Organiser

Malaysian Society for Microbiology

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International Islamic University Malaysia

ABSTRACT BOOK

The Malaysian Society for Microbiology Postgraduate Symposium 2022

MSMPS 2022

Microbes & Planetary Health: A Sustainable Affair

10 - 11th August 2022 | Virtual Symposium

Microbes & Planetary Health: A Sustainable Affair

INTERNATIONAL ISLAMIC UNIVERSITY MALAYSIA

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FOREWORD
President, Malaysian Society for Microbiology

Assalamualaikum w.b.t and Greetings to all,

On behalf of the society, it is my pleasure to welcome all of you to the MSM Postgraduate Symposium 2022 (MSMPS2022). The society has always strived to provide avenues for nurturing an inclusive and resilient science landscape in the country, and the MSMPS is a designated platform for dissemination of knowledge aimed at promoting science amongst our postgraduates and the younger scientific fraternity.

This year, the symposia operates under the theme "Microbes and Planetary Health: A Sustainable Affair". The role of microbial communities, or microbiomes towards balancing a myriad of ecosystems have recently taken centre stage in many scientific discourses. Thriving microbiomes are crucial for sustainable environmental health and flourishing ecosystems. Research has demonstrated that crop yield and growth are transcendent of healthy soil microbiomes; water microbiome systems become harbors of a vast range of marine species and corals; and a thriving gut microbiota leads to robust immune systems and overall good health in animals. The role of microbes and the science of microbiology remains classically relevant, and its importance to planetary health is more relevant against the dynamic backdrop of the world we live in today. Through MSMPS2022, we hope this message will be reflected in the many wonderful presentations by the future of science – our postgraduates.

This year the symposium is organized once again via online conventions, an initiative the MSM hopes would be able to provide opportunities for interaction that bridge our postgraduate researchers together within conducive grounds to communicate their work to colleagues, academics and interested parties from various universities nationwide. This year, the symposium provides ample microbiological discourse through presentations in the fields of General Microbiology, Food Microbiology, Environmental Microbiology, Industrial Microbiology, Medical Microbiology, Agricultural Microbiology, and Microbial Omics.

I would like to record my utmost appreciation to the Kuliyyah of Science, International Islamic University (UIA) as our gracious Co-Organizers for MSMPS2022. The organization of this symposia is a consequent reflection of the wonderful collegial and collaborative efforts from the committee members and showcases the strength as well as focus of the research being carried out by our postgraduates nationally. I would also like to extend my heartfelt acknowledgements to the Guests of Honor, Keynote and Plenary speakers, sponsors, and seminar participants for making this event a success.

Thank you once again for your involvement in the MSMPS2022 and we look forward to your active participation and support in future events under the banner of the Malaysian Society for Microbiology.

I wish you all a satisfying and fulfilling scientific interaction.

Mas Jaffri Masarudin

FOREWORD
Organizing Chair, MSMPS2022

Assalammualaikum warahmatullahi wabarakatuh and Greetings!

On behalf of the committee, I would like to extend a warm welcome to all participants to the Malaysian Society for Microbiology Postgraduate Symposium 2022 (MSMPS2022). It is our hope that this two-days virtual symposium will serve as an avenue for aspiring research students to exchange knowledge in the field of microbiology as well as opportunity to make new acquaintances.

The COVID-19 pandemic has evidently affected the life of many of us. The challenges also inspire us, to adapt and innovate while doing microbiology research. During pandemic too, we realised the vital relationship of microorganism with different dimensions of sustainability. The effort to create an environmentally sustainable future might be at stake if we underestimate the importance of understanding microorganisms and their significant role in balancing the earth biosphere. Wherever there is life there are microbes! Therefore, the theme for our symposium this year is, “Microbes and Planetary Health: A Sustainable Affair”.

I am honoured that International Islamic University Malaysia has been invited by Malaysian Society for Microbiology to co-organise MSMPS this year. I would like to express my sincere gratitude and appreciation to the Kulliyyah of Science, Kulliyyah of Allied Health Sciences and Kulliyyah of Dentistry, International Islamic University Malaysia (Kuantan Campus) for the support in organising MSMPS2022. The organising committee has continuously shown their dedicated commitment and enormous efforts to ensure that the symposium will be a success.

My utmost gratitude also to our guests of honour, keynote speaker, plenary speakers, sponsors and all participants of the MSMPS2022 for their contributions and immense support.
Thank you for joining us, and I wish you a very pleasant and rewarding 2-days interactive virtual meet!

Assoc. Prof. Ts. Dr. Suhaila Mohd Omar

Organizing Committee

Malaysian Society for Microbiology Postgraduate Symposium 2022

(MSMPS2022)

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Programme MSMPS2022

10-11 August 2022

International Islamic University Malaysia
(ZOOM)

DATE	**10 August 2022**
TIME	**Agenda**
8.30 – 9.00	Log into ZOOM https://iium.zoom.us/j/94444842841?pwd=LzVpMVhucXdDMVJETUhBNDZqYVN3dz09
9.00 – 9.05	Doa recitation by Br Mohamad Azimi Shaharudin and Negaraku anthem
9.05 – 9.15	**OPENING CEREMONY**: Welcome speech by MSM President, Assoc. Prof. Dr. Mas Jaffri Masarudin **MC**: Dr. Widya Abdul Wahab
9.15 – 9.30	**OFFICIATING CEREMONY**: Officiating speech by Prof. Dr. Azmi Md Noor, Campus Director, International Islamic University Malaysia, Kuantan.
9.30 – 10.30	**KEYNOTE**: **Prof. Emerita Datuk Dr. Asma Ismail** *Impact of microbes and planetary health in transforming the research landscape post COVID era*
10.30 – 10.35	Group photo on ZOOM
10.35 – 10.45	**BREAK**
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11.00 – 11.15	**ORAL02 Antimicrobial activities of culturable fungal endophytes from *Cymbidium* and *Dendrobium* orchids.** Chua Ru Wei, Monash University Malaysia
11.15 – 11.30	**ORAL03 Microbial community and functional characteristic of leachate from Jeram and Jabor landfill using metagenomics approach.** Siti Marhamah Drahaman, International Islamic University Malaysia
11.30 – 11.45	**ORAL04 Community structure of phenol-degrading bacteria enriched from palm oil mill effluent.** Izzati Sabri, Universiti Putra Malaysia

11.45 – 12.00	**ORAL05 Enzybiotic from *Pseudomonas otitidis* phage isolated from infected tilapia as potential antimicrobials.** Tee An Nie, Universiti Putra Malaysia
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2.00 – 2.15	**ORAL06 The expression of virulence genes in Group B *Streptococcus i*solated from symptomatic pregnant women with term and preterm delivery.** Ayesha Bahez, International Islamic University Malaysia
2.15 – 2.30	**ORAL07 Potential Effects of bacteriocin against cariogenic oral pathogens.** Malathi Ganeson, Universiti Kebangsaan Malaysia
2.30 – 2.45	**ORAL08 Dynamic of mixed genotype HCV infection in plasma and peripheral blood mononuclear cells of chronic Hepatitis C hemodialysis patients.** Siti Nurul Fazlin Abdul Rahman, International Islamic University Malaysia
2.45 – 3.00	**ORAL09 Diversity of acetyltransferase-type toxin-antitoxin loci in *Klebsiella pneumoniae*** Ying-Xian Goh, Shanghai Jiao Tong University
3.00 – 3.15	**ORAL10 *Streptococcus gallolyticus* infection: a neglected marker for colorectal cancer?** Che Muhammad Khairul Hisyam Ismail, International Islamic University Malaysia
3.15 – 3.30	**ORAL11 Antibacterial evaluation of dimeric sesquiterpene compound from basidiomycetes strain FRIM550 in vivo in a MRSA skin infection mouse model.** Vimalah Vallavan, Universiti Kebangsaan Malaysia
3.30 – 3.45	**ORAL12 Thermostability improvement of *Glomerella cingulata* cutinase via iterative site-saturation mutagenesis (ISM) on *cut*1 gene** Wan Norhidayah Wan Hanapi, Universiti Kebangsaan Malaysia
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4.00 – 4.05	**POS02 Epidemiology of extrapulmonary tuberculosis in a tertiary teaching hospital from year 2016-2021:** **A retrospective study**

