AM), indicating that AM was being used as a carbon source. The mats were also found to degrade AM efficiently within 28 days of incubation under aerobic conditions, while very slow rates were observed under anaerobic conditions. Aerobic mat incubations at 500 ppm and 1000 ppm AM resulted in 95 ± 0.1% and 90 ± 10.6% AM degradation, respectively. Moreover, independent growth of bacterial and algal isolates in AM revealed interesting degradation efficiencies, where some strains have fully degraded AM up to 1000 ppm after 7 days and 34 days, respectively. It was concluded that wetland microbial mats adapt well to AM, and could maintain their respiration and hydrocarbon degradation activities in the field.

Keywords: Bioremediation, Microbial mats, Produced water, HPAM, Acrylamide

P85: The Role of Algal Mat Microbiome In The Bioremediation Of Hexavalent Chromium In Mining Sites

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ABSTRACT

In heavy metal-contaminated mining sites, algal mats comprised of a diverse array of microorganisms have been encountered. The key microbiomes found in these mats include metal-resistant bacteria, metal-reducing bacteria, sulfate-reducing bacteria, ironoxidizing bacteria, and phototrophic microorganisms. The multiple microbiomes in algal mats are believed to play a crucial role in the remediation of heavy metal-contaminated sites via the immobilization, detoxification, and removal of heavy metals. MiSeq sequencing of algal mats near a chromium mining site in Oman revealed high proportions of sequences related to *Proteobacteria*, *Firmicutes*, and *Actinobacteria*. When the mats were incubated with Cr(VI) 1 mg L1, the bacterial community changed in favor of *Alphaproteobacteria* and *Verrucomicrobiae*. Aerobic heterotrophic bacteria with the ability to remove Cr(VI) have been isolated from these mats and the removal mechanism has been studied in detail. The obtained isolates were representatives of the *phyla Firmicutes* and *Proteobacteria*, which have been dominantly detected in the original mat. All isolates fell phylogenetically into the genera *Bacillus*, *Enterobacter*, *Klebsiella*, and *Cupriavidus*. The strains could tolerate up to 2000 mg L1 Cr(VI) and exhibited the highest Cr(VI) removal rate at 100±9 mg L-1 d1 . Using scanning electron microscopy (SEM) coupled with elemental analysis, the strains were shown to adsorb Cr(VI) at their cell surfaces. The functional groups OH, NH2, Alkyl, Metal-O, and Cr(VI)-O were involved in the biosorption process. In addition, the strains were shown to reduce Cr(VI) to Cr(III) with the involvement of chromate reductase enzyme. We conclude that chromium-polluted algal mats harbor assorted microbiomes dominated by *Firmicutes* and *Proteobacteria*, our aerobic heterotrophic bacteria fell in the same phyla that possess the ability to remove Cr(VI).

Keywords: Algal mat, microbiome, chromium, bioremediation, chromate reductase

P86: Diverse Functional Characterization of Microbial Communities From 16s Metagenomic Analysis Of River And Sewage Water Ecosystems

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ABSTRACT

Since microbial communities are essential to nutrient cycling, pollutant degradation, and ecosystem health, a thorough understanding of their many ecological niches is essential to the taxonomic and functional profiling of river and sewage water. In addition to being used for irrigation, sewage water is released into rivers and other bodies of water after being properly treated. Notably, antimicrobial resistance genes (ARG) are also stored in sewage samples. The goal of the study is to comprehend the taxonomic and functional potentiality of 16S metagenomic data that were collected from river and sewage water samples of Gujarat region. The investigation uncovered a wide range of taxonomic levels containing *Novosphingobium*, *Chryseobacterium*, and *Cupriavidus*, among other known and unknown bacterial taxa. In order to determine the probability of the presence and assimilation of antimicrobial resistance (AMR), functional classification of microbial communities and predicted Antimicrobial Resistance Genes (ARG) were carried out from the 16S metagenome data utilising a variety of platforms. Consequently, the purpose of this study is to assess the implications of changing environmental conditions for the management and conservation of aquatic ecosystems.

Keywords: 16S metagenome, functional analysis, wastewater, NGS, Antimicrobial resistant genes

P87: Microbial Community Dynamics and Associations During the Development of Harmful Algal Blooms

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ABSTRACT

The interaction between microorganisms and algae during bloom events significantly influences their physiological processes, resulting in alterations to local chemistry and consequential effects on ecosystem diversity. Recognizing the pivotal role of these interactions in bloom progression, our hypothesis establishes a connection between microbial community structure and bloom initiation, unraveling associations among taxa within the phycosphere. Leveraging advanced techniques—16S/18S rRNA amplicon sequencing and metagenome sequencing—we delved into the intricate patterns of bacterial and eukaryotic constituents during a harmful algae bloom induced by the dinoflagellate *Karenia brevis*. Over a span of nine months, a low bloom emerged in March, gradually dissipating in April, followed by an intensified high bloom from May to August. Through 18S rRNA amplicon sequencing, distinct phytoplankton communities emerged during both bloom and non-bloom periods. Similarly, 16S rRNA analysis of attached bacterial communities unveiled diverse compositions between bloom and non-bloom conditions, with free-living bacteria exhibiting no significant differences. Notably, Gammaproteobacteria and Bacteroidetes dominated the initial bloom, while Alphaproteobacteria, Actinobacteria, and Cyanobacteria witnessed increased abundance during the onset of the bloom. Among environmental factors, only pH displayed a negative correlation with bloom events. Furthermore, our study yielded 197 high-quality metagenome-assembled genomes (MAGs), unveiling the genetic diversity intrinsic to the microbial community. Aligning with previous findings, we detected cyanobacterial MAGs, potentially serving as a grazing resource for *K. brevis*, and Roseobacter MAGs showcasing complete vitamin B1, B7, and B12 synthesis pathways, potentially aiding *K. brevis* growth. Significantly, Roseobacter MAGs demonstrated a positive correlation with *K. brevis* numbers during the bloom. This finding was substantiated through laboratory experiments, where a Roseobacter clade strain stimulated K. brevis growth under vitamin-depleted conditions, reinforcing the intricate ecological interplay within this ecosystem. These findings underscore the potential of bacterial communities to facilitate *K. brevis* development, thereby deepening our understanding of complex ecological dynamics.

P88: Comprehensive analysis of Taxonomic and Antibiotic Resistance of Microbiome from Solid Waste Landfill Sites in Gujarat, India employing Whole Genome Shotgun Metagenomics Approach

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ABSTRACT

The enrichment of drug-resistant organisms is facilitated by the presence of pathogens and antimicrobial resistance (ABR) genes within municipal solid waste dumping sites, which can be attributed to inadequate practices in the disposal of solid waste. The implementation of an effective solid waste management system is imperative, as failure to do so can result in the creation of an antibiotic-resistant gene pool (ABR gene pool), which has the potential to adversely impact both human and animal health. Hence, the objective of this work was to conduct a comprehensive assessment of the taxonomic analysis of different solid waste disposal locations, in addition to performing ABR gene analysis by the utilization of whole genome shotgun sequencing and bioinformatics methodologies. The study involved the collection and processing of samples from municipal solid waste disposal sites in Rajkot, Surat, and Ahmedabad. Metagenomic DNA extraction was performed on these samples, followed by metagenomic library creation and sequencing using the Illumina platform. The obtained sequences were subjected to taxonomic analysis using One Codex, revealing the presence of different pathogens including *Corynebacterium sp*. and *Vibrio sp*. The investigation also included an assessment of the presence of resistance genes against beta-lactams, macrolides, and tetracyclines using the same platform. Comparative analysis was conducted for all sites. In all sample types, the prevalence of macrolide resistance genes, specifically ermA (identified in 85.1% to 100% of samples) and ermF (identified in 80.1% to 100% of samples), was consistently higher compared to the presence of beta lactam resistant genes. The Surat solid waste disposal site had the lowest presence of beta-lactamase genes, whereas the Ahmedabad sample displayed the lowest occurrence of tetracycline resistance genes. Hence, the existence of ABR genes at waste disposal sites provides a rationale for the ongoing surveillance and monitoring of ABR gene prevalence. This is necessary to address the global issue of Antimicrobial Resistance to some degree.

Keywords: Antimicrobial resistance, wastewater, NGS, Antimicrobial resistant genes

P89: Bioprospecting as a strategy to uncover potential value-added products in extremophilic microalgae based in the Sultanate of Oman

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ABSTRACT

The exploration of biological sources for novel commercially valuable products, or bioprospecting, has played a vital role in the development of many industries, mainly including pharmaceuticals, agriculture, aquaculture and cosmetic industries. Microalgae have been targeted specifically in bioprospecting due to their high secondary metabolite content that translates to high potential for value-added products. Microalgae grown in extreme conditions portray a different composition of secondary metabolites than algae grown in ideal conditions that help them to deal with the stress in their environments. Eight indigenous extremophilic microalgae have been isolated from Oil fields in Nimr within the Sultanate of Oman. The secondary metabolite composition and potential for value-added products has never been explored in Oman prior to this paper, particularly microalgae grown in extreme conditions, which could lead to new discoveries in the region. This research aims to study the macromolecular and biochemical composition of these 8 microalgae, followed by an examination of their potential for industrial use, specifically as a bio-stimulant and anticancer agent. This was achieved through a variety of assays that had been modified to work with the extremophilic indigenous microalgae. The results showed that despite their microscopic diversity, all extremophilic microalgae showed relatively low macromolecule content, accompanied by a high pigment and phenolic content. Through testing for industrial application, these algae showed no bio-stimulant effects when added to the soil as whole algae. However, they had a high anti-proliferation effect in the anticancer assay. These results help to outline a potential use for extremophilic microalgae within the pharmaceutical industry and further testing of these microalgae could lead to a valuable marketable product.

Keywords: Bioprospecting, microalgae, bioactive compounds, biostimulant, cytotoxicity

P90: Study of Antimicrobial-Resistant Microorganisms from Sewage Wastewater Treatment Plant in Taiwan

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ABSTRACT

The increasing prevalence of antimicrobial-resistant bacteria (AMR) in Sewage wastewater treatment facilities (WWTPs) is a significant concern for global health. The study examined the prevalence, variety, and types of AMR bacteria in Taiwan's sewage wastewater treatment facilities. Samples were collected from the NPUST campus at various points along the treatment process, including sludge storage tanks, clarifiers, bar racks, equalization basins, oxidation ditches, and clarifiers. In-depth microbiological and molecular studies were conducted to identify AMR bacteria, with carbapenem and Penicillin resistance being the most common. The study found a significant incidence of AMR germs in the sewage wastewater samples, and different bacterial species showed resistance to various antimicrobial substances. Bacterial species like *Plesiomonas shigelloides*, *Escherichia coli, and Aeromonas sp.* were found resistant to carbapenem-class antibiotics.16S rRNA sequencing and overall genomics are more widely used in microbiology research because it reveals the diversity of unknown microscopic life and understands the occurrence and classification of complex microbial communities or environments. The findings have significant health-related significance, providing insight into the spread of AMR and emphasising the need for efficient surveillance and intervention techniques. Understanding the elements influencing AMR dissemination in the wastewater environment can help create focused strategies for reducing transmission and containing the spread of resistant bacteria. The study's findings contribute to our understanding of AMR's spread and serve as a foundation for public health interventions and antimicrobial stewardship initiatives.

Keywords: Antimicrobial resistance, Sewage Wastewater Treatment Plant, antimicrobial susceptibility, Carbapenem resistance, Penicillin resistance,16S rRNA sequencing

P91: Isolation and Identification of Pigment-Producing Fungi, and Their Potential Application as Non-Cytotoxic Food Colorants

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ABSTRACT

A large number of food colorants being used in today's world come mainly from synthetic sources. These chemical colours can pose a wide variety of threats like being immunosuppressive, carcinogenic, and various other major deleterious health effects like they can harm the natural microbiome of the human gut in the long run. Recent studies show that Long-term exposure to synthetic red food dye triggers inflammatory bowel diseases (IBD). To counter these hazardous effects posed by synthetic colours, there is a rising demand for natural pigments from natural sources. Microbial pigments have gained widespread popularity due to greater stability of the pigments, and availability of cultivation technology in laboratories. Apart from use as natural colorants, the microbial pigments can also act as better therapeutic agents like immunomodulators, antiproliferative, anticancer and antioxidants, and so on. The current study focuses on isolating novel pigment producing fungi by air sampling and identifying them by traditional method of studying their morphological features as well as by MALDI-TOF MS, purification by column chromatography and TLC and characterization of pigments for their structure elucidation and compound annotation. The study involves antioxidant assays by DPPH, antimicrobial studies of the pigments and toxicity analysis thereby leading to the final application of the pigments as nontoxic edible colorants in the food and beverages industry with the least or no lethal side effects. Currently, the study is in the initial stage dealing mainly with the mass isolation of pigmentproducing fungi and identification of the fungi by MALDI-TOF MS, categorization, optimization and submerged fermentation for mass production of pigments in liquid media.

Keywords: Food colorants, Fungal pigments, MALDI-TOF, Antimicrobial, Toxicity

P92: Rhodobacteraceae Are Key Members Involved in Microbiome Assembly of The Diatom Asterionellopsis Glacialis

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ABSTRACT

The multitude of interactions between bacterioplankton and phytoplankton have prompted numerous studies that investigate phytoplankton microbiomes with the aim of characterizing beneficial or opportunistic taxa and elucidating core bacterial members. Oftentimes, this information is garnered through 16S rRNA gene profiling, over time and across locations. In the laboratory, phytoplankton cultures are typically maintained in synthetic, nutrient rich media which may skew our understanding of the microbiome. In this study, we aimed to identify taxa that are central to structuring and establishing the overall microbiome of the diatom *Asterionellopsis glacialis*. We introduced a diverse environmental bacterial community to *A. glacialis* in a continuous culture set-up in both nutrient-rich (F/2) and nutrient-poor media (filtered sea water). The bacterial community was profiled over a period of 7 day using 16S amplicon sequencing. Cyanobacteria (*Coleofasciculaceae*) and *Rhodobacteraceae* dominated the microbiome early on and maintained a strong presence throughout the incubation period. By employing differential abundance, network and differential association analyses, it was discovered that specific members of the family *Rhodobacteraceae*, particularly, *Sulfitobacter* species, likely funtion as keystone species. In the presence of the diatom, *Sulfitobacter* species and other *Rhodobacteraceae* develop positive associations with taxa that are typically in high abundance in marine ecosystems (*Pelagibacter* and *Synechococcus*) leading to restructuring of the microbiome in comparison to diatom-free controls. Moreover, we observe that these associations develop predominantly under oligotrophic conditions, highlighting the importance of investigating phytoplankton microbiomes in as close to natural conditions as possible to avoid biases that may develop under routine laboratory conditions.