	Liow Yii Ling, Universiti Malaya
4.05 – 4.10	**POS03 Distribution of staphylococcal enterotoxins among clinical isolates of methicillin-susceptible *Staphylococcus aureus* (MSSA) from Terengganu, Malaysia** Ainal Mardziah Che Hamzah, Universiti Sultan Zainal Abidin
4.10 – 4.15	**POS04 Agarose gel electrophoresis as a classical method to confirm recombinant vector sizes: Towards an amplification of ABA392 Haemorrhagic septicaemia (HS) vaccines B:2** Nur Nazirah Md Nasir, Universiti Malaya
4.15 – 4.20	**POS05 The antibiotic and biocide susceptibility profile of *Acinetobacter baumannii* clinical isolates from Terengganu –** Nurul Saidah Din, Universiti Sultan Zainal Abidin
4.20 – 4.25	**POS06 Vaccines as Sustainable Approach to Infectious Diseases: EPS-MH Adjuvanted Vaccine Against Mannheimiosis** Ghaith Hussein Mansour, Universiti Malaysia Terengganu
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10.55 – 11.00	**POS08 Genome analysis of clinical *Acinetobacter soli* isolates from Terengganu** Farahiyah binti Mohd Rani, Universiti Sultan Zainal Abidin
11.00 – 11.05	**POS09 Effect of domain manipulation in the Staphylococcal Phage 88 endolysin** Melvina Krishnan, Universiti Putra Malaysia
11.05 – 11.10	**POS10 Air-liquid biofilm formation: A potential virulence factor in**

	clinical carbapenem-resistant *Acinetobacter baumannii.* Ng Heng Kang, Universiti Malaya
11.10 – 11.15	**POS11 Antimicrobial activity produce from *Paenibacillus polymyxa* KP10 against Methicillin Resistant *Staphylococcus aureus.*** Farah Syahrain Roslan, Universiti Putra Malaysia
11.15 – 11.20	**POS12 Extraction of *Senna alata* (l.) roxb leaves using soxhlet, maceration and subcritical fluid method and antibacterial activities against *Staphylococcus aureus* and *Staphylococcus epidermidis.*** Nadirah Abd Rahim, International Islamic University Malaysia
11.20 – 11.25	**POS13 In vitro wound healing activity of Sidr and Manuka honey on skin dermal fibroblast cells.** Asma Mohammed Al-Sayaghi, University of Cyberjaya
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2.55 – 3.00	**POS15 Actinomycetes from bris soil: Investigation of potential candidate as new drug leads**. Amirah Ahmad, Universiti Pendidikan Sultan Idris
3.00 – 3.05	**POS16 Isolation and characterization of beneficial endophytic bacteria from *Oryza Sativa* cultivated in acid sulfate soil** Nor Adilah A.Rani, International Islamic University Malaysia
3.05 – 3.10	**POS17 Microalgae from Antarctic Soil.** Nor Syafawati Mohamad Pauzi, International Islamic University Malaysia
3.10 – 3.15	**POS18 Characterization of heavy metal tolerance Rhizobacteria and its potential in bioremediation.** Emyrah Ilya Maisarah Azamuddin, International Islamic University Malaysia
3.15 – 3.20	**POS19 Analysis of microbial community composition found in Malaysian bris soil.** Hamizah Hazmeen Hairi, Universiti Pendidikan Sultan Idris

3.20 – 3.45	**BREAK**
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P1	**Environmental change and microbes** Assoc. Prof. Dr Lee Choon Weng
P2	**Using 'omics' to shed light on the role of microorganisms in the environment** Prof. Dr Evelyn Doyle
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ORAL02	**Antimicrobial Activities of Culturable Fungal Endophytes from Cymbidium and Dendrobium Orchids** Ru Wei Chua, Keang Peng Song, Adeline Su Yien Ting
ORAL03	**Microbial Community and Functional Characteristic of Leachate from Jeram and Jabor Landfill Using Metagenomics Approach** Siti Marhamah Drahaman, Noor Faizul Hadry Nordin, Hamzah Mohd. Salleh, Husna Ahmad Tajuddin
ORAL04	**Community Structure of Phenol-degrading Bacteria Enriched from Palm Oil Mill Effluent.** Izzati Sabri, Norhayati Ramli, Mohd Zulkhairi Mohd Yusoff, Nor Azlan Nor Muhammad, Ho Li Sim
ORAL05	**Enzybiotic from *Pseudomonas otitidis* Phage Isolated from Infected Tilapia as Potential Antimicrobials.** Tee An Nie, Chong Chou Min, Shaufi bin Mohd Asrore, Khatijah binti Mohd Yusoff and Adelene Song Ai Lian
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ORAL07	**Potential Effects of Bacteriocin Against Cariogenic Oral Pathogens.** Malathi, G, Zaleha, S, Zamirah, ZA, Noraziah, MZ, Mazlina, MS.
ORAL08	**Dynamic of Mixed Genotype HCV Infection in Plasma and Peripheral Blood Mononuclear Cells of Chronic Hepatitis C Haemodialysis Patients.** Siti Nurul Fazlin Abdul Rahman, Hairul Aini Hamzah, Mohammed Imad A. Mustafa Mahmud.
ORAL09	**Diversity of Acetyltransferase-type Toxin-antitoxin Loci in Klebsiella pneumoniae.** Ying-Xian Goh, Peifei Li, and Hong-Yu Ou.

ORAL10	**Streptococcus gallolyticus infection: a neglected marker for colorectal cancer?** Che Muhammad Khairul Hisyam Bin Ismail, Edre Bin Mohammad Aidid, Hairul Aini Binti Hamzah, Mohd Shaiful Ehsan Bin Shalihin, Azmi Bin Md Nor
ORAL11	**Antibacterial Evaluation of Dimeric Sesquiterpene Compound from Basidiomycetes Strain FRIM550 In Vivo in a MRSA Skin Infection Mouse Model.** Vimalah, V., Getha, K., Zin, N. M., Abdul-Latif, M., Azahar, M. S., Syed Abdul-Rahman, S. N.
ORAL12	**Thermostability improvement of Glomerella cingulata cutinase via iterative site-saturation mutagenesis (ISM) on cut1 gene** Wan Nurhidayah Wan Hanapi, Iuan-Sheau Chin, Nor Muhammad Mahadi, Abdul Munir Abdul Murad & Farah Diba Abu Bakar
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POS06	**Vaccines as Sustainable Approach to Infectious Diseases: EPS-MH Adjuvanted Vaccine Against Mannheimiosis** Ghaith Hussein Mansour, Mohd Effendy, Laith Abdul Razzak
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POS12	**Extraction of *Senna alata* (l.) roxb leaves using soxhlet, maceration and subcritical fluid method and antibacterial activities against *Staphylococcus aureus* and *Staphylococcus epidermidis*.** Nadirah Abd Rahim, Sahena Ferdosh, and Nur Sabrina binti Ahmad Azmi
POS13	**In Vitro Antibacterial and Wound Healing Activity of Sidr and Manuka Honey on Skin Dermal Fibroblast Cells.** Asma Mohammed Al-Sayaghi, Abdelkodose Mohammed Al-Kabsi, and Mohammed Abdullah Alshawsh
POS14	**Characterization of Indazoles and Thiazoles as anti-amoebic agents.** Thevashree Rajanderan
POS15	**Actinomycetes from bris soil: Investigation of potential candidate as new drug leads**. 'Amirah Ahmad1 , Hamidah Idris, Hamizah Hazmeen Hairi, Muhammad Adib Zakwan Azman, Noraziah Mohamad Zin, Muhd Danish Daniel Bin Abdullah
POS16	**Isolation and characterization of beneficial endophytic bacteria from *Oryza Sativa* cultivated in acid sulfate soil** Nor Adilah binti A. Rani, Md Hoirul Azri bin Ponari, and Muhd Fahmi bin Yunus
POS17	**Microalgae from Antarctic Soil.** N. S. Mohamad Pauzi, Z.A. Zainal Abidin, Z. Zainuddin, A.J.K. Chowdhury
POS18	**Characterization of heavy metal tolerance Rhizobacteria and its potential in bioremediation.** Emyrah Ilya Maisarah Binti Azamuddin, Md Hoirul Azri bin Ponari, Ahmad Zaim Fahmi Bin Abdullah, Che Nurul Aini Binti Che Amri, and Mohd Fauzihan Bin Karim
POS19	**Analysis of microbial community composition found in Malaysian bris soil.** Hamizah Hairi, Hamidah Idris, Amirah Ahmad, Adib Zakwan, Noraziah Mohamad Zin, Muhd Danish Daniel Abdullah

KEYNOTE

IMPACT OF MICROBES AND PLANETARY HEALTH IN TRANSFORMING THE RESEARCH LANDSCAPE POST COVID ERA

Prof Emerita Datuk Dr Asma Ismail
President, Academy of Sciences Malaysia and
Ibn Sina Chair for Medicine
International Islamic University Malaysia
Kuantan Campus, Pahang

Our humanity and planet are under threat based on our own actions. Urgent action, taken together, is needed to change course and reimagine our futures. Planetary health is based on the understanding that human health and human civilisation depend on flourishing natural systems and the wise stewardship of those natural systems. Planetary health is the balance between human, animal and the environment. Unfortunately, since economic advancement takes precedence over societal and environmental spheres, our natural systems are being degraded to an extent unprecedented in human history. This has resulted in the COVID 19 pandemic that has hugely affected our lives and livelihood. Covid 19 has shown that Zoonotic diseases are becoming riskier to humans based on encroachment of wildlife habitats and encroachment of land for food security. The pandemic has also revealed the stark weaknesses in almost every health care system. Within and between countries we have witnessed how already vulnerable and marginalized populations bear disproportionate burden of infection and issues due to the pandemic including mental health. Our effect on climate change, encroachment on wildlife habitats via environmental degradation and the borderless global travel help to circulate the animal-borne diseases. Combined with urbanization, over population, food security and the global trade, we basically have set the scene for more pandemics to come. Solutions to pandemics can no longer be siloed and treating it as a health agenda. We need to be concerned about the interplay of the bigger ecosystems called planetary health (with the balance between human, animal and environment) especially for countries in the tropics.

Covid 19 has highlighted the critical value of science in providing answers and solutions to the pandemic and for a fast economic recovery plan. To combat COVID 19 we see the need for sustained investment not only in global health research but also planetary health issues that comprises of human health, animal health, environmental degradation and climate change that are intricately combined. Lessons learned from COVID 19 showed that solutions-based research and innovations should be performed in a responsible manner. We need to move from desk-based research to research with impact. Performing responsible research should not be technology –centric but rather people centric, nature centric and values-centric**.** The ability to tackle issues and challenges in attaining collective societal response will be the tipping point for preventable measures of future pandemics. This paper will discuss how Covid 19 is influencing research trends globally and in Malaysia as stipulated in the 10-10 *My*STIE niche areas to ensure future pandemic preparedness and resilience.

PLENARY 1

ENVIRONMENTAL CHANGE AND MICROBES

Assoc. Prof. Dr. Lee Choon Weng
Laboratory of Microbial Ecology
Institute of Biological Sciences
Institute of Ocean and Earth Sciences
Universiti Malaya

A major problem facing us is the climate change brought about by increasing atmospheric CO_2. As oceans are a major sink of CO_2, it is pertinent to understand the main microbial processes that govern CO_2 flux i.e., respiration and photosynthesis. From our measurements of bacterial and primary production in the coastal waters of Peninsular Malaysia, we found evidence of possible net heterotrophy. Further investigation into bacterial respiration showed that this microbial process is governed by organic matter concentration, lability and temperature. Some coastal waters sites are a net source of CO_2. The effects of environmental change on other microbial components in the aquatic food web will also be discussed.

PLENARY 2

USING 'OMICS' TO SHED LIGHT ON THE ROLE OF MICROORGANISMS IN THE ENVIRONMENT

Prof. Dr Evelyn Doyle
School of Biology & Environmental Sciences
University College Dublin, Republic of Ireland

Microorganisms are key drivers of biogeochemical nutrient cycling and play an important role in environmental processes such as soil fertility, plant growth, greenhouse gas production and dissipation, pollutant transformation and wider ecosystem functioning. However, because less than 10% of microbes in environments such as soil can be cultured in the laboratory it was traditionally not possible to get a complete picture of microbial diversity (who is there?) and function (who is doing what?) in complex environments. The advent of molecular ecological techniques such as amplicon sequencing, metagenomics and metatranscriptomics has provided microbial ecologists with the means to examine microbial diversity and function in the environment. In this talk I will review the various 'omic methods used in microbial ecology and describe how our research group has used some of them to elucidate the microbes involved in pollutant degradation, to examine microbial dynamics in the rumen with a view to developing methods for the mitigation of methane from livestock and to unravel bacterial-fungal interactions in plant roots.

ORAL01

ISOLATON OF FUNGAL ENDOPHYTES ON DIFFERENT MEDIA FROM DIFFERENT LEAF STAGES

Nur A'fina binti Ahmad Mokhtar[1*], and Kamarul Zaman bin Zarkasi[1]

[1]School of Biological Sciences, Universiti Sains Malaysia, Penang

*****Corresponding author: finamokhtar93@gmail.com

Abstract: Endophytic fungi are one of the valuable sources of antimicrobial compounds. They live symbiotically with host plants and survive in the plant tissue. The multifaceted interaction between endophyte and host plant is what makes endophyte a unique source to search for new bioactive compounds with antibacterial activities. The more intriguing aspect of endophyte is the ability to produce similar compounds as the host plant which can be very beneficial for large scale use in broad potential areas. Therefore, this present study was conducted to isolate the fungal endophytes from *Ocimum basilicum* host plant. A total of 82 fungal endophytes were isolated on three different media compositions which are potato dextrose agar (PDA), potato dextrose agar supplemented with host plant powder (PDA + PP) and potato dextrose agar with host plant water extract (PDA + PWE). Endophytes were isolated from young, matured, old and senescent leave stages. Based on the study, endophytes were successfully isolated from all leave stages. Fungal endophytes densely colonized PDA with 40.18% of colonization percentage followed by PDA+PWE (35.27%) and PDA+PP (24.33%). Most of the fungal endophytes were recovered from old and senescent leave stages which are 35.30% and 34.14% respectively. There are 23.15% fungal endophytes isolated from matured leaves and only 7.20% isolated from young leaves. As a conclusion, healthy old leaves without any supplementation in the PDA media were the best leaf stage and culture medium to obtain more fungal endophytes.

Keywords: fungal endophytes, *Ocimum basilicum*, isolation, leaf stage

ORAL02

ANTIMICROBIAL ACTIVITIES OF CULTURABLE FUNGAL ENDOPHYTES FROM *Cymbidium* AND *Dendrobium* orchids

Ru Wei Chua, Keang Peng Song, Adeline Su Yien Ting*

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Abstract: Endophytic fungi are microorganisms that reside in the inner tissues of living plants without causing any harm or pathogenic infection to the host. These asymptomatic microbes are ubiquitous in nature and are better known as producers of bioactive compounds. In this study, fungal endophytes were harnessed from common orchids, *Cymbidium* and *Dendrobium* sp. in Malaysia, and their antimicrobial activities evaluated. Culturable endophytes were identified via molecular approaches then tested for their antibacterial and antifungal activities via the agar well diffusion assay and dual culture technique, respectively. Results revealed a total of 59 fungal endophytes were isolated, with *Fusarium spp.* being the most frequently isolated (62.7%). Seven of the isolates demonstrated strong antibacterial activities (5.33 ± 0.58 to 25 ± 0.00 mm) against the tested pathogenic bacteria (*Bacillus cereus, Staphylococcus aureus, Escherichia coli* and *Pseudomonas aeruginosa*). For antifungal activities, all of the endophytic isolates impeded the growth of at least one tested fungus albeit with varying efficacy (1.16 to 91.86% inhibition). Two endophytic isolates showed greater antimicrobial potential. *Fusarium incarnatum* (C4) resulted in significant zones of inhibition against *B. cereus* (21.00 ± 1.00 mm) and *S. aureus* (25.00 ± 0.00 mm). *Trichoderma asperellum* (D17) also produced the highest inhibition against *Ganoderma boninense* (91.86 ± 4.03%) and *Pythium ultimum* (87.6 ± 1.83%). This study highlights the potential of fungal endophytes from common orchids as a natural and sustainable source of novel bioactive compounds which may be exploited for medicinal, agricultural, and industrial applications.

Keywords: antibacterial, antifungal, bioactive compounds, endophytic fungi, orchids

ORAL03

MICROBIAL COMMUNITY AND FUNCTIONAL CHARACTERISTIC OF LEACHATE FROM JERAM AND JABOR LANDFILL USING METAGENOMIC APPROACH

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Abstract: The municipal landfill is an example of human-made environment that harbours some complex diversity of microorganism communities. To evaluate this complexity, the structures of bacterial communities in active landfills in Malaysia were analysed with culture independent 16S amplicon sequencing approaches. Several points of leachate samples were collected in Jeram and Jabor landfill sites. The DNA from the leachate sample was extracted and purified prior to sequence the 16S rRNA gene for statistical and bioinformatics analyses. As a result, bacterial OTUs sequenced for Jeram landfill was 265 and Jabor landfill was 273. The data from both landfills showed that the predominant phyla belonged to Firmicutes. On average, Bacteroidetes was the second highest phylum followed by Proteobacteria for Jabor landfill. While the phyla for communities in Jeram landfill were phyla from Proteobacteria and Actinobacteria. Diverse bacterial genera associated with various functions such as cellulolytic bacteria (e.g., *Taibaiella*) with a percentage abundance of 0.3% and hydrogen-reducing bacteria (e.g.,Anaerobic digester metagenome) with a percentage abundance of 0.375% were detected abundantly in the Jabor and Jeram landfill leachate respectively. In addition, the Shannon index which account for species diversity of Jabor leachate was lower than that of the Jeram leachate, and the Simpson index which refer to random selection of the sample was higher than that of the Jabor leachate with no significant different. Thus, both leachate sample shown diverse species with random selection has dominates the site. As such, the composition of bacterial communities suggests some variances between the bacterial communities found in Jabor and Jeram landfills. Based on PICRUSt2, 10 metabolism pathways belonging to KEGG pathway groups were predicted in all landfill leachate samples. Thus, this study provides an important insight into the composition and functional characteristics of the microbial communities in landfill leachate.

Keywords: Landfill leachate, metabolism pathway, microbial community, PICRUSt2 prediction, 16S amplicon sequencing.

ORAL04

COMMUNITY STRUCTURE OF PHENOL-DEGRADING BACTERIA ENRICHED FROM PALM OIL MILL EFFLUENT

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Abstract: Phenol is a priority pollutant due to its carcinogenicity, toxicity and solubility. Various strategies have been adopted to remove phenol, particularly physical, chemical and biological methods. Biological method is preferable due to its low cost and no generation of secondary pollutants. The palm oil mill effluent (POME) biotreatment system has been shown to successfully remove 91% of phenol. Hence, it is hypothesised that POME comprises of a complex phenol-degrading bacteria community that is beneficial in phenol biodegradation. However, the community structure of phenol-degrading bacteria and its potential degradation pathways is poorly understood. In this study, POME samples from anaerobic (AN) and algae (AG) ponds with high phenol degrading activity were selected and enriched with increasing initial phenol concentration (300-500 mg/L). The 16S rRNA gene for AN and AG was sequenced via amplicon sequencing on the Illumina MiSeq platform. The results revealed that AN and AG degrade 97% and 74% of 500 mg/L of phenol within 24 hours, respectively. Bioinformatics analysis of 16S rRNA amplicon sequencing via Quantitative Insights into Microbial Ecology 2 (QIIME2) unravel phenol degrading bacteria such as *Acinetobacter*, *Pseudomonas*, *Flavobacterium* and *Sphingobacterium* in the AN and AG mixed-culture. In addition, the Phylogenetic Investigation of Communities by Reconstruction of Unobserved States 2 (PICRUSt2) prediction revealed that AN and AG comprised of nine metabolic pathways involved in phenol degradation, suggesting that phenol-degrading consortia were successfully enriched from the original POME samples. The findings demonstrate that the enriched AN and AG mixed-culture could be potentially used in phenol bioremediation applications.