Keywords: diatom, microbiome, phytoplankton-bacteria interactions

P93: Production of Microalgal Biomass, As Potential Biofertilizer, Using Wastewater Leading To Removal Of Pollutant And Pathogenic Load

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ABSTRACT

With a growing population, droughts, land degradation, global climate change, weather extremes and inappropriate use of freshwater resources caused detrimental effects on the overall ecosystem. The unnecessary usage of agrochemicals to achieve food security and conventional wastewater treatment strategies has possessed significant barriers to sustainable crop production. Interestingly, Microalgae is employed as an eco-friendly and cost-effective biological recourse to be used as a potential biofertilizer in modern agriculture and wastewater treatment. The goal of this research was to investigate the potential strains of Microalgae for wastewater treatment and sustainable crop production. In this study, isolation, physicochemical characterization and molecular identification of Microalgal strains were carried out. The physicochemical based comparative analysis of wastewater before and after treatment was performed. Moreover, real time implementation of Microalgal biomass by performing pot experiment on different crops and analyzing plant growth parameters and soil physiochemical properties were also conducted. Results of this study confirmed that the identified species showed similarity with Tetradesmus nygaardii, Chlorella vulgaris and Closteriospsis strains. The identified strains of microalgae also revealed that the industrial wastewater was more contaminated as compared to the other wastewater samples. Moreover, ------- crop outperformed in all plant physiological analysis. This study concludes that the identified strains of microalgae have a potential to be used as a biofertilizer and a green method for wastewater treatment. These findings potentially influence the future of sustainable agriculture by proving the efficacy of microalgae as a biofertilizer, creating multiple options for innovation, commercialization, and governmental assistance in the agricultural sector.

Keywords: Microalgal Microbiome, Green biofertilizer Innovation, Wastewater treatment, Soil Microbiome, water pathogens

P94: Metagenomic Screening Strategies for Bioprospecting Enzymes from Polluted Water

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ABSTRACT

A metagenomic technique was utilized to initiate a comparative taxonomic and functional microbial profiling of a contaminated location along the Gaoping River in Kaohsiung, Taiwan. The Gaoping River is typically associated to pollution difficulties related to high BOD, COD, color, and toxicity, etc. The present study was conducted to decode the microbial community exists from polluted water. After sequencing on Illumina platform, a total of 72107 reads and a mean G + C% of 53 were observed. Onecodex, DADA2, SILVA138 and QIIME2 were used for the taxonomic and functional screening. Sequencing metagenome reported about 3516 species belonged to 154 different dominant phyla Pseudomonadota, Bacteroidota, Planctomycetota, Actinomycetota, and dominant species Streptomyces griseocarneus, Ignavibacteria bacterium, Salifodinibacter halophilus, Flavobacterium succinicans, and Megasphaera cerevisiae were observed. The metagenomic approach has emerged as promising way towards replacing conventional microbial techniques with culture-independent methods. There are two primary methodologies, i.e., functional-based and sequence-based, to identify and characterize industrially valuable biocatalysts from the environmental microcosms. By culture dependent study 45 bacterial species were isolated from the polluted water and each isolates have been screened based on the extracellular production of amylase, cellulase, xylanase, protease and laccase enzymes. There are 21 isolates with potential for enzyme hydrolases among these bacteria. Based on the findings, it is suggested that cultivable and uncultivable methods be used for bioremediation process. The study provides the foundational data for developing a commercial-scale use of bacteria for the removal of organic contaminants from wastewater.

Keywords: Community Metagenome, Functional Metagenome, Enzyme, Wastewater

P95: Composition and Function of The Coral Pathobiome In White Syndrome-Affected Corals

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ABSTRACT

Corals thriving in the extremes represent a unique opportunity to study populations experiencing end-of-century temperatures such as those of the Arabian Gulf. Within the gulf, corals are exposed to large fluctuating sea surface temperatures (reaching 11°C in the Winter and exceeding 36°C in the Summer). These conditions exceed the survival limits of most corals on the planet, that lead to recurrent episodes of bleaching and temperature-driven diseases, including the infectious disease white syndrome (WS). Here, we generated paired shotgun metagenomic and metabolomics data from colonies of the coral *Acropora pharaonis* from the gulf to investigate structural and functional changes in the coral microbiome associated with WS manifestations. Corals were sampled at both WS lesion and adjacent lesion sites in WS-affected colonies along with healthy colonies as control. Diversity and richness indices were significantly higher in the lesion and adjacent lesion sites compared to healthy colonies. Moreover, the microbial consortium differed significantly between the three groups, with significant increases in select bacterial families at WS lesion sites forming the core constituents of the WS pathobiome. To understand the potential functional roles of these bacterial assemblages, we assembled 11 high-quality metagenomic-assembled genomes (MAGs) from the WS-affected colonies, three of which belonged to Rhodobacteraceae (MAG2, MAG6, and MAG7), Granulosicoccaceae (MAG9), and Oleiphilacaea (MAG11) whose relative abundance increased with disease. Using functional annotations of these MAGs and metabolomics collected simultaneously with metagenomic sampling, we uncover the role these bacteria play in disease manifestation. These microbial species and molecules could further be used as WS bio-markers to better understand and predict WS etiologies, which remain elusive.

Keywords: coral, microbiome, pathobiome, metagenome, climate change

P96: Metagenomic Profiling of Microbial Communities in Estuarine Sediments: Phylogenetic, Functional, and Pollutant-Related Insights

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ABSTRACT

The phylogenetic and functional characteristics of microbial communities that reside in sediments that were collected from the estuaries of the Rivers Amlakhadi (AK) and Khajod (KJD) in the southern region of the Gujarat State in India were evaluated with the help of metagenomic profiling. Another sediment sample of Tapi River was obtained from near the shore far from estuaries, used for contrast. Gammaproteobacteria were the most common type of bacteria found in the sediments. According to the enzyme profiles found in the Kyoto Encyclopaedia of Genes and Genomes (KEGG), dominant enzymes were discovered in estuarine sediments. These enzymes included 2-oxoglutarate synthase, acid phosphatases, and lipases, and their levels increased significantly. The majority of the pathways in the KEGG pathway profiles were also dominated by specific metabolism in these sediments and showed a marked increase. This includes the metabolism of alanine, aspartate, and glutamate, as well as carbon fixation pathways in prokaryotes and aminoacyl-tRNA biosynthesis. The amount of pollution in the river water that entered the estuary caused the bacterial diversity there to change. The function of the bacterial community in the sediment was impaired to a greater degree in the estuary that received river water from the river with the highest level of pollution. The characterization of the bacterial communities that live in estuary sediment revealed that toxic chemicals may reduce the natural variability that exists within microbial communities while simultaneously increasing the number of microbial metabolic enzymes and pathways. From these 3 Sampling sites screened 52 bacterial isolates for their resistance/tolerance to Heavy Metal, PAH and pesticides. Out of 20 multi-metal resistant isolates, 5 were able to tolerate anthracene, phenanthrene and pyrene PAH at different concentration. One of the bacterial isolates MAK1 (Identified as Exiguobacterium profundum by 16S rRNA) exhibited maximum degradation efficiency (65%) was further tested for further anthracene degrading ability in the presence and absence of glucose in a mineral salt medium; and a number of metabolites were produced and detected by GC-MS. The PAH degradation efficiency of the isolates was assessed using spectrophotometer with 100µg/ml to anthracene and observed different degree of degradation ranging from 35-55% after 96h of incubation. The DNA derived from PAHs tolerant bacteria were PCR amplified using specific primers and positive PCR products.

Keywords: Metagenomics, Biodegradation, Polycyclic aromatic hydrocarbon, Metabolites

P97: Genomic of Detection Sars-Cov-2 Variants From Waste Water Treatment Plant Of Vadodara City, Gujarat, India

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ABSTRACT

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), a novel member of the Coronaviridae family has been identified as the etiologic agent of covid-19 pandemic. This pandemic has exposed global domino effects including public health, food security, and economic stability. Tracking the initiation of the virus, its spread, and trends is a daunting task, especially at population-wide scales. Rapid diagnostic testing is the main tool for identifying infected individuals, but wastewater surveillance method provides early stage detection of COVID-19 variant outbreaks. From December 2022 to February 2023, Total four sewage samples were collected from Sewage treatment plant (STP) of Vadodara city located in Gujarat, India. All samples were processed for RNA concentration through ultracentrifugation and polyethylene glycol precipitation followed by RT-PCR. RT-PCR results reflected incidence of COVID-19 cases in the city. All four samples were detected positive with low CT value of N gene and subjected to COVID-19 genome sequencing on the Ion S5 plus sequencing platform. The genome analysis of sequenced samples has been identified as BA.2, VOC, Omicron with important genetic mutations in different proteins of SARS-CoV-2 structure. Simultaneously, 422 Genome sequences from Vadodara region of Omicron variant till March 2023 from GISAID database were analysed similarly. The highest mutation found in Spike protein followed by nsp3 and N protein. From total 86 Mutations, 27 mutations were identified as Transversions mutations and 59 mutations were Transition type mutations. Most mutations were SNP and deletion type, resulting in synonymous and missense annotation. Mutation site has been identified to locate changes in the amino acid of a particular protein. Total six marker mutations of BA. 2 in spike protein such as T19I, V213G, S371F, T376A, D405N, R408S were also observed in wastewater sample. The detection of key finding mutation in sewage sample mirrors the public health information and characterize variants of SARS-CoV-2 circulating in a community. In summary, wastewater surveillance can serve as a prediction tool for infection within a specific population. Therefore, sewage surveillance for COVID-19 can be an effective way to monitor and discover novel variants with low cost and better long-term efficacy at the community level.

Keywords: SARS-COV-2, Wastewater surveillance, Environmental Monitoring, Variant Analysis

P98: Ecomicrobiome of Winogradsky Columns Established with Solid Waste Sediments and Enriched With Ldpe Plastic

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ABSTRACT

The waste landfills are utilized to discard waste including organic waste, paper, cloths, rubber, wood, plastic, leather, etc., creating a unique anthropogenic ecosystem. Discarded plastics are rapidly increasing in solid waste landfills and resistant to biodegradation leading to pollution that is harmful to the ecosystem. The Winogradsky column is a useful model microbial ecosystem to study environmental influences on microbial community structure and dynamics. This complex community can be maintained or manipulated under controlled laboratory conditions with the addition of compounds in the column. In the present study, Pirana solid waste sediment and leachate samples were used to build Winogradsky column with normal and LDPE enriched condition. After 13 weeks of incubation and maturation columns were intended to extract metagenome by using HiPurA™ Soil DNA Purification Kit (MB542). The 16s rRNA gene amplicon sequencing libraries were prepared and V3-V4 region of 16S rRNA gene was targeted using 341F and 805R primers with Illumina adapters. Libraries were verified and quantified using Qubit v3. The libraries were sequenced on Illumina MiSeq using 250 x 2 paired end chemistry. The community study was done with ONE CODEX. MEGAN and STAMP operate for comparative and statistical analysis. METAGENassist and IVikodak were used for phenotypic mapping and predicted functional attributes of the dataset. Higher abundance of Proteobacteria, Spirochaetes and Bacteroidetes which were identified for polymer degradation. Candidatus Saccharibacteria bacterium, Prolixibacteraceae bacterium XSD2 spp. was found in metagenome. Analysis of the microbial attributes narrated oxygen requirement, energy requirement that exhibit the presence of anaerobic organisms, autotroph and ammonia oxidizer. The predictive functional profiling revealed the presence of enzymatic groups and pathways involved in biodegradation of xenobiotics and methane metabolism. The study will explore the polluted site for the removal of pollution and microbial community stimulated by Winogradsky column can be used for LDPE depolymerization.

Keywords: Winogradsky, Metagenome, Plastic degradation, Solid waste, LDPE.

P99: Microbial Diversity and Resistance Patterns in Tropical River Sediments: Evaluating Human Impact and Implications for Health, Monitoring, and Remediation.

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ABSTRACT

In this research, we delve deep into the previously uncharted microbial realm of the Periyar River sediments in Southern India. Using advanced sequencing techniques for 16S rRNA genes, qPCR, and ICP-OES, we mapped out the geographic spread of microbial communities, their resistance profile, and the complex ties with their surrounding environmental factors. Our exploration revealed an impressive diversity of species within the river's ecosystem, highlighted by dominant groups such as Proteobacteria, Firmicutes, Bacteroidetes, Chloroflexi, and Planctomycetes. Notably, specific microbial groups were associated with distinct pollution levels, pointing to methanogenic and sulfur-reducing bacteria as key respondents to different contamination degrees. We also identified several bacteria with potential for remediation. A deeper dive into our data unveiled various pollution markers linked to fecal/sewage contamination, along with harmful bacterial species. A striking relationship was seen among these marker genera, hinting at a shared origin. Our in-depth examination revealed that factors like TDS, salinity, EC, and temperature play critical roles in shaping microbial diversity. The presence of resistance genes correlated with the river's pollution level. Interestingly, this is the first study to assess the antibiotic and metal resistance genes in this river's metagenome, revealing numerous resistance markers, including class 1 integrase (Intl1), and genes resistant to aminoglycoside (aadA), Quinones (qnrS), and copper (CopA). The factors contributing to the rise of resistance genes and their potential transfer to harmful bacteria were also assessed. One key takeaway is that diverse pollution levels result in similar microbial community structures, but with variations in taxonomic composition and resistance genes that mirror the pollution spectrum. This highlights the potential of microbial communities as early-warning systems for pollution. Such insights can guide environmental monitoring and mitigation measures. In conclusion, our study offers a comprehensive understanding of the Periyar River's ecological health, laying a crucial groundwork for directed pollution control measures.