Keywords: bioinformatics, bioremediation, metagenomics, mixed culture, phenol

ORAL05

ENZYBIOTIC FROM *Pseudomonas otitidis* PHAGE ISOLATED FROM INFECTED TILAPIA AS POTENTIAL ANTIMICROBIALS

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Abstract: A new *Pseudomonas* species, *Pseudomonas otitidis* was first known as an otic infectious agent in human and its potential to cause serious hospital-acquired infections was highlighted recently. The rarity in detection and possible underestimation of the occurrence of this species, especially in the aquaculture field, are possibly accounted by the phenotypic similarity to *Pseudomonas aeruginosa*. *P. otitidis* isolated from an infected tilapia fish farm was characterized through whole genome sequencing and its antibiotic susceptibility profile was determined. This β-haemolytic *P. otitidis* strain was resistant to several β-lactam antibiotics due to the presence of an inherent metallo-β-lactamase gene (POM-1) found in all *P. otitidis* species. As an antibacterial approach, a bacteriophage targeting *P. otitidis* was also isolated and characterized. Due to the temperate nature of the bacteriophage isolated, its lytic enzyme, endolysin that can degrade the peptidoglycan in the bacterial cell wall was cloned and expressed in *E. coli* as a potential enzybiotic. The native endolysin (POE) was found to be active against *P. otitidis* only in the presence of ethylenediaminetetraacetic acid (EDTA), which functions to permeabilize the outer membrane that blocks access to the peptidoglycan. However, POE fused with its holin (Hol-POE), a phage transmembrane protein, showed successful lysis on both plate and broth reduction assays even without EDTA treatment, implying that the engineered endolysin could permeabilize the outer membrane and lyse *P. otitidis*. This study could lead to the development of enzybiotics against *P. otitidis* in the aquaculture or clinical setting.

Keywords: Bacteriophages, endolysin, enzybiotics, holin, *Pseudomonas otitidis*.

ORAL06

THE EXPRESSION OF VIRULENCE GENES IN GROUP B STREPTOCOCCUS ISOLATED FROM SYMPTOMATIC PREGNANT WOMEN WITH TERM AND PRETERM DELIVERY.

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Abstract: During pregnancy, group B streptococcus (GBS) colonization is one of the risk factors for preterm delivery and neonatal infections. Previous studies have revealed the crucial roles of GBS virulence factors including hemolytic pigment (CylE), hyaluronidase (HylB), serine rich protein (Srr) and bacterial surface adhesion of GBS (BsaB) in mediating GBS colonization and intrauterine ascending infection, that triggers preterm delivery. The aim of this study is to investigate the association between mRNA expression of virulence genes in GBS isolates obtained from symptomatic pregnant women and preterm delivery. GBS isolates were obtained from high vaginal swabs of pregnant women (n=40) with gestational age less than 37 weeks and symptoms including preterm labour, preterm premature rupture of membrane (pPROM), vaginal discharge and vaginal bleeding. RNA was extracted from these GBS isolates and RT-qPCR was performed to determine the relative mRNA expression of GBS virulence genes including *CylE, HylB, Srr* and *BsaB*. Women with preterm labour and pPROM who delivered prematurely were demonstrated with higher expression of *CylE* gene and a trend towards an increased expression of HylB gene, in comparison to women with term delivery. The expression of *Srr* and *BsaB* genes were both similar between symptomatic pregnant women who delivered at term and prematurely.These results suggest that following vaginal colonization, both *CylE* and *HylB* genes possibly contribute to intrauterine ascending infection and inflammation, causing preterm delivery in humans. These virulence factors may be targeted for the pre-clinical stages of vaccine development or therapeutic intervention.

ORAL07

POTENTIAL EFFECTS OF BACTERIOCIN AGAINST CARIOGENIC ORAL PATHOGENS

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Abstract: Probiotics are live microorganisms that confer a health benefit on the host when administered in sufficient amounts and can modify oral microbiotas. It is extensively studied in the scope of prevention and treatment of oral diseases including dental caries and periodontal diseases. Meanwhile, bacteriocins are ribosomal-synthesized peptides produced by probiotics that indicate antibacterial activities against microorganisms closely related to bacteria. Bacteriocin-producing microorganisms are open fields for the development of recombinant bacteriocin with antimicrobial peptides that offer a promising strategy against pathogens with increasing resistance to antibiotics and bacteriocin currently. Some studies on probiotics from natural sources have been conducted, but the available data are scarce. This review is aimed to investigate studies on the potential antibiotic effects of bacteriocins against cariogenic pathogens, current treatment, and their prospects and focuses on investigating bacteriocins' applications in the medical and dental industries particularly in promoting oral health benefits through commercial oral care products. Electronic database searches in Scopus, PubMed, Google scholar, Proquest and WOS with the keywords "bacteriocin AND probiotic AND caries AND antimicrobial activity" were conducted. A total of 589 articles were screened which include studies on probiotics and bacteriocins (72 articles), the antimicrobial activity of bacteriocin against oral pathogens including *in vivo* or *in vitro* and genomics studies (56), the bacteriocin against cariogenic pathogen studies(31), the antimicrobial activity of bacteriocin against cariogenic pathogen studies(28) and review articles on bacteriocin applications (19). No clinical study was found on bacteriocin application.

Keywords: Antimicrobial activity, Bacteriocin, Dental caries, Probiotic.

ORAL08

DYNAMIC OF MIXED GENOTYPE HCV INFECTION IN PLASMA AND PERIPHERAL BLOOD MONONUCLEAR CELLS OF CHRONIC HEPATITS C HEMODIALYSIS PATIENTS

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Abstract: Hepatitis C virus (HCV) infection is common among dialysis patients. The virological diagnosis is the detection of viral RNA within plasma samples. It is however reported that HCV can be found in extra-hepatic sites like peripheral blood mononuclear cells (PBMCs). Multiple HCV genotype (mixed genotype) may occur from these dual detection on the same individuals which can directly affects the outcome of patients and disease severity. The aim is to investigate the presence of mixed genotype HCV infection in dialysis setting after dual detection of viral RNA in both plasma and PBMCs sample. Ten blood samples of dialysis patients with chronic hepatitis C were processed using Ficoll-gradient centrifugation method. HCV RNA was extracted and subjected to RT-PCR assay using primers targeted 5'UTR and NS5B regions. Sequencing assay was used to obtain their nucleotide sequences. Bioedit and Mega 6x4 software were used for sequence alignment and constructing phylogenetic tree, respectively. Mixed genotype HCV infection were found in 5 out of 10 samples. A combination of HCV genotype 1a and 3a was the main mixed-genotype found in this study. However, there was one sample with the combination of HCV genotype 1a, 3a and 6. This may resulted from repeated exposure to HCV. Meanwhile, five out of 10 samples demonstrated mono HCV genotype in all assays with four of them were infected with genotype 3a and one was infected with genotype 1a. In summary, having dual detection on both of these samples demonstrated the presence of mixed genotype HCV infection in dialysis setting.

Keywords: Hepatitis C, HCV genotypes, Mixed-genotype, PBMC

ORAL09

DIVERSITY OF ACETYLTRANSFERASE-TYPE TOXIN-ANTITOXIN LOCI IN *KLEBSIELLA PNEUMONIAE*

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Abstract: Type II toxin-antitoxin (TA) systems play a crucial role in regulating bacterial physiology, while *Klebsiella pneumoniae* is a multidrug-resistant pathogen that causes a wide range of recalcitrant infections. A previous study has shown that overexpression of KacT, an acetyltransferase-type toxin, inhibits cell growth and enhances antibiotic tolerance in *K. pneumoniae*. KacT, a Gcn5-related N-acetyltransferase (GNAT) toxin, usually pairs up with KacA, a ribbon-helix-helix (RHH) antitoxin, forming a typical type II GNAT-RHH TA module. This study investigates the distribution of GNAT-RHH TA loci in 3,013 completely sequenced *K. pneumoniae* genome available in NCBI RefSeq using TAfinder. The KacT toxins can be phylogenetically classified into four distinct clades (KacT1-4) and the *kacAT* TA loci of different clades coexist in a strain. Although the BLASTp identities across KacT1-4 are low, all KacT1-4 inhibit bacterial growth when being overproduced, and their toxicities are neutralized by cognate antitoxins in a *K. pneumoniae* model. Using PCR, we also proved that all *kacAT1-4* TA loci are transcripted in a bicistronic fashion. All these evidences confirmed that KacAT1-4 are classical type II TA systems. Furthermore, using different plasmid combination, we mixed the plasmids containing cognate and noncognate TA to study potential cross-interactions between TA pairs. Interestingly, a cross-interaction between chromosomal and plasmid-borne GNAT-RHH TA pairs was observed, where a chromosomal KacT2 can be neutralized by KacA2 (its cognate RHH antitoxin) and KacA3 (a non-cognate RHH antitoxin found on plasmid). This phenomenon suggests that TA module might involves in a more extensive cellular regulatory network.