Keywords: River microbiome, Resistance gene, Pollution, Amplicon sequencing, Periyar.

P100: Screening of Plant Growth-Promoting Activity Of Bacterial Isolates From Vechur Cow Dung: A Promising Plant Bio-Stimulant

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ABSTRACT

Plant growth-promoting bacteria (PGPB) are an integral part of sustainable agriculture that can transfigure the agricultural economy. The immediate advantage is the reduced reliance on huge quantities of chemical fertilizers and pesticides. The constant usage of these chemicals weakens soil biodiversity, fertility, and ecosystem health. The application of potential microbial inoculants for promoting plant growth and disease management is an emerging alternative. However, broader approaches for developing microbial formulations as plant bio-stimulants targeting agricultural crops lag far behind. Commercial production of bio-formulator products that aim at sustainability is of vital need which could satisfy the ever-expanding demand for crop production. Cow dung is a repository of natural plant growth-enhancing bio-resources. It comprises of a broad range of microbes that can be used as potential plant growth promoters. In the present study, the plant growth-promoting effect of bacterial isolates from the dung of an indigenous cattle breed of Kerala, India -Vechur cow was studied. Five bacterial strains (VC41, VC42, VC43, VC45, and VC54) isolated consisted of both gram-positive and gram-negative bacteria. These isolates exhibited plant growth-promoting qualities like phosphate solubilization, and IAA production, along with biocontrol activities like chitinolytic activity, HCN, and siderophores production. Genotypic identification using 16S rRNA sequencing identified two *Bacillus* strains (VC41 and VC45), one each of *Pseudomonas* (VC42), *Acinetobacter* (VC43*), and Alcaligenes* (VC54*)*. Phenotypic analysis of the seedlings raised from seeds treated with the bacterial isolates from Vechur cow showed promising results in terms of increased seed germination and plant growth in Rice. Thus, combining the functional efficiencies of these compatible microbial species into an efficient bio-formulation for enhancing plant growth and crop yield is a propitious opportunity for sustainable agriculture.

Keywords: Plant growth-promoting Bacteria (PGPB), Cow dung, seed germination, bio-formulation, Sustainable agriculture.

P101: Multi-temporal Soil Salinity Mapping in the United Arab Emirates Using Landsat 8

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ABSTRACT

Soil salinity is a significant environmental challenge in the arid and semi-arid regions of the United Arab Emirates (UAE). Elevated salinity levels in the soil adversely affect agricultural productivity, water quality, and overall ecosystem health. To effectively manage and mitigate these detrimental effects, accurate and up-to-date soil salinity mapping is essential. The research involves the integration of multi-temporal satellite imagery, ground-based data, derive precise and spatially explicit soil salinity maps. Landsat 8 satellite data for the years 2016 to 2022 were used for producing multi-temporal soil salinity maps. Ground truth data collected from field surveys and laboratory analyses were used. EC values for 36 samples collected across UAE were measured in micro siemens per cm and 18 samples were used for calibration and 18 for validation purposes. The methodology includes preprocessing and radiometric corrections of satellite imagery, followed by spectral indices computations, such as Normalized Difference Salinity Index (NDSI), Normalized Difference Vegetation Index (NDVI), and Soil Adjusted Vegetation Index (SAVI). Supervised classification algorithm was used for the study. The results of the study showcase detailed soil salinity maps at 30m spatial resolutions, offering valuable insights into the spatial distribution and temporal severity variations of salinization across different regions in across the UAE. The spatial data layers produced resulting soil salinity maps can serve as essential inputs for land use planning, precision agriculture, and natural resource management. With an accuracy of 75%, the generated maps highlights the reliability and credibility of the applied methodology.

Keywords: Soil Salinity, Salinity Index, Landsat 8, spectral indices, Spatial data.

P102: Biological Cultivated Sage (*Salvia officinalis* L.): A Potential Source of Antioxidants with biofilm inhibitory properties

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ABSTRACT

Bacterial biofilms pose substantial health risks across clinical and industrial contexts, necessitating effective and safe antibacterial agents to control their formation. Sage (*Salvia officinalis* L.), a medicinal plant rich in bioactive compounds with antioxidant and antibacterial traits, was investigated in this study. The total polyphenolic content (TPC), antioxidant potential (AOX), and polyphenolic profile of Tunisian sage's methanolic extract (MSE) were measured. To investigate its efficacy against biofilm-producing bacteria, the minimum inhibitory concentrations (MICs) and minimum bactericidal concentration (MBCs) were screened using disc diffusion and micro-dilution methods, against biofilm-producing bacteria: *Staphylococcus aureus* (ATCC 25923), *Salmonella typhimurium* (DT 104), *Pseudomonas aeruginosa* (ATCC 27853), and *Vibrio alginolyticus* (ATCC 17802). The MSE's minimum biofilm inhibitory and eradication concentrations (MBICs and MBECs) against the above-mentioned pathogens were determined via crystal violet test. The TPC of the MSE was 41.65 mg GAE/g DW and the IC_{50} value was calculated as 13.21 µg/ml. HPLC analysis revealed that rosmarinic acid and myrecetin were the predominant compounds. The MSE's inhibition zone diameters (ZOI) measured 14.3±0.5mm, 13.6±1.5mm, 11.5±1 mm and 10.4±0.5 mm against *P. aeruginosa*, *S. typhimurium*, *S. aureus* and *V. alginolyticus* respectively. MSE exhibited low MIC values against *S. typhimurium*and *P. aeruginosa* (17.4 mg/mL and 21.84 mg/mL, respectively), whereas it was two times higher for the other strains. MBC values, also, were lowest for *S. typhimurium* and *P. aeruginosa* (21.72±7.5 mg/ml and 26.2±0 mg/ml, respectively), compared to *S. aureus* and *V. alginolyticus*. MBICs were 6-12.5% and MBECs 50% of the MSE on biofilm formation for most of the tested bacteria, with greater than 90% inhibition and eradication capacities. Identified phenolic compounds correlated significantly with these biological activities ($p<0.05$) establishing MSE's strong antioxidant and antibiofilm attributes, against the studied bacteria.

Keywords: *Salvia officinalis* L., polyphenolic compounds, antioxidant activity, antibacterial activity, antibiofilm activity.

P103: Fungi in Flux: How Saline Groundwater Irrigation Reshapes Arid Soil Ecology

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ABSTRACT

Saline groundwater irrigation is adopted as a pivotal agricultural practice in arid regions as they face the challenge of freshwater scarcity. Despite its widespread use, the repercussions of this irrigation method on soil fungal communities and their ecological functions remain elusive. This study investigates the effects of irrigation water sources, comparing saline groundwater to fresh water, on the diversity, structure, and assembly processes of soil fungal communities using Illumina Miseq sequencing targeting the internally transcribed fungal spacer gene (ITS). Our findings reveal that, intriguingly, there were no significant alterations in soil fungal diversity between the two irrigation water sources. Remarkably, only 27.1% of the total operational taxonomic units (OTUs) were unique to saline groundwater irrigation. Soil fungal richness exhibited a negative correlation with soil pH. Distinct variations emerge in the composition of soil fungal communities, primarily influenced by electrical conductivity (EC) and pH of the irrigation water. Notably, transient effects of irrigation water selected fungal communities adapted to varying salinity and pH conditions in the bulk soil of date palms. Furthermore, soil fungal guilds displayed differential structuring patterns in response to irrigation water properties. Saprotrophs display sensitivity to water EC and pH, while pathotrophs exhibit disparities based on both water and soil EC. Ectomycorrhizal fungi (ECM) responded significantly to the EC of irrigation water. Collectively, the outcomes underscore that saline groundwater irrigation distinctly shapes soil fungal communities, even without inducing discernible shifts in overall diversity. The decline in saprotrophic fungi holds the potential to disrupt nutrient cycling in the soil and foster pathogen incursion in the agroecosystem. These insights emphasize the importance of holistic irrigation management strategies to safeguard soil health, sustain crop productivity, and foster resilient agroecosystems in arid regions.

Keywords: Arid agroecosystem; Fungal community; High throughput sequencing; Irrigation source; Soil salinization

P104: Occurrence of multidrug-resistant bacteria in marine beach sand and water with excellent microbial quality

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ABSTRACT

Antibiotic-resistant bacteria (ARB) are resistant to natural and synthetic antibiotics and are termed multidrug-resistant (MDR) if they are resistant to 3 or more antibiotics and have become a health concern worldwide. This study aimed to evaluate the occurrence of antibiotic-resistant bacteria on a public beach in Dubai, UAE. In total, 18 samples (6 marine water and 12 beach sand) were collected from six crowded and non-crowded areas. The VITEK-2 system was used to identify and determine antibiotic resistance profiles of bacterial isolates. IDEXX and Quanti-Tray/2000 were used to evaluate the bacteriological quality of the beach water and sand samples. The beach sand samples were tested for catalase and oxidase enzymes, and all isolates tested positive for both enzymes. The identified gram-positive bacteria were Staphylococcus lentus, Staphylococcus aureus, and Leuconostoc mesenteroides. S. aureus & S. lentus isolates were multidrug-resistant and showed resistance to oxacillin, erythromycin, rifamycin, benzylpenicillin, clindamycin, quinupristin/ dalfopristin, and vancomycin. E. coli, Enterococci, and Pseudomonas aeruginosa were detected in six beach water samples. However, total coliform levels in crowded areas were found to be in the range of 73-161 MPN/100 mL whereas non-crowded sampling sites had 132.9 MPN/100mL. Overall, the bacteriological quality of beach sand and water samples was excellent. However, a few samples with gram-positive bacterial isolates were found with a high level of resistance to commonly used modern antibiotics. A detailed and long-term systematic study with more samples is needed to evaluate the potential risk of antibiotic-resistant bacteria in the marine beach environment in the UAE.

Keywords: Antibiotic-resistance, multidrug resistance, VITEK-2, IDEXX, public health, marine environment.

P105: An approach to isolate axenic culture of centric and pennate diatoms

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ABSTRACT

Diatoms are ubiquitous and contribute 20% of net primary production, along with ecological it also offers biotechnological promise for things like biofuel, nutraceutical products, and nanoparticles. The axenic cultures are required to understand the diatom-bacteria interaction, also for genomic and proteomic studies. The production of axenic cultures is still a major challenge due to the complex and variable interaction between the diatoms and their associated bacteria. The production of axenic cultures of microalgae is a time-consuming process, and establishing and maintaining axenicity is frequently problematic. Hence, this study focused on the isolation of an axenic culture of the marine-centric diatom Odontella sp. And Pennate diatom and Amphora sp. (from Indian Ocean water) and Navicula sp. (from Mandovi River). The isolation of axenic culture involves mechanical removal, such as filtration and cell washing as well as antibiotic treatment, which includes treating cells using the selected antibiotic (Streptomycin, Ampilox (Ampicillin+ Cloxacillin), Ampicillin, Nystatin, Penicillin), with repeated filtration steps. The antibiotic Streptomycin was effective for Odontella sp. and Amphora sp., while Ampilox showed an inhibitory effect on Navicula-associated microorganisms. These cultures were maintained through subsequent subculturing in the 12H: 12H Day: night photocycle. The agar plate method, staining method- DAPI, and 16S rRNA sequencing verified the axenic nature of the cultures. The axenic culture obtained will be used for the physiological responses of the diatoms during acclimatisation to the stress conditions.

Keywords: Axenic, Antibiotic, Diatom, Filtration, Diatom associated micro-organism

P106: Exploring the Microbial Communities and Their Plastic Degrading Enzymatic Activity Patterns in Extremely Micro-plastic Polluted Mangrove Forests

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ABSTRACT

Plastic production worldwide reached a staggering 390.7 million tones in 2021, with over 250,000 tones being dumped into the oceans. Due to the low rate of degradation, (micro)plastics remain in the ecosystem for long periods. There is currently a knowledge gap and growing interest in seeking green alternatives to mitigate marine plastic pollution, and fortunately, they may be susceptible to biodegradation by certain groups of microorganisms that live in the environment. However, the process of degradation of synthetic polymers by microbes is not globally well developed.

The Red Sea coast of Saudi Arabia is home to unique marine ecosystems. Mangrove sediment contains diverse microbial communities and has been found to act as a long-term sink for microplastics. Here, we apply metagenomics and dilution to stimulation approaches to investigate the mechanisms of how microbial consortia degrades microplastics. Synthetic microplastic was used as the sole carbon source in the enrichment culture. The Stimulated Raman Scattering (SRS) microscopy technique was used to classify microplastics in environmental samples collected in different mangrove forests along the Red Sea. We estimate that our results will show several genes and microorganisms associated with the degradation of microplastics and open space for the mining of genes or enzymes involved in the degradation of complex polymers (hydrolases, laccase, etc.). There will be correlation between the abundance of these microplastics and these genes. We believe that our results will help to select consortia and build a framework to, in the future, engineer the microbial community and its metabolic activity to accelerate the degradation process.

Keywords:

P107: Investigation of Micro- and Macro-Fouling on Biocidal and Non-biocidal Antifouling Coatings in the Sea of Oman

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ABSTRACT

Biofouling is the major problem in all submerged surfaces in non-sterile environments. Although antifouling marine coatings have been used to limit or prevent biofouling, not much is known about their effect on the composition of attached micro- and macro-organisms. The current study aims to assess the abundance and diversity of biofouling communities on substrata protected with biocidal and non-biocidal antifouling coatings and not protected ones in the Sea of Oman (Muscat) over 1 year. Biofilms were harvested in 2 months (April 2022), 7 months (September 2022), and 12 months (February 2023). Bacterial diversity was investigated using the 16S rRNA MiSeq sequencing. Macrofouling species were identified visually using photos. Additionally, the total percentage of cover, chlorophyll concentrations and the weight of biofouling were studied. The data suggested that different coatings have different micro- and macrofouling communities. The differential performance of tested antifouling coatings and abundance of biofouling species may be attributed to several factors including varying environmental conditions, differences in microfouling communities, duration of exposure and chemical and physical properties of antifouling coating.