Keywords: acetyltransferase, GNAT-RHH, toxin-antitoxin system, *Klebsiella pneumoniae*

ORAL10

Streptococcus gallolyticus INFECTION: A NEGLECTED MARKER FOR COLORECTAL CANCER?

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Colorectal cancer (CRC) is the second leading cancer in Malaysia with mostly detected at later stage, III and IV due to lack of awareness of CRC symptoms and signs. CRC is a multifactorial, however the clinical association of *Streptococcus gallolyticus* (*S. gallolyticus*) infection with the development of colorectal cancer were reported. Thus, a case-control study was conducted to identify the correlation and predictors of *S. gallolyticus* infection towards CRC among patients attending Sultan Ahmad Shah Medical Centre@IIUM. A total of 33 stool sample from patient diagnosed with CRC and 80 stool sample from patient without CRC attending Sultan Ahmad Shah Medical Centre@IIUM were collected and proceeded with iFOBT test and PCR assay for detection of *S. gallolyticus*.. In this study, the proportion of *S. gallolyticus* infection was higher among CRC patients (48.5%) as compared to the control group (20%). The Pearson's, χ^2 or Fisher's exact analysis shows that the presence of occult blood in stool, *S. gallolyticus* infection, and family history were significantly associated with the development of CRC (p-value < 0.05). The best multivariate logistic regression model showed that positive stool PCR for *S. gallolyticus* had the lowest relative standard error (RSE) and almost 5 times the odds to develop CRC after controlling other factors (adjusted odds ratio= 4.7, 95% confidence interval= 1.7 – 12.6, RSE = 59.6%). This finding suggested that the *S. gallolyticus* infection was the strongest predictor towards development of CRC and potentially be used as a predictive marker for early detection of disease progression.

Keywords: Case study, Colorectal cancer, Predictors, *S. gallolyticus*, Stool PCR.

ORAL11

ANTIBACTERIAL EVALUATION OF DIMERIC SESQUITERPENE COMPOUND FROM BASIDIOMYCETES STRAIN FRIM550 *IN VIVO* IN A MRSA SKIN INFECTION MOUSE MODEL

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Abstract: Methicillin-resistant *Staphylococcus aureus* (MRSA) is recognised as one of the major pathogens associated with the development of antimicrobial resistance (AMR). A dimeric sesquiterpene (DS) compound isolated from a wild basidiomycetes species, strain FRIM550, has proven strong *in vitro* activity against Gram positive bacteria. The objective of this study was to evaluate the *in vivo* efficacy of DS to be used topically for treating MRSA wound infections. Punch biopsy wound model in female Balb/C mice infected with MRSA ATCC 33591 and kept in individually-ventilated cages, was used to test the efficacy of DS at concentrations of 0.5%, 1% and 2% (w/v). Compound DS at 2% concentration just needed two days of treatment, while 0.5% and 1% DS required five days of treatment to show effective reduction in MRSA colonisation in wounds (zero colony forming units, CFU/mL) with complete wound healing in mice. Colony counts of MRSA showed that the 0.5%, 1.0%, 2.0% DS-treated and mupirocin-treated groups exhibited significant difference ($p<0.005$) compared to the untreated MRSA-infected group in one-way ANOVA analysis. In histology study, less inflammatory cells were observed in the treated groups compared to non-treated group. The wound size significantly reduced after 7 days of treatment in the DS-treated groups at 85.5%, 82.1% and 79.7% reduction for 0.5% DS, 1.0% DS and 2.0% DS, respectively. The compound exhibited better healing potential in MRSA-infected wounds compared to the mupirocin-treated group which showed 43.2% reduction in wound size. Studies are needed to explore further the therapeutic values of DS as an anti-MRSA agent for topical application.

Keywords: Basidiomycetes; *in-vivo* wound infection model; anti-MRSA

ORAL12

THERMOSTABILITY IMPROVEMENT OF *Glomerella cingulata* CUTINASE VIA ITERATIVE SITE-SATURATION MUTAGENESIS (ISM) ON *cut*1 GENE

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Abstract: Thermostability is one of the key features in various industries demanding for stable enzymes capable of withstanding harsh conditions in certain bioprocesses. Naturally-occurring enzymes are susceptible to denaturation in non-natural catalyses involving high temperatures. Cutinase is an important biocatalyst in industries pertaining to hydrolysis of soluble esters and emulsified triacylglycerols. The aim of this research is to enhance the thermostability of the *Glomerella cingulata* cutinase via the iterative site-saturation mutagenesis (ISM) approach. It is postulated that increasing the rigidity of certain amino acids in an enzyme increases its thermostability. Thus, certain amino acids at positions of high mobility identified by B-factor values derived from the *G. cingulata* cutinase three-dimensional structure were targeted in this mutagenesis approach. Megaprimer PCR was employed to introduce mutations at selected codons on the *cut*1 gene by randomisation using NNK degenerate primers. About 576 transformants were selected for screening of positive cutinase variants for each amino acid chosen. The screening of variants from the first round of saturation mutagenesis resulted in the selection of a single mutation cutinase variant T40E. The enzyme activity of T40E using crude extract was almost 4.83-fold higher as compared to the wild-type cutinase when exposed at 50°C for 2 h. The second round of mutagenesis using the T40E as template resulted in the selection of the cutinase variant T40E/N177G. Cutinase T40E/N177G was observed to be more thermostable with a 3.3-fold increase in activity as compared to the wild-type enzyme and about 1.94-fold higher than the single mutated cutinase variant T40E after an exposure to 60°C for 2 h. Therefore, this variant was selected for further enzyme characterisation. The substitution of amino acids at locations of high mobility/flexibility in the *G. cingulata* cutinase had increased the ability of this enzyme to withstand higher temperatures than its unmodified counterpart. This study provides valuable information regarding thermal stability of cutinases.

POS01

ANTIBIOTIC SUSCEPTIBILITY PROFILES OF CLINICAL ISOLATES OF *Klebsiella* spp. FROM HOSPITAL PENGAJAR UNIVERSITI PUTRA MALAYSIA (HPUPM)

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Abstract: *Klebsiella* spp. are one of the leading causes of nosocomial infections worldwide. Misuse of antibiotics in the clinical sectors has caused the emergence of multidrug-resistant *Klebsiella* spp. which pose a threat to human health. The rise of extended-spectrum-β-lactamase (ESBL) and carbapenemases producing strains in *Klebsiella* spp. clinical isolates are worrying, and its causing resistance to carbapenems, the last resort of antibiotics. Studies on antimicrobial susceptibility patterns and distribution is crucial in understanding the mechanism of resistance in clinical isolates. Therefore, this study aims to investigate the antibiotic susceptibility profile of *Klebsiella* spp. clinical isolates obtained from ill patients in Hospital Pengajar UPM (HPUPM). Fifty-four *Klebsiella* spp. clinical isolates were collected from HPUPM between January to June 2022. The antibiotic susceptibility profiles of the isolates were determined using Kirby-Bauer disk diffusion method against different classes of antibiotics. The findings showed that among 54 *Klebsiella* spp. isolates, all were resistant towards ampicillin and ciprofloxacin. In terms of carbapenems, the isolates were more resistant towards meropenem (46%) compared to imipenem (13%). In addition, 78% of isolates were resistant towards cephalosporins indicative of ESBLs producing strains. Besides beta-lactams, these isolates were also resistant towards kanamycin (52%). Overall, most of the isolates are ESBLs but not all are carbapenem-resistant Enterobacteriaceae (CRE). In conclusion, the emergence of ESBL and carbapenemases producing strains is a concern, as it causes limitations of the antimicrobial agent against treating patients optimally.

Keywords: antibiotic susceptibility, carbapenemases, extended-spectrum-β-lactamase (ESBL), Klebsiella spp.

POS02

EPIDEMIOLOGY OF EXTRAPULMONARY TUBERCULOSIS IN A TERTIARY TEACHING HOSPITAL FROM YEAR 2016-2021: A RETROSPECTIVE STUDY

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Abstract: Extrapulmonary tuberculosis (EPTB) is often underestimated, especially in Malaysia. The clinical presentation of EPTB is atypical and nonspecific, so it is difficult to obtain the correct microbiological samples to confirm EPTB, thus delaying the diagnosis. The objective of the study was to determine the epidemiology of EPTB disease amongst patients in tertiary teaching hospital, University Malaya Medical Centre (UMMC) between year 2016 - 2021. The data were collected using the Laboratory Information System (LIS) databases archive. The 5 1/2-year retrospective study showed that 328 patients with EPTB were diagnosed at the UMMC, Kuala Lumpur. Total of 11042 samples were received and out of these, 352 (3.2%) samples from 328 patients were positive for EPTB and 50 of them were foreigners. Male to female ratio were 1.1:1. The patients were mainly Malaysians (84.8%), male (52.7%), Malay (55.0%), age group between 25-44 years old (38.7%), and 41.5% had PTB co-infection. The most frequently positive EPTB sample types were pleural fluid 83 (23.5%), followed closely by lymph nodes 76 (21.6%). Plus, 271 (77.0%) of the samples were smear negative but culture positive, with the sensitivity and specificity of the ZN direct smear being 23.3% and 66.7%, respectively. Overall, the EPTB isolates are pan sensitive (94.0%). The Gene Xpert MTB/RIF Ultra assay was performed on 21 of the culture positive EPTB samples, of which *Mycobacterium tuberculosis complex* was detected in 13 samples (62%). Only 1 out of the 13 samples (4.8%) had rifampicin resistance detected.