Keywords: Biofouling, Antifouling, Microfouling, Macrofouling, Bacteria, MiSeq.

P108: Responses of Gut Microbial Community Composition of the snails (Terebralia palustris) to Microplastics in Mangrove Habitats in Oman

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ABSTRACT

Microplastic pollution has become a global concern, with its detrimental effects on aquatic ecosystems receiving increasing attention. In mangrove habitats, microplastics can accumulate and potentially affect resident organisms. This study aimed to investigate the impact of microplastics on the gut microbial community composition and function of Terebralia palustris snails in mangrove habitats of Oman. Snail specimens were collected from two mangrove sites: one with high microplastic pollution and the other with low microplastic pollution. Gut microbial community composition was assessed using high-throughput sequencing of the 16S rRNA gene. Functional potential of the gut microbiome was inferred using predictive metagenomics analysis. High microplastic pollution were detected in mangroves of Al-Sawadi lagoon, however, AlQurum mangroves located in the Muscat city have the lowest microplastic pollution. Our results revealed distinct differences in gut microbial community composition between snails from the two sites. The relative abundances of certain groups especially potentially beneficial groups of bacteria were impacted by microplastic pollution. Furthermore, functional analysis indicated potential disruptions in microbial metabolic pathways in snails exposed to microplastics. These findings suggest that microplastic pollution in mangrove habitats can significantly impact the gut microbial community of T. palustris snails, potentially affecting their overall health and ecological interactions. Further investigations are needed to understand the specific mechanisms by which microplastics influence gut microbial communities and their subsequent implications for the overall health and ecological functions of mangrove ecosystems.

Keywords: Terebralia palustris, gut microbiota, microplastic, 16S rRNA gene , Illumina MiSeq.

P109: Maximizing Food Waste Utilization: The Potential Health Benefits of the Bioaccessible Portion of Fermented Date Pomace by Selected Yeast Isolates

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ABSTRACT

Microbial exposures play a vital role in our overall health, impacting both our internal microbiome and the organisms we encounter in the environment. Food microbiomes, especially fermented foods, hold a unique position as they bridge these two aspects. Fermented foods are created through intentional microbial growth and enzymatic transformations of food components. This research aimed to (i) investigate the physiochemical properties of fermented date pomace (FDP) by selected yeast isolates, which were determined via U-HPLC to analyze sugar, organic acids and phenols, and HS-SPME to identify volatiles, (ii) evaluate the health benefits of FDP samples both preand post-digestion; and (iii) analyze the untargeted metabolites and carbohydrate metabolites in the bioaccessible portions using UPLC-QTOF. Two probiotic yeast candidates, S. cerevisiae and P. kudriavzevii, which have been isolated from food sources, were utilized to ferment date pomace (DP) at 25˚C for 6 days. The sugars in DP were efficiently converted during the fermentation process, leading to elevated concentrations of lactic acid and acetic acid in the FDP. S. cerevisiae resulted in higher levels of alcohols, while P. kudriavzevii produced more esters. This emphasizes the importance of selecting the suitable fermentation agent to effectively control the chemical composition of volatiles. Following fermentation, the levels of phenols in DP samples, particularly (-)-epicatechin, gallic acid, and tyrosol, showed an increase. Higher phenol content in FDP could enhance its health-promoting properties compared to nonfermented DP. The utilization of yeast species for DP fermentation can improve the health benefits of DP, including amylase inhibition and cytotoxicity. The results of the untargeted metabolomics analysis indicate that fermentation significantly influences the 2 metabolization pathway of C5-branched dibasic acids. Additionally, the analysis of carbohydrate metabolites unveiled the presence of three terpenoid compounds: triterpenoids, monoterpenoids, and tutinolide. These findings highlight the potential of yeast fermentation to augment the functionality of DP.

Keywords: Date pomace, Amylase, Glucosidase, ACE-inhibition, Cytotoxicity

P110: Assessments of Agrobacterium Tumefaciens strains for plant transformation.

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ABSTRACT

Background: The first transgenic plant was created about 40 years ago using Agrobacterium tumefaciens-mediated transformation, which is still the preferred approach for gene transport into plants today. Agrobacterium tumefaciens has been used to perform both transient and stable plant changes. These transformation approaches have been utilized in a variety of domains, including agricultural improvement, protein synthesis in plant cells, and gene functional analysis. However, other plants have substantially lower transient gene transfer and stable transformation rates, posing a technological hurdle that must be overcome.
Objective: A. tumefaciens strains (EHA105, AGLI, and LBA4404) were utilized in this work to assess the effectiveness of transformation in Nicotiana tabacum in both transient and stable transformation.
Methods: Salt tolerance was assessed in Mesembryanthemum crystallinum, Salsola soda, Atriplex hortensis, and Spinacia oleracea at 0, 100, 200, and 300 mM NaCl. Halophyte plants were treated with NaCl for 4 weeks to evaluate survival. The DNA encoding salt tolerance is transferred to Agrobacterium Then to plants.
Results: In total, seventy-six transgenic plants were isolated and evaluated for transgene expression and salt tolerance in vitro and in vivo, respectively. This study shows that transgenic tobacco overexpressing AhBADH6 and SoBADH5 were more salt tolerant at germination and seedling phases than wild-type tobacco. Transgenic plants survived exposure to 350 mM NaCl, while wild-type plants died after a week of treatment. The overexpression of AhBADH6 and SpBADH5 transgenic lines retained more chlorophyll and accumulated more proline as single gene transformants, and used enhanced osmoregulatory capability, which decreased the toxic impact of Na+.
Conclusion: Notably, A. tumefaciens strains is the most effective and powerful tools for plant genetic engineering and selectable marker analyses. Because the system has a plasmid harboring the Nptt genes, it might be employed in conjunction with other significant strains like EHA105, LBA4404, and AGL1. Agrobacterium tumefacient might be a revolutionary application for advancing molecular plant science research methodologi

P111: Soil type nested with Plant growth stage are key factors shaping pigeonpea root microbiom

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ABSTRACT

Pigeon pea (Cajanus cajan L. Millsp.) is one of the most important legumes in the world and is the primary source of protein for more than a billion people, with India accounting for approximately 80% of global production. Significant issues associated with pigeon pea growing soils are insufficient nodulation and low yield. Multiple types of pigeonpea are cultivated in various regions, and there are very few investigations on host specificity in nodulation and nitrogen fixation. During various phases of plant development, soil samples from various root zone fractions have been collected for the purpose of primarily isolating nodule-forming Rhizobiales members. It is unknown which of genotype, vegetative state, or soil type controls the microbiome associated with pigeon pea. In leguminous plants, the diversity of root microbiome fractions, i.e. bulk soil, rhizosphere, rhizoplane, and endosphere, is limited, and its evolution in pigeon pea is unknown. In order to answer these questions, an experiment was designed with three genotypes and three soil types, and various root samples were isolated during the vegetative and flowering stages of the plant, respectively. It is the first study of its kind on pigeon pea to identify plant state and soil type as critical factors influencing the root microbiome. It is observed that none of the Rhizobiales members observed to be biological indicators being a classical example of legume-nodule symbiosis.

Keywords: pigeonpea, nodule, rhizosphere, microbiome, biological nitrogen fixation

P112: Mung bean endophytic microbiome: a potential agent to improve Mung bean growth under sustainable agriculture production

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ABSTRACT

Mung bean (Vigna radiata) are known as a good source of protein, vitamins, and different types of micro and macro nutrients for human health. But recent study showed that the growth of mung bean is decreased due to the biotic and abiotic stress. Research suggest that different biological option are available to reduce the effect of stress in mung bean productions. Here, we focused on the effect of mung bean plant microbiome on the mung bean growth, development and disease resistance against different pathogens in in-vitro condition. The endophytic microbes was selected on the basis of plant growth promoting biochemical activity like IAA production, phosphate solubilization, Zinc solubilization, ammonia, siderophore, catalase and biocontrol activity against pathogenic fungi like Fusarium sp., Rhizoctonia sp., Sclerotinia sp., and Alterneria sp. We observed that some endophytic microbes treated mung bean plant showed significant increase in height, biomass, leaf number, roots number, chlorophyll contents and nutrient contents (protein, carbohydrate). The effect of endophytic microbes was tested against plant pathogenic fungi and result showed some of the endoptytes able to inhibit the growth of plant pathogens in in-vitro condition. Therefore it is evident that endophytic microbes can be used as an alternative option of agrochemicals in mung bean production. Further study is required to standardize the microbial dose, molecular cross talk between the microbes and plant metabolisms on their effect on yield, growth development and disease protections. The results provide a direct evidence for the presence of beneficial endophytes and suggest these isolates could be further developed into potential bio-inoculants for improving diseases management and sustainable increase in agriculture productivity

Keywords: Mung bean (Vigna radiata), Endophyte, Microbiome, Plant growth promotion, Sustainable agricultur

P113: Root Endophyte Induced Plant Thermotolerance by Constitutive Chromatin Modification At Heat Stress Memory Gene Loci

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ABSTRACT

Date palms (Phoneix dactylifera) are widely cultivated in arid agroecosystems, where knowledge of irrigation water source effect on below-ground fungal communities is limited. We studied soil and root-associated fungal (RAF) communities of date palms under different irrigation water sources (freshwater vs saline groundwater) across seven farms in UAE in using ITS2 metabarcoding. RAF diversity was lower and fungal communities were distinct between compartments which indicated root effect. Co-occurrence analysis showed a relatively complex and connective (average degree, clustering coefficient and density) as well as highly co-occurring RAF community compared to soil. The RAF and soil fungal communities were also distinct between irrigation water sources; wherein water pH and electrical conductivity (EC) were the major structure factors, while soil pH and EC chemistry were additional factors in soil. Drift (stochastic) was the dominant process in both root and soil under saline groundwater irrigation and its relative importance was higher in root than soil. Saline groundwater irrigation enriched the abundance of specific saprotrophic genera in root (Acrocalymma, Coprinopsis and Myrothecium) and soil (Chaetomium and Preussia) compartments. In addition, the abundance of saprotrophs was higher in root under saline groundwater irrigation, while opposite pattern was observed in soil. Taken together, we show that the RAF communities are complex and connective; saline groundwater irrigation distinctly alters fungal communities in root and soil, in which fungal communities mainly assemble through drift process and select specific saprotrophic fungi (i.e., Acrocalymma-root and Chaetomium-soil) useful for plant growth promotion and nutrient cycling under extreme conditions of saline agroecosystems.

Keywords: Arid agroecosystem; Date palm (Phoenix dactylifera); Desert environment; Fungal community; Irrigation source; Soil salinization

P114: Unveiling the Potential of Catharanthus roseus Rhizobacteria for Stimulating Wheat (Triticum aestivum) Growth: Insights into Characterization and Growth Promotion Mechanisms

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ABSTRACT

The present study aimed to explore the plant growth-promoting rhizobacteria (PGPR) attributes exhibited by bacterial cultures extracted from the rhizosphere of Catharanthus roseus a medicinal plant. In a laboratory setting, the investigation encompassed crucial PGPR traits such as phosphate solubilization, ammonia, and plant growth hormones like indole acetic acid (IAA) production, along with the synthesis of gibberellic acid. Subsequently, pot experiments were conducted using wheat plants to ascertain the potential growth-promoting effects following the inoculation of carefully selected bacterial isolates. At the culmination of the pot study, diverse growth parameters were analyzed comprehensively. This encompassed root and shoot length assessments, overall plant length, spike count, grain production, biomass, spike length, and chlorophyll content. The experimental design employed a Completely Randomized Design (CRD) with each treatment replicated thrice in the pot experiments. A one-way analysis of variance (ANOVA) was employed to scrutinize the data to unravel the significance of the findings. This study sheds light on the PGPR potential in bacterial isolates sourced from Catharanthus roseus rhizospheres. The laboratory assessments highlighted their diverse capabilities, while the subsequent pot studies demonstrated their potential to enhance the growth of wheat plants. These findings contribute to our understanding of sustainable agricultural practices by uncovering beneficial interactions between plants and specialized bacteria. As such, the study underscores the significance of harnessing such interactions to promote crop growth and productivity.

Keywords: PGPR, Medicinal plant, Rhizosphere, Plant growth hormones

P115: Drought and salinity; Methodologies for engineering the plant-associated microbial communities for sustainability of arid regions

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ABSTRACT

The most significant abiotic factors limiting crop development and output are salinity and drought. Approximately half the entire Earth's surface is thought to be covered by arid regions. At the same instance, there will soon be 900 crore people on the planet, and their fitness to survive depends upon agricultural output. It is expected that these issues will only get worse in the near future along with continuous climate change and global warming. Plants growing in saline or dry soil exhibit low germination rates, short roots, reduced shoot biomass, and seriously impaired photosynthetic efficiency, which results in a large loss in crop output and causes substantial economic harm. Plants, on the other hand, should not be thought of as solitary organisms but rather as superorganisms, or holobionts, resulting from the close interactions between the plant and the associated microbiota. Some of the direct mechanisms consist in nitrogen fixation, production of phytohormones (such as auxins and gibberelins), siderophore production and phosphorous solubilization. Controlled applications of referred plant hormones help them to endure with stress by improving its antioxidant potential, by up-regulation of the antioxidant system and by accumulation of compatible osmolytes using soil and atmospheric microbes. This paper, in a nutshell, examines the researches on how the concept of effective growth of plants (especially crop plants) works in desertified habitats and using regulated microbiota (hypothetically resembles desert farming) and what manipulations need to be applied for a sustainable nourishment of microbe-mediated plant species under the conditions of various environmental stresses.