Keywords: extrapulmonary tuberculosis, epidemiology, microbiology, Malaysia

POS03

DISTRIBUTION OF STAPHYLOCOCCAL ENTEROTOXINS AMONG CLINICAL ISOLATES OF METHICILLIN-SUSCEPTIBLE *Staphylococcus aureus* (MSSA) FROM TERENGGANU, MALAYSIA

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Abstract: *Staphylococcus aureus* is a major infectious pathogen known to be one of the few bacterial species capable of producing superantigenic toxins. One of the most prominent superantigenic toxin is the staphylococcal enterotoxin, which not only causes food poisoning but also plays a role in other types of infections. This study aimed to determine the prevalence of 11 staphylococcal enterotoxin genes among 109 methicillin-susceptible *S. aureus* (MSSA) collected from Hospital Sultanah Nur Zahirah from July 2016 until June 2017. The presence of 11 enterotoxin genes (*sea*, *seb*, *sec*, *seg*, *seh*, *sei*, *sel*, *sem*, *sen*, *seo*, and *ser*) were genotyped by conventional PCR. A total of 22 (20.2%) isolates carried at least one gene and 53 (48.6%) isolates carried more than one gene, while 34 (31.2%) isolates were found negative for any of the enterotoxin genes. The most common enterotoxin genes were *seb* (26.6%, *n*=29), followed by *sea* (24.8%, *n*=27) and *sel* (21.2%, *n*=23) whereas *ser* (9.2%, *n*=10), *sei* and *sen* (8.3%, *n*=9) were the least common enterotoxin genes. A total of 33 different carriage patterns were detected among the 109 isolates. The highest number of enterotoxin gene carriage was six genes detected in three isolates, while another three isolates were found positive for five enterotoxin genes. *sec-sel* was the most prevalent combination with 13 isolates followed by *sea-seb-seh* which was found in 10 isolates. In conclusion, the clinical MSSA isolates in Terengganu harbor high prevalence and high diversity of staphylococcal enterotoxin genes.

Keywords: clinical isolate, methicillin-susceptible *Staphylococcus aureus*, staphylococcal enterotoxin, superantigenic toxin

POS04

AGAROSE GEL ELECTROPHORESIS AS A CLASSICAL METHOD TO CONFIRM RECOMBINANT VECTOR SIZES: TOWARDS AN AMPLIFICATION OF ABA392 HAEMORRHAGIC SEPTICAEMIA (HS) VACCINES B:2

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Abstract: Haemorrhagic septicemia (HS) is a well-known high fatality septicemia disease which results into death and low milk production in cattle and buffaloes. The disease is caused by *Pasteurella multocida* serotype B:2, and it is spread through the intranasal and oral routes in domestic animals. Our previous study has shown that both our recombinant protein vaccine, ABA392/pET-30a, and DNA vaccine, ABA392/pVAX1, significantly reduced the infection in rats. Both of the recombinant vaccines will now be tested in rabbits and cattle. Stability checking and agarose gel electrophoresis (AGE) were performed to check on both recombinant vaccines' stability and sizes. Briefly, both, ABA392/pET-30a, and ABA392/pVAX1 were cut using BamH1 and Hind III. Subsequently, both vectors and inserts were subjected to AGE and run for 40 minutes at 90V. From the AGE, 804bp of inserts (ABA392), 5422bp of vector pET-30a, and 3791bp of vector pVAX1 were found visible on the gel. Therefore, it is proven that AGE is still the best method used for DNA separation. Currently, we are sequencing both recombinant vectors and are in the process of amplifying them to be tested using intranasal route in rabbits. Similar to the previous study, the rabbit will be used to test the recombinant vectors (vaccines) and serum samples will be collected from the rabbit. It is hoped that it will be no inflammatory response observed after the intranasal inoculation in rabbits. We hypothesize that both recombinant vaccines, ABA392/pET-30a and ABA392/pVAX1 are able to protect the animal against HS illness.

Keywords: Haemorrhagic septicemia, *Pasteurella multocida*, Recombinant vaccines, Microbiology

POS05

THE ANTIBIOTIC AND BIOCIDE SUSCEPTIBILITY PROFILE OF *ACINETOBACTER BAUMANNII* CLINICAL ISOLATES FROM TERENGGANU

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Abstract: The Gram-negative bacterium *Acinetobacter baumannii* has been reported as one of the major contributors for the occurrence of nosocomial infections. The emergence of antibiotic-resistant *A. baumannii*, especially multidrug resistant (MDR) strains challenged the effectiveness of available treatments for *A. baumannii* infections. In addition to antibiotics, the widespread use of biocides (antiseptics and disinfectants) to contain these nosocomial infections has led to concerns about the emergence of tolerance to biocides. In this study, the antimicrobial and biocide susceptibilities of *A. baumannii* clinical isolates from Hospital Sultanah Nur Zahirah (HSNZ), the main tertiary hospital in Terengganu, was determined. A total of 189 non-repetitive *A. baumannii* isolates that were obtained from 2017 – 2020 from HSNZ were subjected to antimicrobial susceptibility testing using the Kirby-Bauer disc diffusion method with a panel of twenty antibiotics covering eight antimicrobial categories. Results were interpreted using the Clinical and Laboratory Standards Institute (CLSI) guidelines. The minimum inhibitory concentration (MIC) values for the biocides benzalkonium chloride, benzethonium chloride and chlorhexidine digluconate were determined using broth microdilution. A total of 136 (72%) isolates were categorized as MDR strains as they exhibited resistance to three or more classes of antibiotics whereas 28 (15%) isolates were categorized as non-MDR and the remaining 25 (13%) isolates were susceptible to all class of antibiotics. Majority of the *A. baumannii* isolates showed high MIC values ($\geq$ 32 µg/mL) against chlorhexidine digluconate (87%) and benzethonium chloride (74%) whereas only 15% of the isolates exhibited MIC $\geq$ 32 µg/mL for benzalkonium chloride.

Keywords: *Acinetobacter baumannii*, antibiotics, biocides, multidrug resistant

POS06

Vaccines as Sustainable Approach to Infectious Diseases: EPS-MH Adjuvanted Vaccine Against Mannheimiosis

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Abstract: Animals play many essential roles in humans' lives. Vaccination has made a substantial contribution to the sustainability of animal health by reducing the burden of frequent infectious diseases. Vaccines and other alternative products can help minimize the need for antibiotics by preventing and controlling infectious diseases in animal agriculture. One of the major animal respiratory diseases in Malaysia is a food security threat called mannheimiosis, caused by a pathogen called *Mannheimia haemolytica*. Mannheimiosis becomes irreversible and potentially fatal to infected animals. In order to reduce the incidence of the disease, the efficacy of the laboratory-tested inactivated adjuvanted vaccine (EPS-MH) for mannheimiosis was carried out on Katjang hybrid goats against mannheimiosis in TGG, Malaysia. Goats over 6 months old were given the vaccine intramuscularly, followed by a booster dose, and challenged with wild *Mannheimia haemolytica* infection. The data of goats after the lethal mannheimiosis challenge were collected based on gross pathology and bacterial isolation to confirm the diagnosis. The effect of vaccination was evaluated. There was a significant reduction in bacteria isolates and infected lung lesions when vaccinated were compared to unvaccinated goats. This has clearly shown that vaccines have the potential to improve animal health, reduce antibiotic consumption and safeguard agricultural productivity.

Keywords: *development; sustainability; Mannheimia haemolytica; adjuvant; vaccine; agriculture*

POS07

IN SILICO ANALYSIS AND MOLECULAR DOCKING STUDY OF NIPAH VIRUS V PROTEIN AGAINST STATS FAMILY PROTEIN

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Abstract: Nipah virus is one of the highly lethal pathogenic paramyxoviruses that causes deadly encephalitis. The V protein which is encoded from the P gene by mRNA editing is the key determinant of the virulency of Nipah virus. Many studies have revealed that the N-terminal region (NTD) of NiV V protein plays a vital role in invading innate immune responses particularly in antagonizing interferon by interacting with STATs protein family. There's no experimental determined structure for NiV V protein except for another paramyxovirus Simian virus 5 V protein. In this study, we build the NiV V protein structure from different strain by using homology modelling together with ab initio structure modelling approaches. Two NiV V protein structure from different isolate (pig and bat) were undergone protein-protein docking with STATs family protein (STAT1 and STAT2). The molecular docking and interaction analysis revealed that bat isolate have stronger binding affinity than pig isolate when interacting with STAT1 and STAT2 protein. This have indicated that the amino acid changes in bat isolate have led to stronger interferon antagonizing effect and might exhibit stronger virulency than pig isolate.