Keywords: Phytohormones, antioxidant potential, environmental stresses, osmolytes, desert farming.

P116: Biological Control Efficacy of Indigenous Antagonistic Bacteria Isolated from the Rhizosphere of Cabbage Grown in Biofumigated Soil against Pythium aphanidermatum Damping-Off of Cucumber

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ABSTRACT

Soil biofumigation is the practice of the incorporation of fresh plant materials from the members of the Brassicaceae family into the soil which release antimicrobial volatile organic compounds (VOCs), namely glucosinolates and their hydrolysis products. However, the VOCs may affect non-target beneficial soil biota including microbial biocontrol agents. In this study, native antagonistic rhizobacteria were isolated from cabbage plants grown in biofumigated fields and their potential in the management of Pythium aphanidermatum cucumber damping-off was evaluated with and also without biofumigation. A total of 20 morphologically distinct bacterial strains were recovered from the rhizosphere soil in a biofumigated field, with the largest fraction of the isolates belonging to the genus Bacillus. The other bacterial genera isolated were Pseudomonas, Serratia, Stenotrophomonas, Microbacterium and Priestia. Of the 20 bacterial isolates, Pseudomonas aeruginosa, Pseudomonas indica, Serratia marcescens and Pseudomonas brenneri exhibited inhibitory activity against P. aphanidermatum. The deformation and shrinkage of P. aphanidermatum hyphae due to diffusible antimicrobial compounds were witnessed through scanning electron microscopy. A biofilm was formed by these bacterial strains in vitro and they exhibited compatibility with each other; however, they had no significant plant growth promotion effect on cucumber. These bacterial strains significantly reduced damping-off in cucumber under greenhouse conditions when applied to soil singly, but failed to show a significant effect when combined with biofumigation treatment, though the bacterial population in the soil was maintained at higher levels. Soil biofumigation alone was also not effective in suppressing the damping-off of cucumber. GCMS analysis revealed that 1-butanol, n-butyl butyrate and butyl acetate were the predominant VOCs in the soil amended with cabbage leaf residue. The results suggest that soil biofumigation with cabbage leaf residue has no significant effect on P. aphanidermatum under high inoculum levels; furthermore, it affects the efficiency of the bacterial antagonists in controlling damping-off in cucumber.

Keywords: bacterial antagonists; biofilm; Cucumis sativus L.; damping-off; volatile organic compounds

P117: Characterization Of Pseudomonas Putida For Its Plant Growth Promotion Potential And Bioremediation

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ABSTRACT

Plant growth-promoting rhizobacteria (PGPR) are plant root colonising bacteria used as a biocontrol agent in agriculture to improve plant growth, increase production, and tolerance against abiotic stress. Biopriming of seeds is a useful technique for introducing advantageous microbial inoculum into the soil or rhizosphere. They either directly promote plant growth by assisting in acquiring nutrients like nitrogen, phosphorus, and other essential minerals or by modulating the levels of phytohormones or reduce the detrimental impact of various pathogens on plant growth and development in the form of biocontrol agents. In this study, we tried to characterize the plant growth-promoting ability of Pseudomonas putida, an isolate obtained from the roots of Lemna minor (duckweed). P. putida is screened for plant growth promotion traits and bioremediation potentials like tolerance to heavy metals and salt. We checked the plant growth promotion ability by biopriming with paddy seeds and observed that it increased the root, shoot length and chlorophyll content compared to the control. The improved root colonisation, the synthesis of enzymes, ammonia siderophores and phytohormones along with the ability to fix nitrogen and solubilization of phosphate was found to be efficient in plant growth promotion. We also checked the antagonistic effect of P. putida against selected bacterial pathogens and observed that it could inhibit the growth of different pathogens. When cocultured with the pathogens we observed that P. putida can outcompete the pathogens both in planktonic as well as biofilm state.

The untreated industrial wastes and agrochemicals may lead to the accumulation of toxic heavy metals in soil and water resources. P. putida showed a broad spectrum of tolerance towards different concentrations of heavy metals Cadmium, Zinc, Nickel, Lead, Arsenate, and Copper thus proving its ability in bioremediation. These findings highlight P. putida as an efficient plant growth-promoting bacteria with bioremediation potential.

Keywords: P. putida, Plant growth promotion, biocontrol, agriculture, bioremediation

P118: Chickpea Seed Endophyte Bacillus Subtilis: An Effective PGPB To Improve Chickpea Nutritional Quality Under Sustainable Agriculture

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ABSTRACT

Chickpea (Cicer arietinum L.) used as a rich source of protein and energy both in human and livestock's diets. Moreover, the chickpea foliage can serve as an alternative fodder. Our present study evaluates the effect of chickpea seed endophytes inoculation on the nutritional values in the edible parts of chickpea and productivity. The competent chickpea seed endophyte Bacillus subtilis BHUJPCS-12 (Ac no. MN078050) was selected on the basis of plant growth promoting properties like IAA, phosphate solublization, zinc solubilizaiton, protease activity, ammonia, siderophore production and antagonistic against soil borne phytopathogen Fusarium sp. Pot experiment was conducted with the chickpea seed (P-362) to check the plant growth and development. Chickpea seeds treated with the seed endophytes showed significant increase in plant growth (20%), biomass (19.76%) and nutrients quality in chickpea seed and plant. Additionally, nutritional quantity like total protein (5%, 7%), carbohydrate (14%, 10.90%), flavonoid (33.3%, 25%), micro and macro nutrient were also found significant enhancement in seed and foliage of the endophyte treated chickpea plants as compared to the control plant. Therefore, this potential seed endophyte strains Bacillus subtilis can be used as a plant growth promoting inoculants for enhancing plant growth, nutritional quantity and productivity of chickpea crops under sustainable agriculture. This endophytes can be further used for field demonstration for chickpea productivity. This should be cost effective, economically viable and environment friendly.

Keywords: Chickpea, Plant endophytic microbiome, Bacillus subtilis, Nutrients, sustainable agriculture

P119: In vivo Assay of Multi-Potent Plant Growth Promoting Bacteria

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ABSTRACT

Beneficial plant–microbe interactions in the rhizosphere determine plant health and soil fertility. In the era of sustainable agricultural production, the interactions in the rhizosphere play a pivotal role in transformation, mobilization, solubilization, etc. Plant growth-promoting rhizobacteria (PGPR) are the rhizosphere bacteria that may be utilized to augment plant growth and suppress plant diseases. The objectives of this study were to identify and characterize PGPR indigenous to the groundnut rhizosphere, which increases plant growth in Vigna radiata L. A total of 11 bacteria were isolated from different Saurashtra regions, out of which Acinetobacter calcoaceticus KR-25 (KR-25) was selected based on their in vitro plant growth-promoting attributes for in vivo assay. The selection of KR-25 was influenced by showing one or more Plant growth-promoting (PGP) traits like Nitrogen fixation, Phosphate solubilization ability, Potassium solubilization, Siderophore production, Ammonia production, 1-aminocyclopropane-1-carboxylate deaminase activity, Zinc solubilization and exhibited strong abilities to produced Indole acetic acid. Vigna radiata L. seeds treated with KR-25 strain displayed significantly higher levels of seed germination, growth, and increased length of root and shoot of plants compared to non-treated control plants. Multi potent KR-25 stain was indigenous to the groundnut plant, although it shows a significant positive effect on the growth of Vigna radiata L. germination percentage of treated plants shows 100% as compared to control (87.5%). Further root length was increased by 202% as compared to control plants.

Keywords: PGPR, in vivo assay, Vigna radiata L., Nitrogen fixation, seed germination

P120: Ascending migration and in planta nitrogen fixation of rice foliage endophytic diazotrophic Lysinibacillus sphaericus

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ABSTRACT

Nitrogen is the major limiting nutrient required for rice cultivation next to water. The large potential demand of nitrogen for plant growth is mainly achieved using chemical N fertilizers. Considering the risk factors associated with N over fertilization and requirement of plant growth and yield, Endophytic bacteria forms a major focus on extension of biologically fixed N effectively to non-leguminous plants. The present study used an endophytic N fixing isolate identified as Lysinibacillus sphaericus, which was found to be positive for in planta nitrogenase activity (13.06±2.22 n moles C2H2 gm -1 h-1) compared to uninoculated control plants (2.86±0.32 n moles C2H2 gm – h-1) in the Acetylene Reduction Assay using Gas chromatography. The effect of inoculation of L. sphaericus on colonization as well as yield and nutrient uptake was studied. All the parameters studied showed significantly higher values than that obtained in uninoculated absolute control. The highest yield was given by treatment T7 (seed and foliar) followed by T9 (soil and foliar) and T5 (seed and soil) and were statistically at par. There was no remarkable change in the soil N content in the treatments which received L. sphaericus application revealing the fact that the N content of straw came mainly from biological nitrogen fixation. The highest values of total N were shown by treatment T10 (1.58%) followed by T7 (1.54%). While the soil N content was found to be lower in pots which received treatments of Standard Pseudomonas sp. compared to L. sphaericus. The least N content (1.1%) was recorded in T23 absolute control, where the plant utilized the inorganic nitrogen provided in the soil. It can be deduced from the results, there is a high influence of endophytic bacteria L. sphaericus in plant growth despite the mode of inoculation. This confirms the potential of diazotrophic endophyte L. sphaericus to limit the use of industrial N fertilizers thereby enhancing the fertility of the soil and establishing sustainable agriculture.

Keywords: L. sphaericus, endophytic diazotroph, biological nitrogen fixation, non-leguminous plants

P121: Exploring the Mangrove Plant Microbiome and Comparing the Taxonomic and Functional Composition among Plant and Soil Compartments

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ABSTRACT

The microbiome of mangroves plays a crucial role in maintaining these ecosystem services, yet studies examining the mangrove microbiome in coastal wetlands Linyuan District, Kaohsiung City, Taiwan. In this study, the metagenomic approach is aimed to characterize the microbiome of the mangrove tree and its associated soil compartments. The V3 and V4 region of 16s rRNA based amplicon sequencing was performed using Illumina MiSeq platform. The results revealed significant differences in taxonomic and functional composition among plant and soil compartments, with bacterial communities varying across populations and tissue types. The major detected bacterial phyla were affiliated to Proteobacteria, Flavobacteriia, Terrabacteria, Planctomycetia were the predominant phyla in the mangrove sediments of this area microbial attributes based characterization suggests the presence of the unknown origin which may contribute to the growth and health of these important trees. Additionally, studies have isolated and identified plant growth-promoting rhizobacteria (PGPR) in the microbiome of mangroves. Overall, understanding the differences and similarities between the microbiome of mangrove plants and soil compartments is crucial for maintaining the functioning and resilience of these important ecosystems, particularly in the context of climate change and other anthropogenic stressors. As interest in mangrove restoration increases throughout the region, an understanding of the microbes associated with these habitats will become an increasingly important consideration in conservation initiatives.

Keywords: Mangrove Microbiome, Metagenomic analysis, Bacterial diversity

P122: Native Bacteria Isolated from Roots And Rhizosphere Of Mangrove Trees Increase Tomato Seedling Growth Under A Reduced Chemical Fertilization Regime

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ABSTRACT

Plant growth-promoting bacteria (PGPB) use is a sustainable agricultural strategy that can promote optimal plant growth while preserving the environment. This study aimed to select efficient native PGPBs and evaluate their potential to enhance tomato seedling growth while reducing the use of NPK chemical fertilizers. A total of 41 strains were isolated from the roots and rhizosphere of the mangrove tree, and their in vitro, PGP activities were screened. Two compatible strains, identified as Bacillus wiedmannii and Bacillus licheniformis, were selected for further evaluation. The efficiency of these two strains used individually and in combination, was assessed in a pot experiment with varying levels of chemical NPK fertilization (0, 50, and 100% of their standard needs). The experiment was conducted in a completely randomized design with three replications. After 42 days of sowing, various parameters such as plant height (PH), digital biomass (DB), projected leaf area (PLA), greenness average (GA), the normalized difference vegetation index (NDVI), shoot and root dry weight (SDW, RDW), and content of chlorophyll a (Chl-a), chlorophyll b (Chl-b), and carotenoid (Car) were estimated and analyzed. Interestingly, these increases ensured the highest values similar to or higher than those of plants receiving a full dose of NPK chemical fertilization. The findings of the study indicate that the combination of bacterial inoculation and 50% of NPK chemical fertilization significantly increased the PH (44-51%), DB (60-86%), PLA (77-87), GA (29-36%), NDVI (29%), SDW (82-92%) and RDW (160-205) compared to control plants. Additionally, this combination positively impacted Chl-a by 25-31%, Chl-b by 34-39%, and Car by 45-49%. This research highlights the potential of using native PGP bacteria as a sustainable and environmentally friendly approach for crop cultivation. Nonetheless, further studies are needed to investigate how these inoculants affect the productivity and quality of tomatoes.

Keywords: Plant growth-promoting bacteria, tomato seedling, sustainable agriculture, fertilization practices

P123: Comparative genomics provides insights into plant bacterial pathogen infection mechanisms

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ABSTRACT

The desert is a fragile ecosystem characterized by harsh environmental conditions and limited resources. Developing a sustainable farming system with fertile soil and disease-free crops is challenging. The DARWIN21 project has assembled the world's largest microbial desert biobank, offering sustainable solutions that promote plant growth, suppress phytopathogens, restore soil fertility, and rebalance hyper-arid ecosystems. Here, we aimed to identify specific microbial species or communities that are particularly effective in mitigating the harmful effects of the bacterial pathogen Pseudomonas syringae pv. Tomato (Pst) on plants. By evaluating 117 Pseudomonas strains from the DARWIN21 biobank for their ability to mitigate DC3000 infection on A. thaliana plants, we identified 42 strains that demonstrated varying degrees of efficacy in impeding Pst disease progression. We demonstrated dual beneficial functions for plant defense and growth promotion for strains Z4-20, Z5-35, D1-26, and Z4-24. Moreover, we identified two strains of Pseudomonas zanjanensis (Z1-12 and Z3-6) that are closely related (96.25% whole-genome sequence similarity) but display beneficial or pathogenic effects on Arabidopsis plants, respectively. Using comparative genomics, we identified specific Pseudomonas virulence genes and several candidates for explaining the direct and indirect host immunity suppression of Pst disease. Our work should help to develop sustainable agroecosystem solutions by substituting toxic pesticides with natural microbiomes to provide disease-free plants and healthy food.

Keywords:

P124: Mangrove Forest is a Hotspot of Plant Growth-Promoting Bacteria with Immense Potential For Enhancing Crop Productivity In United Arab Emirates

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ABSTRACT

The mangrove forests are blue carbon ecosystems with a unique ability to sequester carbon, mitigate climate impact, and support high biodiversity. Although the microbiota of mangrove ecosystems has been studied worldwide, there are significant gaps in understanding halophilic microorganisms with plant growth promotion potential from mangrove plants. This study aimed to isolate plant growth-promoting bacteria (PGPBs) associated with the mangrove ecosystem in the UAE. In total, 42 bacterial strains were isolated from the Umm Al Quwain mangrove forest's wet and dry sediments and mangrove roots. Isolated bacterial strains were identified by 16S rRNA sequencing and studied for their plant growth-promoting properties. Most of the isolates belonged to bacillus genera, including endophytes such as Bacillus wiedmannii and Bacillus licheniformis. Screening of mangrove bacterial isolates by in vitro plant growth-promoting assays indicated the high occurrence of PGPB in the mangrove forest. Results suggest that most of the endophytes from mangroves exhibited plant growth-promoting characteristics such as phytohormones, extracellular polymeric substances (EPS) & siderophore production, phosphorous, potassium solubilization, nitrogen fixation, and antagonism against pathogens. Several isolates exhibited growth and morphological characteristics similar to long cable bacteria. These filamentous sulfur-oxidizing bacteria are likely to induce long-distance electron transport in aquatic sediments and could be keystone microbial species in the geochemical cycling of mangroves. Overall, the PGPB isolated in this study can be used for microorganisms-mediated bio-inoculation approaches for mangrove protection and rehabilitation to enhance the circulation of elements in mangrove forests, including various edible crop productivity in the United Arab Emirates.

Keywords: Mangrove endophytes, Salinity, Plant growth promotion, crop productivity, United Arab Emirates

P125: Metagenomic Exploration of the Adventitious Root Microbiome of Black Pepper (Piper nigrum): Unravelling the Microbial Diversity and Functional Potentia

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ABSTRACT

Black pepper (Piper nigrum) is a highly valuable spice crop known as the "King of Spices" or "Black gold." It is widely cultivated in tropical regions and relies on the adventitious roots produced from its nodes to climb. These specialized roots are vital in providing support, anchorage, and nutrient uptake. Despite its significance, the adventitious root microbiome of black pepper remains largely unexplored. Metagenomic approach can unravel the complex interactions between plants and associated microbiome. In this study, we performed metagenomic analysis to characterize the microbial diversity and functional potential of the adventitious root microbiome of black pepper. Root samples were collected from healthy black pepper plants. High-throughput DNA sequencing was performed on the Illumina platform, generating vast amount sequence data. The resulting metagenomic dataset was subjected to comprehensive bioinformatic analyses, including quality control, taxonomic profiling, and functional annotation. Our analysis revealed a diverse array of microorganisms inhabiting the black pepper adventitious roots. The results underscored the dominance of bacteria in the black pepper adventitious root microbial community, accounting for an overwhelming 97.7% of the overall composition. At the phylum level, Proteobacteria and Actinobacteria were the dominant bacterial groups. The functional analysis provided valuable insights into the metabolic capabilities of the root microbiome. Our findings provide comprehensive insights into the dynamic nature of microbial communities within black pepper adventitious roots, shedding light on the potential interactions between the plant and diverse microorganisms. The identification of specific bacterial taxa and their abundance patterns contribute significantly to our understanding of the complex relationships that shape the plant's ecosystem. The study unveils the intricate microbial diversity within black pepper adventitious roots, offering valuable information for developing innovative strategies to bolster crop productivity while ensuring sustainable agriculture practices.

Keywords: Black pepper, Metagenomics, Adventitious root, Microbiome

P126: Microbe Induced Growth Promotion and Stress Tolerance In Arabidopsis Using Endophytes Isolated From Date Palm

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ABSTRACT

Black pepper (Piper nigrum) is a highly valuable spice crop known as the "King of Spices" or "Black gold." It is widely cultivated in tropical regions and relies on the adventitious roots produced from its nodes to climb. These specialized roots are vital in providing support, anchorage, and nutrient uptake. Despite its significance, the adventitious root microbiome of black pepper remains largely unexplored. Metagenomic approach can unravel the complex interactions between plants and associated microbiome. In this study, we performed metagenomic analysis to characterize the microbial diversity and functional potential of the adventitious root microbiome of black pepper. Root samples were collected from healthy black pepper plants. High-throughput DNA sequencing was performed on the Illumina platform, generating vast amount sequence data. The resulting metagenomic dataset was subjected to comprehensive bioinformatic analyses, including quality control, taxonomic profiling, and functional annotation. Our analysis revealed a diverse array of microorganisms inhabiting the black pepper adventitious roots. The results underscored the dominance of bacteria in the black pepper adventitious root microbial community, accounting for an overwhelming 97.7% of the overall composition. At the phylum level, Proteobacteria and Actinobacteria were the dominant bacterial groups. The functional analysis provided valuable insights into the metabolic capabilities of the root microbiome. Our findings provide comprehensive insights into the dynamic nature of microbial communities within black pepper adventitious roots, shedding light on the potential interactions between the plant and diverse microorganisms. The identification of specific bacterial taxa and their abundance patterns contribute significantly to our understanding of the complex relationships that shape the plant's ecosystem. The study unveils the intricate microbial diversity within black pepper adventitious roots, offering valuable information for developing innovative strategies to bolster crop productivity while ensuring sustainable agriculture practices.

Keywords: Black pepper, Metagenomics, Adventitious root, Microbiome

P127: Insights into the Citrullus colocynthis microbiome

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ABSTRACT

Desert plants depend on their microbiomes to thrive amidst water scarcity in arid environments. *Citrullus colocynthis*, a native desert vine, produces water-rich fruits and oil-rich seeds despite lacking apparent water access. The broader research project seeks to investigate the mechanisms behind the adaptation of *C. colocynthis* by exploring the interactions between the plant and its microbiome. Previous research has demonstrated associations with plant-growth-promoting bacteria. Here we delve into potential disparities in the microbiome of *C. colocynthis* across two United Arab Emirates locations: Al Ain and Ras Al Khaimah (RAK), which differ in geographic location, elevation, and annual rainfall levels. Using leaf and root tissue data, our preliminary findings suggest intriguing differences but also shared elements between the sites. Specifically, Al Ain samples contained Actinobacteria and Clostridia, which were absent in RAK samples. Alphaproteobacteria were present in root samples from both locations. To build on these insights, we extended our sampling to include two seasons. This approach aims to ascertain whether seasonal variations, also observed in the microbiomes of other desert plants, influence the microbiome of *C. colocynthis*. The disparities in microbial composition between the Al Ain and RAK plants, coupled with the potential for seasonal variation, may showcase the intricate interplay of environmental factors, plant-microbe dynamics, and microbial communities. These observations serve as a stepping stone for a deeper comprehension of the interactions between *C. colocynthis* and its microbiome. As the study advances, we anticipate uncovering more about the intricate relationships driving desert plant resilience and microbial adaptation.

Keywords: Colocynth, microbiome, desert flora

P128: Metagenome-Directed Investigation Provides Powerful Probiotic Bacteria from The Microbiome of Palm Nectar

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ABSTRACT

Human health may benefit from plant-derived probiotics. Most probiotic studies have focused on human or animal bacteria; however plant-originated bacteria may enhance human health. The aim of the study is to utilize the metagenome-guided approaches to enables the identification and isolation of highly effective probiotic bacteria derived from the microbiome of palm nectars. Two samples of palm nectar named Neera (N) or Toddy (T) were collected aseptically from the Phoenix sylvestris and Borassus flabellifer palm trees in western India. Total DNA was extracted from both samples and subjected to 16s rRNA gene amplification followed by Ion Torrent-based amplicon sequencing. QIIME2 was used to analyze the metagenomic data to determine the dominating species in both samples, and One Codex was used to compare the samples. Culturing was done by selective isolation agar medium (MRS media) after identifying of numerous probiotic bacterial species in metagenomes. Firmicutes and Proteobacteria phyla and Lactobacillaceae and Leuconostocaceae families predominated in both Metagenomic datasets. Different Lactobacillus and Leuconostoc species predominated in both samples, followed by Zymomonas mobilis and Acetobacter species. However, only the T sample had a substantial presence of Pediococcus species. In both metagenomes, more than 20 different species of lactic acid producing bacteria were found. Culture-based isolation on MRS agar media was successful in isolating 17 distinct isolates. Four were identified as Leuconostoc suionicum Y1, Lactiplantibacillus paraplantarum NF2 from the N sample and Lactiplantibacillus pingfangensis MF1, Lactiplantibacillus paraplantarum MF2 from the T sample. All four isolates were tested for probiotic activities, including the production of inulinase, protease, amaylase, and lipase, antibiotic sensitivity, and antibacterial substance production against four food pathogens: E. coli, E. faecalis, B. subtilis, and S. Abony. Each test produced an outstanding result. Acid tolerance, bile salt tolerance, 0.6% phenol tolerance, DPPH-free radical scavenging activity, and bacterial adhesion to hydrocarbons (non-polar solvents) were also tested, and all four isolates were found to tolerate acid, bile salt, and phenol, as well as having good antioxidant activity and cell surface hydrophobicity. All of these qualities may lead to better gut health of human. This metagenomics-based study screens potent novel plant-derived lactic acid bacteria for the first time. The study opens up the possibility of commercializing probiotics for health benefits.

Keywords: Probiotics, Palm nectar, Metagenomics, Lactic acid bacteria

P129: In Vitro Evaluation of Acinetobacter Strain For Physio-Biochemical Traits, Phytohormone Level, Expression Of Defense Related Genes And Cd Detoxification In Maize Cultivars Differing In Cd Retention Potential

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ABSTRACT

Cadmium (Cd) poses serious threats to plant growth and development, whereas the use of plant growth-promoting rhizobacteria (PGPR) has emerged a promising approach to inhibit Cd accumulation in crops. A pot experiment was conducted to evaluate the effect of Cd tolerant strain Acinetobacter sp. SG-5 on growth, phytohormonal levels, defense response and Cd uptake of two maize cultivars (3062, 31P41) under various Cd stress levels (0, 50 and 100 mM CdCl2). Our results revealed that CdCl2 treatment significantly suppressed the growth, photosynthesis, ionic homeostasis together with higher Cd uptake and transport in maize cultivars in a dose dependent and cultivar specific manner with pronounced negative effect in 31P41. However, SG-5 strain exerted positive impact by up-regulating growth indices, photosynthesis-related attributes (Fv/Fm, Fm, qP, ETR and FPSII), enzymatic and non-enzymatic antioxidants, endogenous hormone levels (IAA and ABA) in both maize cultivars but evident results were recorded in Cd sensitive cultivars 31P41. Further, Cd resistant PGPR decreased the formation of reactive oxygen species in terms of malondialdehyde (MDA) and hydrogen peroxide (H2O2) verified through (DAB and NBT) analysis, concomitantly with ATP and ionic exchange capacity (including Ca2+ ATPase and Mg2+ ATPase), expression levels of defense related genes such as (ZmGR1, ZmAPX1, ZmCu/Zn-SOD, ZmNHX1, ZmNHX3, and ZmATPs) in conjunction with diminished Cd uptake and translocation in maize root and shoots as compared to their control counterparts advocating its sufficiency for bacterial-assisted Cd bioremediation. In conclusion, both SG-5 inoculated cultivars exhibited maximum Cd tolerance but substantial Cd tolerance was acquired by Cd susceptible cultivar 31P41 than Cd tolerant cultivar 3062. Current work strongly suggests that the SG-5 strain as a promising candidate for plant growth promotion and bacterial assisted phytomanagement of metal-polluted agricultural soils.

Keywords: Antioxidant activity, Gas exchange, defense related genes, PGPR, nutrient acquisition

P130: Endophytic Actinobacteria Mediated Suppression of Fusarium Solani Induced Sudden Decline Syndrome in Date Palms

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ABSTRACT

Thirty-one endophytic streptomycete and non-streptomycete actinobacteria were isolated from healthy date palm root tissues. In vitro, screening revealed that the antifungal action of isolate #16 was associated with the production of cell-wall degrading enzymes, whereas with diffusible antifungal metabolites in isolate #28, albeit their production of volatile antifungal compounds. According to the 16S rRNA gene sequencing, isolates #16 and #28 were identified as Streptomyces polychromogenes UAE2 (Sp; GenBank Accession #: OK560620) and Streptomyces coeruleoprunus UAE1 (Sc; OK560621), respectively. The two antagonists were recovered from root tissues till 12 weeks after inoculation and efficiently colonized root cortex and xylem vessels, indicating that the date palm roots are a suitable habitat for these endophytic isolates. At the end of the greenhouse experiments, sudden decline syndrome (SDS) development was markedly suppressed by 53% with the application of Sp and 86% with Sc, confirming their potential in disease management. Results showed that the estimated disease severity indices in diseased seedlings were significantly ($P<0.05$) reduced from 4.75 (scale of 5) to 2.25 or 0.67 by either Sp or Sc, respectively. In addition, conidial numbers of the pathogen significantly ($P<0.05$) dropped by 38% and 76% with Sp and Sc, respectively, compared to infected seedlings with F. solani (control). Thus, the suppression of disease symptoms was superior in seedlings pre-inoculated with S. coeruleoprunus, indicating that the diffusible antifungal metabolites were responsible for F. solani retardation in these plants. This is the first report of actinobacteria that naturally exist in date palm tissues acting as microbial antagonists against SDS on date palms.