POS08

GENOME ANALYSIS OF CLINICAL *ACINETOBACTER SOLI* ISOLATES FROM TERENGGANU

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Abstract: The Gram-negative bacterium *Acinetobacter soli* is a rare member of the genus *Acinetobacter* that was first isolated from forest soil in 2008 but has since been implicated in several hospital-associated infections. This study presents genome data on two *A. soli* clinical isolates from Hospital Sultanah Nur Zahirah (HSNZ), the main tertiary hospital in Terengganu. A total of 384 *Acinetobacter* spp. clinical isolates from HSNZ were screened by *rpoB* gene sequencing, leading to the identification of two *A. soli* strains designated AC1511 and AC15148. Antimicrobial susceptibility test using a panel of 21 antibiotics encompassing 8 different classes indicated that both *A. soli* isolates were susceptible to all antibiotics tested. Genome sequencing was performed on the Illumina HiSeq platform (2 × 150-bp paired-end reads) and assembled using Unicycler v.0.4.8. The total genome size for AC1511 was 3,320,693 bp and 3,260,687 bp for AC15148. Core genome phylogenetic analysis with a selection of forty *A. soli* strains obtained from GenBank revealed that AC1511 was closely related to *A. soli* As186, a clinical isolate from the United States and OCU-Ac9, which was isolated in Japan. On the other hand, *A. soli* AC15148 was more closely related to *A. soli* NIPH2899, a clinical isolate from the Czech Republic. Both AC1511 and AC15148 were unable to be typed by both the Pasteur and Oxford schemes for *Acinetobacter* multilocus-sequence typing (MLST). No resistance genes could be detected from AC1511 and AC15148 using ResFinder, which confirmed their susceptible phenotypes.

Keywords: *Acinetobacter soli*, clinical isolates, whole-genome sequencing, phylogenetic analysis

POS09

EFFECT OF DOMAIN MANIPULATION IN THE STAPHYLOCOCCAL PHAGE 88 ENDOLYSIN

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Abstract: The rise of antibiotic resistance in *Staphylococcus aureus* warrants the discovery of novel antimicrobials that do not elicit bacterial resistance. Bacteriophage-encoded endolysins also known as peptidoglycan hydrolases hold potential as prospective antimicrobials, triggering lysis of bacterial cells at the end of the viral life cycle for release of progeny viruses. However, most naturally occurring endolysins may not be efficient antimicrobials in terms of lytic activity and host range. The Staphylococcal Phage 88 endolysin targeting Multi-Drug Resistant *Staphylococcus aureus* has a tri-domain structure – an N-terminal Cysteine, Histidine-dependent Amidohydrolase/Peptidase (CHAP) domain, a central amidase domain and a C-terminal SH3b cell wall-binding domain (CBD). Engineered staphylococcal endolysins have been shown to confer enhanced properties as compared to their wild-type counterparts. In this study, two deletion constructs of the Staphylococcal Phage 88 endolysin comprising the CHAP and CHAP-Amidase enzymatic domains respectively were designed. The recombinant mutants were developed via conventional cloning and expressed using the pET expression system. Proteins were purified using His-tag affinity chromatography and confirmed via SDS-PAGE and Western Blot. Both constructs still retained its lytic activity, despite some reports showing that the loss of the CBD could disallow binding to the host thus diminishing lytic activity. Future studies to determine the host range of the mutant endolysins are underway as deleting the CBD could extend the host range of the endolysin. Engineered endolysins could hold tremendous potential as novel antimicrobials to alleviate the rising global antimicrobial resistance issue.

Keywords: Bacteriophages, endolysin, domain mutagenesis, Multi-Drug Resistant *Staphylococcus aureus*

POS10

AIR-LIQUID BIOFILM FORMATION: A POTENTIAL VIRULENCE FACTOR IN CLINICAL CARBAPENEM-RESISTANT *Acinetobacter baumannii*

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Abstract: Bacterial biofilm formation is well-known for causing therapeutic impasses by increasing their resistance to antibiotics and desiccation for environmental survival. Biofilms are not limited to solid-liquid or solid-air interfaces but also form at air-liquid interfaces (pellicle) that provide a favourable niche for direct oxygen uptake from air and nutrients from liquid media. In this study, we aimed to investigate the pellicle-forming ability in 96 clinical carbapenem-resistant *A. baumannii* isolates (63 respiratory- and 33 non-respiratory-related specimens) collected from the intensive care unit at University Malaya Medical Centre (2015–2016). Pellicle formation assay was performed in Mueller-Hinton (MH) and Luria-Bertani (LB) mediums using borosilicate and polypropylene tubes and biomass was quantified using crystal violet staining. A total of 4.2% (4/96) isolates displayed pellicle-forming ability with biomass OD_{570} (1.165±0.091–3.325±0.946). These isolates have higher pellicle-forming rates in borosilicate tubes (MH:4/4; LB:4/4) and nutrient-richer MH medium (Borosilicate:4/4; Polypropylene:3/4) compared to polypropylene tubes (MH:3/4; LB:1/4) and LB medium (Borosilicate:4/4; Polypropylene:1/4), implying the influence of different nutrient compositions and abiotic surfaces. Low rate of pellicle-forming isolates observed in our study was also documented in studies from Australia (14.8%, 8/54) and India (3.4%, 2/60), suggesting pellicle is an uncommon phenotypic-trait. Interestingly, all four pellicle-forming isolates were recovered from respiratory-related specimens: bronchoalveolar lavage, sputum, tracheal-secretion, and tracheal-swab (n=1 each) which is in accordance with a study from India. Such observation questions the relationship between pellicle-forming capabilities and the potentially enhanced virulence in respiratory-related isolates (instead of other clinical origins), thus, the exact mechanism involved in pellicle formation warrants further investigation.

Keywords: Carbapenem-resistant *Acinetobacter baumannii*, Malaysia intensive care unit patients, Pellicle, Respiratory-related

POS11

ANTIMICROBIAL ACTIVITY PRODUCE FROM *Paenibacillus polymyxa* KP10 AGAINST METHICILLIN-RESISTANT *Staphylococcus aureus*

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Abstract: By the 21st century, the emergence of antimicrobial pathogens around the world are rising critically and becomes a major problem in healthcare. This is due to the unregulated usage of antibiotics in the treatment that leads to high morbidity and mortality. Methicillin-resistant *Staphylococcus aureus* (MRSA) is one of the multidrug-resistant pathogens that cause chronic infections. Treatment of these infections using conventional antibiotic are ineffective due to antimicrobial resistance. This has propelled the search for alternative antibiotic therapy using antimicrobial peptides (AMPs). AMPs are small protein molecules that have a broad spectrum of antimicrobial and immune-modulatory activities against pathogens. *Paenibacillus polymyxa* is a gram-positive bacteria that is able to produce AMPs against the pathogen. This study aims to screen antimicrobial activity produced from *P. polymyxa* against MRSA. Firstly, cell-free culture supernatant (CFCS) isolated from *P. polymyxa* KP10 will be prepared. Then, the antimicrobial activity of CFCS against nine MRSA clinical isolates will be determined using the agar well diffusion method. The sensitivity of antimicrobial activity of CFCS in various pH, temperature, and proteolytic enzymes will be analysed. The findings from this study will provide insight into the potential of AMPs produced from *P. polymyxa* KP10 with antimicrobial properties against MRSA.

Keywords: Methicillin-resistant *Staphylococcus aureus*, antimicrobial, antimicrobial peptides, *Paenibacillus polymyxa.*

POS12

EXTRACTION OF S*ENNA ALATA* (L.) ROXB LEAVES USING SOXHLET, MACERATION AND SUBCRITICAL FLUID METHOD AND ANTIBACTERIAL ACTIVITIES AGAINST *Staphylococcus aureus* AND *Staphylococcus epidermidis*

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Abstract: *Senna alata* (L.) Roxb., which belongs to the family of Fabaceae, has been used traditionally for the treatment of skin diseases, ringworm infection, and constipation. In the evaluations of traditional claims, it is important to study the active ingredients and find scientific evidence for the herbal activities. This study was aimed to assess the total yield percentage and the antibacterial activity from *S. alata* leaves extracts using three different extraction methods which were maceration, Soxhlet and Subcritical Fluid and the methanol extracts were subjected to screening against *Staphylococcus aureus* and *Staphylococcus epidermidis* using the standard protocol Disc Diffusion Method (DDM) and resazurin based microdilution method. The antibacterial activities were assessed by the bacterial growth inhibition zone, minimum inhibition concentration and minimum bactericidal concentration values. This study resulted the highest total yield percentage was the maceration method (25.14 % ± 0.59), followed by Soxhlet (20.34 % ± 0.66) and the least was Subcritical Fluid (1.49 % ± 0.19). It was observed that there were inhibition zones for all extracts against both strains ranging from 3-18 mm with the highest from maceration method whereas the lowest inhibition from subcritical fluid method. Meanwhile the MIC and MBC values ranging from 83-166 mg/mL. This study proves that the methanol extracts of *S. alata* leaves from maceration method produces the highest total yield and antibacterial activities. This study also showed that *S. alata* leaves can be used as natural cure for bacterial infections.

Keywords: Disc diffusion, maceration, microdilution, minimum inhibition concentration, resazurin, *Senna alata,* Soxhlet, Subcritical fluid.

POS13

IN VITRO ANTIBACTERIAL AND WOUND HEALING ACTIVITY OF SIDR AND MANUKA HONEY SAMPLES ON SKIN DERMAL FIBROBLAST CELLS

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Abstract: wound healing is a complex process that required to be started immediately after injury. Contamination is the biggest impediment to wound healing processes resulting in granulation tissue damage and exposure to bacterial infection. Antibiotics are often effective in treating vulnerable microbial infections, however, some of them have undesirable side effects. For this reason, scientists are exploring medicinal plants and their bioactive constituents as a potential safe source of wound healing agents. Honey is a natural product made by bee from floral nectar. It has been used as a traditional treatment for skin tissue infections. Hence, this study aimed to investigate the antibacterial susceptibility activity against four bacterial strains as well as *in vitro* cell migration rate of skin dermal fibroblast cells treated with Sidr honey (SH) and Manuka honey (MH) using a wound healing assay. *E.coli* was the only strain that showed an inhibition zone at 700 mg/disc and was chosen to determine the MBC. The percentage of wound closure treated with honey samples at 1000 µg/ml was significantly inducing wound healing in a time-dependent manner compared to untreated control cells. SH was more efficiently enhanced the cell proliferation and migration of fibroblasts through time intervals than MH. Overall, both tested honey samples were found to be effective in inhibiting bacterial growth of *E.coli* as well as accelerating the closing of the injured area and this could be attributed to a variety of antioxidant compounds in honey such as polyphenolic compounds that play a principal role in wound healing.

Keywords: Bacterial activity, Cell migration, Manuka honey (MH), Sidr honey (SH), Wound healing assay.

POS14

CHARACTERIZATION OF INDAZOLES AND THIAZOLES AS ANTI-AMOEBIC AGENTS

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Abstract: *Acanthamoeba castellanii* is a disease-causing amoeba that shows resistance towards medications when in cyst form. Amoebic infections are usually treated with anti-fungal drugs; however, cases of unsuccessful treatments (if late diagnosis) and relapse are reported. Over the years, anti-microbial research had been conducted using azole compounds due to their effectiveness as therapeutic compounds especially as anti-fungal. Therefore, this paper characterize the effect of Indazoles and Thiazoles as potential anti-amoebic agents via different anti-amoebic assays and effects on gene expression of apoptotic and cell proliferation genes. Results showed that compounds RR64, FM23. FM50, FM55 and RR65 performed significantly well as an anti-amoebic agent for all assays conducted, while the other compounds had their advantages and disadvantages. Also, qPCR findings of selected genes NACHT, GSK3-β and RAS-like protein genes imply the role of apoptosis in treatment by Indazoles and Thiazoles. In conclusion, compounds RR64, FM23. FM50, FM55 and RR65 can be further studied on as an anti-amoebic agent and hopefully can be utilised for therapeutic purposes, in the future.

POS15

ACTINOMYCETES FROM BRIS SOIL: INVESTIGATION OF POTENTIAL CANDIDATE AS NEW DRUG LEADS

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Abstract: The emergence of antibiotic resistance has been recognized globally in which new drugs are needed to combat this problem. Actinomycetes have been noted as the major potent drugs producer. The information of actinomycete diversity from BRIS soil and their antibacterial activity remains scarce specifically from Rhu tapai and Baging series. In the present study, selective isolation of actinomycetes were performed from both soil series and screening for antibacterial potential of the actinomycete isolates using plug assay method were conducted. Colony forming unit (CFU/g) was recorded for both soil series. The highest CFU/g recorded for Rhu tapai series is $3.7*10^5$ and $24.2*10^5$ for Baging series. 87 isolates were purified and 75 isolates showed various significant activity against ESKAPE pathogens while only one isolate showed weak antibacterial activity against all of the pathogens tested. The outcome of this study would be a profound platform in drug discovery and in proposing potent candidates with significant antibacterial potential as well as uncover the potential of BRIS soil as source to find new drug producers.

Keywords: actinomycetes, antibacterial activity, BRIS soil, ESKAPE pathogen

POS16

ISOLATION AND CHARACTERIZATION OF BENEFICIAL ENDOPHYTIC BACTERIA FROM *Oryza Sativa* CULTIVATED IN ACID SULFATE SOIL

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Abstract: Pyrite (FeS_2) oxidation in acid sulfate soil led to high acidity and aluminium (Al) and/or iron (Fe) toxicity to the plant. This problem causes nutrient deficiency and root inhibition, which retards plant nutrient uptake efficiency for growth. Plant-microbe interaction is one of the most important determining factors in influencing plant's nutrient uptake and growth in acid sulfate soil. Thus, this research aims to isolate and characterize the beneficial endophytic bacteria from *Oryza sativa* cultivated in acid sulfate soil. The *O. sativa* samples were collected from a paddy field in Nenasi, Pekan, Pahang. Eight endophytic bacteria were isolated using serial dilution methods after surface sterilization of plant samples were achieved. All isolated bacteria showed different capacities for plant growth-promotion features, including production of plant growth hormone, solubilization of phosphate and converting atmospheric nitrogen into a plant-usable form. This preliminary analysis found that the isolated bacteria have potential application in integrated plant nutrient management that promotes vegetation growth in acid sulfate soils.

Keywords: plant growth-promoting bacteria, indole 3-acetic acid, phosphate solubilization, biological nitrogen fixation.

POS17

MICROALGAE FROM ANTARCTIC SOIL

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Abstract: The source of fatty acids such as Omega-3 PUFAs is considered valuable due to its significant role in the fields of medical, pharmaceutical, and aquaculture. However, this promising source is at scarce considering that currently it can only be acquired from fish. Consequently, this occurrence gains interest among researchers in utilizing microalgae as alternatives for potential producers of fatty acids. Several studies have claimed that Antarctic microalgae are likely to contain a high concentration of fatty acids that can be beneficial for human and animal health. Six soil samples from the Antarctic, S6, S10, S11, S21, S26, and S30, were collected and cultured in 3 different liquid media of BBM, 3N-BBM+V, and JM. After two months, only soil samples S26 and S30 showed the growth of green microalgae in every nutrient media, with an exception for JM media, which did not revive the microalgae from soil sample S26. The type of soil from samples S26 and S30 are similar, which is fine-grained sandy loam while the remaining samples were coarse-grained sand. The fine-grained texture of the sandy loam soil samples may affect soil fertility, which in consequence influenced the presence of microalgae communities. These findings provide information on the type of soil and specific nutrient media that suits the growth of microalgae from the Antarctic soil, creating further possibilities for further analysis such as identification and chemical compound manipulation.

Keywords: Microalgae, Antarctic, isolation, fatty acids

POS18

Characterization of Heavy Metal Tolerance Rhizobacteria and its Potential in Bioremediation

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Abstract: Lead (Pb) is a toxic heavy metal released into the environment through either natural sources or human activity. It can cause harmful effects on plants, human health, and microorganisms. Beneficial microorganisms such as plant growth-promoting rhizobacteria (PGPR) can be used for microbial-assisted phytoremediation processes. However, not all PGPRs are tolerant to a high concentration of heavy metals. Thus, this research aims to analyze the plant growth-promoting features of indigenous rhizobacteria isolated from heavy metal contaminated soil and their tolerance toward Pb toxicity. The heavy metal-contaminated soil collected from a mining site in Tasik Chini, Kuantan, Pahang, was used for rhizobacteria isolation. All rhizobacteria from the soil were screened for phosphate solubilization activity, IAA production, and nitrogen fixation ability. Then isolates that showed the most promising plant growth-promoting features were selected and analyzed for their heavy metal resistance toward Pb. A total of 14 rhizobacteria were successfully isolated from the soil samples. Nine isolates were categorized as gram-positive, while the remaining were gram-negative. Analysis of plant growth-promoting features found that five isolates showed a positive result for all screening tests. Subsequently, heavy metal tolerance analysis of different Pb concentrations found that all isolates can grow at a low concentration of Pb. Interestingly, one isolate (C4) showed growth at concentrations of 4 and 5 mmol L-1. Overall, the study successfully screened the potential rhizobacteria for microbial-assisted phytoremediation.

Keywords: Plant growth-promoting rhizobacteria, heavy metal resistant rhizobacteria, lead (Pb), bioremediation.

POS19

ANALYSIS OF MICROBIAL COMMUNITY COMPOSITION FOUND IN MALAYSIAN BRIS SOIL

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Abstract: Globally, the rapid emergence of resistant bacteria has been a major threat to public health, threatening the efficiency of antibiotics in treating infections. The urgency in new drug discovery is desperately needed to combat this crisis posed by antimicrobial resistance. However, the rediscovery of known compound has been one of the main hurdles in finding new drug in natural resources. It is suggested to explore underexploited or extreme habitat conditions in efforts to avoid the rediscovery of known compound. Hence, Beach Ridges Interspersed with Swales (BRIS) soil is selected as the study sample since, they possess soil characteristics which can be considered as unhealthy or problematic soil and there are lack of study done particularly on BRIS soil that can be found in Malaysia. This study is intended to investigate the microbial community composition in BRIS soil using metagenomics and culture-dependent approach and to determine the effect of BRIS soil physico-chemical characteristics on microbial community composition and then to isolate Actinomycetes from BRIS soil and identify their antimicrobial potential. The culture-dependent approach focused on the selective isolation, screening and dereplication of Actinomycetes from BRIS soil. A total of thirty-two Actinomycetes strains were successfully isolated from BRIS soil using soil serial dilution and spread plate method. The colony-forming unit (CFU) of actinobacterial colonies to the bacterial colonies showed high percentage in the samples. Out of thirty-two Actinomycetes isolates, six isolates showed their antimicrobial activity against ESKAPE pathogen by inhibiting the growth of one or more strains from six selected ESKAPE pathogen through primary screening. It is expected from this study is to reveal the microbial community composition of Malaysian BRIS soil present in both culturable and non-culturable and their relationship with the physico-chemical properties of BRIS soil and to identify the Actinomycetes isolated from BRIS soil that possess antimicrobial activity which can open a pathway to the discovery of a new potential antimicrobial producer to serve as novel drug leads.

Keywords: microbial community, microbial composition, Malaysian BRIS soil, BRIS soil, Actinomycetes

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