P131: The function of CAZymes class glycoside hydrolase in the rhizosphere microbiome of the wild plant Moringa oleifera

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ABSTRACT

Moringa oleifera is a wild plant belonging to the family Moringaceae. This species is a large tree commonly known as the horseradish tree, which is native to several habitats, including the western region of Saudi Arabia. This wild plant has many health benefits as it harbors several important bioactive and antioxidant compounds. Carbohydrate-Active enZymes (or CAZymes) as they build and break down complex carbohydrates in the soil. The most abundant bacteria harboring these CAZymes include phylum Actinobacteria and its genus Streptomyces and phylum Proteobacteria and its genus Microvirga. The utilization of next-generation sequencing (NGS) in terms of the metagenomic whole genome sequencing (mWGS) approach allows the cataloging of soil microbial genes that can be used to detect more accurate soil microbial composition and function. The results of this study indicate that CAZy class glycoside hydrolases (GH) and its α-amylase family GH13 in rhizobiome are the most abundant among CAZy classes and families. In general, we can conclude that class GH is the most abundant among CAZy types in microbiomes surrounding the roots of M. oleifera. These microbiomes can be a source of industrially important enzymes acting on starch hydrolysis/biosynthesis. In the present study, we have searched CAZymes of rhizosphere soil microbes that are encoded by the most abundant microbial genes that allow cross-talking with roots of M. oleifera to reach insights as to how plants and microbes interact and mutually benefit from carbohydrates with different levels of complexities. This will allow the engineering and integration of root microbiomes in breeding programs of domesticated plants to enhance their growth by monitoring the availability of required nutrients and the ability to withstand biotic and abiotic stress conditions.

Keywords: Moringa oleifera, microbiome, glycoside hydrolases, Actinobacteria, Proteobacteria.

P132: The highly abundant CAZyme encoded genes in rhizosphere microbiome of Moringa Oleifera

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ABSTRACT

Moringa oleifera is a small tree of the family Moringaceae that is grown in the wild in Saudi Arabia. It is an edible plant with a high nutritional value, as it is rich in proteins, vitamins, oils, fatty acids, micro/macro elements, and phenolics. Extensive research on this wild plant might lead to the recovery of novel agents to be used commercially to lower human blood sugar and cholesterol levels, in addition to many other medical applications. The genomes of the microbial communities in rhizosphere region and bulk soil of Moringa oleifera are highly abundant in genes encoding carbohydrate active enzymes. These enzymes are named Carbohydrate Active enZymes (or CAZymes) as they act in building/degrading soil carbohydrate. CAZymes were assigned to CAZy classes (level 1) and families (level 2). The rhizosphere microbiome was studied via metagenomic wholegenome shotgun sequencing (mWGS) in comparison with a bulk soil microbiome of Moringa oleifera. The results indicated that microbiome signatures and corresponding CAZy datasets differ between the two soil types. We assume that microbiome of the wild plant Moringa oleifera is a good source of industrially important enzymes that act on starch hydrolysis and/or biosynthesis. In addition, metabolic engineering and integration of certain microbes of this microbiome can also be used in improving growth of domestic plants and their ability to tolerate adverse environmental conditions.

Keywords: Moringa oleifera, Rhizosphere, CAZy, mWGS, Carbohydrates

P133: Unraveling Drought-Induced miRNAs through Next Generation Sequencing and Their Contrast to miRNAs Under Salt Stress in Niger (Guizotia abyssinica Cass.)

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ABSTRACT

MicroRNAs (miRNAs) play pivotal roles in directing gene regulation, particularly in plant responses to drought stress. Extensive investigations have illuminated a multitude of miRNAs and their target candidates in diverse plant species experiencing varying stress conditions. In our pursuit to identify drought-responsive miRNAs, we harnessed the power of Illumina deep sequencing technology to construct and analyze small RNA libraries extracted from both control and drought-stressed Niger seedlings. This approach yielded a total of 4,326,902 and 6,905,026 raw sequences for the respective conditions. Our meticulous analysis unveiled 111 conserved mature miRNAs and 2 novel miRNAs in the control samples, whereas the drought-stressed samples exhibited 95 conserved mature miRNAs and 5 novel miRNAs. Through differential gene expression (DGE) analysis, we ascertained 74 known miRNAs that displayed expression in both control and drought-stressed conditions. Among these, 12 miRNAs were up-regulated, 27 were down-regulated, and 35 exhibited no significant change in expression levels. Validating our findings, quantitative real-time PCR (qRT-PCR) corroborated the differential expression pattern of 10 conserved miRNAs. Notably, miR6478, miR167d, miR319b, miR156, and miR858b were up-regulated, while miR167b, miR166a, miR156q, miR166b, and miR319d-3p were down-regulated under drought stress. Employing the psRNA Target tool, we conducted target prediction and identified 5,509 targets for conserved miRNAs and 381 targets for novel miRNAs across both libraries. Furthermore, Gene Ontology (GO) annotations of the target genes highlighted their potential involvement in ATP binding and as integral membrane components, suggesting their role in modulating the plant's response to drought stress. In addition, we conducted a comparative analysis of miRNAs in niger under both salinity and drought conditions, shedding light on their distinct contributions to target gene expression, particularly in the context of abiotic stress responses.

Keywords: microRNA, drought stress, salt stress, next-generation sequencing, differential gene expression, qRT-PCR, target prediction, Gene Ontology, abiotic stress response.

P134: Optimization of cultural condition for bio cellulose production by acetobacter isolated form local UAE dates

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ABSTRACT

Bacterial cellulose is the most renewable, versatile, and multifaceted biopolymer, with a wide range of applications and still in use today. Great interest towards the BC is due to its 3-dimensnional structure and gelatinous structure that can make it a good candidate for different medical applications as well. Natural BC consists of nanofiber mesh in pure cellulose form without hemicellulose and lignin. Bacterial cellulose (BC) can be synthesized in fine nature from several microbiological sources, such as bacteria. The objective of our current studies is to isolate a an acetobacter bacteria from waste and rotten dates in local western region of UAE and production of bio-cellulsoe from the isolated bacteria. Different fruits (Apple, grapes, and dates) were screened for BC production and potent bacterial strain was isolated from the rotten Khalas dates, local UAE farms. Acetobacter was isolated from Khalas dates using GYC media, nutrient agar (12.5g), yeast extract (2 g), glucose (2g), calcium carbonate 98% (4g) with final volume of distilled water (250 ml). Inoculum for bacterial strain was prepared using same cultural conditions without agar in shaker incubator at 30℃, 180 rpm for 48 hrs. For Bio cellulose production fermentation mixture was used with nutrient composition mention as above and different parameters (pH, Temperature and inoculum size and incubation time) were optimized for the maximum production of BC. Based on the optimized conditions, bio cellulose production increased with increased medium size, pH 4.5, 12 days of incubation at temperature of 30℃, with 4% inoculum size. Bio cellulose produced can be used in food and pharmaceuticals, for producing high-quality paper, wound dressing material, and nanocomposite films for food packaging.

Keywords: Biocellulose, Acetobacter, Khalas dates, Cultural condition

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P135: Rhizobiome Signature and Its Alteration Due toWatering in the Wild Plant Moringa oleifera

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ABSTRACT

Metagenomic approach was used to detect microbial gene abundance and relative abundance in the rhizosphere of Moringa oleifera and surrounding bulk soil and to detect the responseof soil microbes to watering. Expectedly, the number and abundance of non-redundant genes were extremely higher in bacteria followed by archaea, eukaryota and viruses. Results demonstrated unexpected high abundance of some microbes (ex., endophyte genus Nocardioides) in the rhizosphere that are supposed to exist mainly in other rhizocompartments. We suggest this differential distribution of microbes is due to the specific pattern of host-microbe interaction. Other endosymbiont microbes, ex., fungi Mucoromycota and Ascomycota, were highly abundant in the bulk soil possibly because they are phytopathogens where plant exudates might inhibit their growth or force these fungi to approach reverse chemotaxis. Our data indicated high abundance of other symbiont microbes in the rhizosphere of M. oleifera at phylum (ex., Actinobacteria) and genus (ex., Streptcmyces) levels. Watering experiment indicated that phylum Actinobacteria and the descending genus Streptomyces are among the highest. Rhizobiome of M. oleifera seems to harbor a wealth of new species of the genus Streptomyces that are required to be deciphered for function in order to be eventually utilized in pharmaceutical and agricultural applications.

Keywords: Actinobacteria; Streptomyces; rhizocompartment; phytopathogen; endophyte; symbiont; Drought

P136: Functional Interpretation of Cross-Talking Pathways with Emphasis on Amino Acid Metabolism in Rhizosphere Microbiome of the Wild Plant Moringa oleifera

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ABSTRACT

The functional processes and mutual benefits of the wild plant Moringa oleifera and its rhizosphere microbiome were studied via metagenomic whole-genome shotgun sequencing (mWGS) in comparison with a bulk soil microbiome. The results indicated high gene abundance of the four KEGG categories, “Cellular Processes”, “Environmental Information Processing”, “Genetic Information Processing”, and “Metabolism”, in the rhizosphere microbiome. Most of the enriched enzymes in rhizobacteria are assigned to the pathway “Amino acids metabolism”, where soil-dwelling microbes use amino acids as a defense mechanism against phytopathogens, while promoting growth, colonizing the cohabiting commensal microbes and conferring tolerance against abiotic stresses. In the present study, it was proven that these beneficial microbes include Bacillus subtilis, Pseudomonas fluorescens, and Escherichia coli. Mineral solubilization in these rhizobacteria can make nutrients available for plant utilization. These rhizobacteria extensively synthesize and metabolize amino acids at a high rate, which makes nitrogen available in different forms for plants and microbes. Amino acids in the rhizosphere might stand mainly as an intermediate switcher for the direction of the soil nitrogen cycle. Indole acetic acid (IAA) was proven to be synthesized by these beneficial rhizobacteria via route indole-3-pyruvate (IPyA) of the pathway “Tryptophan metabolism”. This hormone might stand as a shuttle signaling molecule between M. oleifera and its rhizobacteria. Tryptophan is also metabolized to promote other processes with important industrial applications. Rhizobacteria were also proven to breakdown starch and sucrose into glucose, which is the primary metabolic fuel of living organisms. In conclusion, we assume that the metabolic processes in the rhizosphere microbiome of this wild plant can be eventually utilized in boosting the sustainability of agriculture applications and the plant’s ability to benefit from soil nutrients when they are not in the form available for plant root absorption.

Keywords: mWGS; phytopathogen; rhizobacteria; solubilization; tryptophan; glucose

P137: Functional Interpretation of Cross-Talking Pathways with Emphasis on Amino Acid Metabolism in Rhizosphere Microbiome of the Wild Plant Moringa oleifera

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ABSTRACT

Genes of the rhizospheric virome of the wild plant species Moringa oleifera were investigated for their ability to encode useful CAZymes and other KEGG (Kyoto Encyclopedia of Genes and Genomes) enzymes and to resist antibiotic resistance genes (ARGs) in the soil. Abundance of these genes was higher in rhizospheric microbiome than in that of bulk soil. Detected viral families include Siphoviridae, Myoviridae, Podoviridae and Potyviridae with bacteriophages mainly associated with bacterial genera Pseudomonas, Streptomyces and Mycobacterium. Viral CAZymes in this soil mainly belong to glycoside hydrolase (GH) families GH43 and GH23. Some of these CAZymes participate in KEGG pathway “Amino sugar and nucleotide sugar metabolism” with actions included debranching and degradation of hemicellulose as well as biosynthesizing biopolymer of the bacterial cell wall and the layered cell wall structure of peptidoglycan. Other CAZymes promote plant physiological activities such as cell-cell recognition, embryogenesis and programmed cell death (PCD). Other viral KEGG enzymes participate in KEGG pathways “Glyoxylate and dicarboxylate metabolism”, “Terpenoid backbone biosynthesis”, “Protein export”, “Mismatch repair”, “Purine metabolism” and “Pyrimidine metabolism”. Enzymes of these pathways help reduce the level of soil H2O2 and participate in the biosynthesis of glycine, malate, isoprenoids, as well as isoprene that protects plant from heat stress. Other enzymes act in promoting both the permeability of bacterial peroxisome membrane and carbon fixation in plants. They also participate in balanced supply of dNTPs, successful DNA replication and mismatch repair during bacterial cell division. They also catalyze the release of signal peptides from bacterial membrane prolipoproteins. Phages with the most highly abundant antibiotic resistance genes (ARGs) transduce bacterial genera Pseudomonas, Streptomyces and Mycobacterium. Abundant mechanisms of antibiotic resistance in the rhizosphere include “antibiotic efflux pump” for ARGs soxR, OleC and MuxB, “antibiotic target alteration” for parY mutant, and “antibiotic inactivation” for arr-1. These ARGs can act synergistically to inhibit several antibiotics including tetracycline, penam, cephalosporin, rifamycins, aminocoumarin and oleandomycin. The study investigated the possible occurrence of horizontal transfer of ARGs to clinical isolates and human gut microbiome.

Keywords: CAZyme, KEGG, ARG, HGT, cell membrane, antibiotics

P138: The Microbiome of Suaeda monoica and Dipterygium glaucum From Southern Corniche (Saudi Arabia) Reveals Different Recruitment Patterns of Bacteria and Archaea

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ABSTRACT

Soil and plant interact differently in response to the same stress (e.g., salinity) and recruit certain bacteria. The southern corniche (Saudi Arabia) has limited plant growth, which could be due to the high temperature and salinity. The study aimed to determine the soil microbiome of selected plants and the interactions between soil and these plants. Suaedan monoica and Dipterygium glaucum soil samples were collected from the crust (surface) and rhizosphere, while soil with no plant growth from the nearby area was used as control. High-throughput hypervariable V3–V4 region of the 16S rRNA gene was used to evaluate the shifts in soil microbiome due to growth of plant growth. The analysis detected up to 16% archaeal strains in S. monoica-associated samples, while D. glaucum and control samples contained 100% bacterial strains. The top 10 phyla composition of the soil samples were Proteobacteria, Actinobacteria, Firmicutes, Gemmatimonadota, Bacteroidota, Halobacterota, Cyanobacteria, Cloroflexi, Planctomycetota, and Myxococcota. The V3–V4 region analysis successfully clustered the 5 samples into 3 clusters (control, D. glaucum, and S.

monoica) at higher-order classification but not at the species level due to unidentified bacteria. The main differences between soil samples were due to halophyte S. monoica samples containing high amounts of halophilic archaea and halophilic bacteria. This showed that selected plants interacted differently with the soil. EC- and KO-based analyses of functional genes and pathways showed that 5 pathways were specific to control, 11 pathways were observed only in D. glaucum samples, 12 pathways were expressed in S. monoica samples only, and 9 pathways were common in all samples. The study also detected numerous relatively novel genera in high abundance such as Aliifodinibius, Pontibacter, and Lacunisphaera. This showed that the soil in the sampling area is not well explored and that novel species could be isolated from the soil samples and used for future research.

P139: Tomato Leaf Curl Palampur Virus: A Tomato Infecting Bipartite Begomovirus Detected from Papaya And Wild Melon In Oman

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ABSTRACT

Tomato leaf curl Palampur virus (ToLCPlV) is a major threat to tomato and other vegetable crops in South Asia (India and Pakistan) and in Iran. Moreover, weeds plants also serve as a reservoir of Begomoviruses. In the ongoing study, wild melon (Cucumis melo) and papaya (Carica papaya) plants showing leaf curling and color breaking symptoms and severe symptoms of leaf curling, vein thickening, downward leaf cupping and stunted growth, respectively were collected and used in for Begomovirus amplification. Cloning, sequencing and bioinformatics analysis revealed the association of a bipartite begomovirus isolates with the diseased C. melo and C. papaya hosts. The complete genome of DNA-A of a bipartite Begomovirus isolate exhibited maximum (> 99%) nucleotide similarity with DNA-A of tomato leaf curl Palampur virus (ToLCPalV) reported from Iran ([IR: Jir8:T58P:08] FJ660431). Further pairwise identity derived implemented in sequence demarcation tool identified that the DNA-B showed highest (> 98%) sequence identity to the corresponding DNA-B of ToLCPalV ([IR: Jir-T65X:08] JF501720). The phylogenetic dendrogram of DNA-A and DNA-B genome components grouped respectively with ToLCPalV DNA-A and DNA-B of Iran isolates and far from Pakistan and India clade. This study provides the first identification of a bipartite Begomovirus ToLCPalV from C. melo and C. papaya in Oman and indicates the requirement for more investigation of ToLCPalV, as ToLCPalV is a major threat particularly to tomato crops in India and Pakistan and recently introduced in Iran.

Keywords: Bipartite begomovirus, diversity, whitefly, C. papaya, C. melo

P140: Use of Root Endophytic Enterobacter SA187 To Improve Abiotic Stress Tolerance of Tomato Grown Under Greenhouse Conditions

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ABSTRACT

Root-associated bacteria form complex co-associations with their host plant, and may play a critical role in alleviating salinity stress and promoting plant growth. They accumulate osmolytes and antioxidant enzymes for maintaining cell viability and replication under high saline conditions. In a previous work, the root endophyte Enterobacter sp. SA187 was reported to induce thermotolerance in wheat in the laboratory as well as in open-field agriculture. In this study we will investigate the impact of the endophyte Enterobacter sp. SA187 colonization on the growth of tomato seedlings grown in greenhouse under normal and abiotic stress conditions (salinity, drought, and heat). Several plant growth parameters, such as fresh and dry mass of the plant, lateral roots density, total chlorophyll content, Na+ and K+ ions contents, and antioxidant enzymatic activities such as CAT, SOD, POD will be monitored. Comparison between inoculated and non-inoculated tomato seedlings challenged with the different abiotic stresses will be performed to elucidate the role of this Enterobacter sp. in improving the growth parameters and protecting the plants from the negative aspects of the different applied abiotic stresses. To identify genes, pathways and biological processes involved in growth promotion and abiotic stress tolerance conferred by the endophyte Enterobacter sp. SA187, the root transcriptome will be analyzed by using RNAseq technology of colonized and non-colonized seedlings with salinity (200 mM NaCl), drought (withholding irrigation for 10 days), and heat (by exposing the seedlings to 42°C for 2h). Up-regulated candidate genes will be cloned and validated by qRT-PCR.

Keywords: Root Endophyte, Abiotic Stress

P141: Constructing a database of Endophytic bacteria by isolation in Prosopis cineraria and Zygophyllum dumosum

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ABSTRACT

Plants could serve as residence to a wide range of advantageous microbes. Endophytic bacteria live symbiotically with plants, enriching them in a variety of ways. The current study's goal is to create a database by isolating endophytic bacteria from Prosopis cineraria and Zygophyllum dumosum samples taken from various locations in Al-Ain, United Arab Emirates. Then, determine and evaluate the level of genetic diversity. Based on morphological and biochemical basis of endophyte characterisation, as well as the 16S rRNA sequencing technology. This research, however, is considered ongoing, and further data is being collected.

Keywords: Endophytic bacteria, Prosopis cineraria, Zygophyllum dumosum, 16S rRNA

P142: Plant Growth Promoting (PGP) Capabilities Assessment And Whole Genome Sequencing Of Mangrove Root Endophytic Bacteria Bacillus Wiedmannii E1 Strain

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ABSTRACT

Abiotic stresses, such as limited precipitation and high temperature, impose constraints on plant growth. However, certain flora, like mangroves, exhibit remarkable resilience in extreme environments, and plant growth-promoting (PGP) bacteria are pivotal in stress management. Our focus here is to delineate the PGP traits inherent to the endophytic bacteria, isolated from the root system of the Avicennia marina sp., a prevalent mangrove species thriving in the Umm Al Quwain region of the United Arab Emirates, using in-vitro analyses and comprehensive genome characterization. In the controlled laboratory assessments, the E1 strain showed remarkable growth under elevated salinity of up to 11% salt concentration. Furthermore, the bacterium demonstrated affirmative attributes of the production of siderophore, ammonia, and indole acetic acid (IAA) and displayed adeptness in phosphorous and potassium mobilization. Genomics analyses classified the bacterium as Bacillus wiedmannii strain, encompassing a substantial genome size of 51.3 megabases. We identified the occurrence of genes responsible for nitrogen fixation, exemplified by nifs, hcnC, fepC, and sirC and critical processes like hydrogen cyanide synthesis, siderophore transport, and iron-siderophore transport. The plant growth promotion potential of Bacillus Wiedmannii (E1 strain) was observed by inoculating the Cucumis sativus seeds. The treated Cucumis sativus crop, compared to the untreated group, showed higher germination rate, SPAD, and leaf area index, including higher averages in the number of leaves per plant, NDVi readings, and shoot height average over a period of 8 weeks under controlled shade house conditions. This study's findings imply PGP bacterial contribution towards mitigating stress for its host plant. Such insights stand poised to drive the development of stress-tolerant crops, representing a crucial stride towards the commercial and industrial utilization of these bacteria within the realm of sustainable agriculture.

Keywords: Bacillus Wiedmannii; Endophyte; Mangrove ecosystem; Plant growth promoting (PGP) bacteria; Sustainable agriculture

P143: Saline groundwater irrigation alters fungal community patterns and enhances drift-based assembly in root and soil compartments of Date palm (Phoenix dactylifera)

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ABSTRACT

Date palms (Phoneix dactylifera) are widely cultivated in arid agroecosystems, where knowledge of irrigation water source effect on below-ground fungal communities is limited. We studied soil and root-associated fungal (RAF) communities of date palms under different irrigation water sources (freshwater vs saline groundwater) across seven farms in UAE in using ITS2 metabarcoding. RAF diversity was lower and fungal communities were distinct between compartments which indicated root effect. Co-occurrence analysis showed a relatively complex and connective (average degree, clustering coefficient and density) as well as highly co-occurring RAF community compared to soil. The RAF and soil fungal communities were also distinct between irrigation water sources; wherein water pH and electrical conductivity (EC) were the major structure factors, while soil pH and EC chemistry were additional factors in soil. Drift (stochastic) was the dominant process in both root and soil under saline groundwater irrigation and its relative importance was higher in root than soil. Saline groundwater irrigation enriched the abundance of specific saprotrophic genera in root (Acrocalymma, Coprinopsis and Myrothecium) and soil (Chaetomium and Preussia) compartments. In addition, the abundance of saprotrophs was higher in root under saline groundwater irrigation, while opposite pattern was observed in soil. Taken together, we show that the RAF communities are complex and connective; saline groundwater irrigation distinctly alters fungal communities in root and soil, in which fungal communities mainly assemble through drift process and select specific saprotrophic fungi (i.e., Acrocalymma-root and Chaetomium-soil) useful for plant growth promotion and nutrient cycling under extreme conditions of saline agroecosystems.

Keywords: Arid agroecosystem; Date palm (Phoenix dactylifera); Desert environment; Fungal community; Irrigation source; Soil salinization

P144: The Impact of Utilising Machine-Processed Fruits and Vegetables Waste Fertilizer on the Growth of Cherry Belle Radish in the United Arab Emirates

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ABSTRACT

Food waste is increasingly recognized as a significant global issue, given its association with both global climate change and various diseases. The recycling of food waste in the United Arab Emirates encompasses several effective approaches. In order to enhance these methods, novel techniques have been employed to facilitate the conversion of fruits and vegetables waste generated at the United Arab Emirates University (UAEU) canteen into agricultural fertilizer. The objective of this study was to investigate the impact of fertilisers derived from fruit and vegetable waste on the growth of Cherry Belle Radish plants. The experimental method involved the testing of various concentrations (10%, 25%, and 50%) of fruit and vegetable waste, which were then compared to control samples, as well as samples treated with chemical fertilisers and vermicompost fertilisers. It is important to note that all other variables, including temperature, were kept constant across all plants. The experiment was conducted in the greenhouse of UAEU in April 2023. The source of the food waste used to produce the fertiliser was collected from the canteen of UAEU and processed using a thermochemical machine. The experimental results indicate that the tested fertilisers yielded similar outcomes to the control group, which consisted of chemical fertilisers and vermicompost. Conclusion: It is plausible to consider the utilization of fruit and vegetable fertilisers as a viable alternative to conventional chemical fertilisers, given their comparable efficacy to vermicompost fertilisers. This approach holds potential for enhancing waste recycling practices, particularly in the context of the United Arab Emirates' pursuit of environmentally sustainable land management and clean energy initiatives.

P145: Polycystic Ovary Syndrome and Endometrial Cancer: A Scoping Review of the Literature on Gut Microbiota

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ABSTRACT

Gut dysbiosis has been associated with polycystic ovary syndrome (PCOS) and endometrial cancer (EC) but no studies have investigated whether gut dysbiosis may explain the increased endometrial cancer risk in polycystic ovary syndrome. The aim of this scoping review is to evaluate the extent and nature of published studies on the gut microbiota in polycystic ovary syndrome and endometrial cancer and attempt to find any similarities between the composition of the microbiota. We searched for publications ranging from the years 2016 to 2022, due to the completion date of the 'Human Microbiome Project' in 2016. We obtained 200 articles by inputting keywords such as 'gut microbiome', 'gut microbiota', 'gut dysbiosis', 'PCOS', and 'endometrial cancer' into search engines such as PubMed and Scopus. Of the 200 identified in our initial search, we included 25 articles in our final review after applying the exclusion and inclusion criteria. Although the literature is growing in this field, we did not identify enough published studies to investigate whether gut dysbiosis may explain the increased EC risk in PCOS. Within the studies identified, we were unable to identify any consistent patterns of the microbiome similarly present in studies on women with PCOS compared with women with EC. Although we found that the phylum Firmicutes was similarly decreased in women with PCOS and studies on women with EC, there was however significant variability within the studies identified making it highly likely that this may have arisen by chance. Further research pertaining to molecular and microbiological mechanisms in relation to the gut microbiome is needed to elucidate a greater understanding of its contribution to the pathophysiology of endometrial cancer in patients with polycystic ovarian syndrome.

P146: Algicidal activity of a ubiquitous marine bacterium against the red tide species *Karenia brevis*

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ABSTRACT

Utilizing a biotic approach to regulate algal blooms, particularly through the implementation of algicidal bacteria during bloom termination phases, offers a viable ecological strategy to effectively control harmful algal blooms. This approach mimics natural ecological processes, leading to bloom termination, and holds promise for bloom control in an ecologically balanced manner. In this study, a ubiquitous bacterium, *Croceibacter atlanticus*, was isolated from blooms of the toxigenic dinoflagellate *Karenia brevis* in the Gulf of Mexico and has been shown to have antagonistic effects on the dinoflagellate growth in a laboratory setting. We show that the algicidal activity of *C. atlanticus* is cell-density dependent. Bacterial concentrations of 10^6 cells/mL caused strong inhibition of *K. brevis* while low concentrations of 10^4 and 10^5 cells/mL did not exhibit algicidal activity. This phenomenon could be linked to quorum-sensing mechanisms, a cell-to-cell communication mechanism often linked to coordinating bacterial behaviors by cell population density. The decline in growth was concomitant with a change in morphology of *K. brevis,* showing decreased size and loss of the characteristic dinoflagellate grooves with flagella. Comparative genomic analysis of *C. atlanticus* genomes indicated the gene for anthranilate synthase, an enzyme that is linked to quorum-sensing, is highly conserved. The absence of motility across all strains can also indicate quorum-sensing mechanisms for interactions amongst bacteria and the algae. Ongoing work is examining the molecular mechanisms of the bacterial algicidal activity on *K. brevis* via multi-omics that can be useful in controlling future blooms.

Keywords: algicidal bacteria, dinoflagellate, harmful algal blooms, bloom termination, quorum-sensing

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