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September 2020 | Volume 03
Journal of Microbiology and Biotechnology Reports

Proceedings of

5th World

Biotechnology Congress

&

3rd International Conference on

Microbiology and Infectious Diseases

September 23, 2020 | Webinar

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Scientific Program

Scientific Program

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35 YEARS IN ASSESING THE IMPACT OF HEALTHCARE RESEARCH

Webinar
Time Zone: London, UK

September 23, 2020

Introduction 10:00-10:10

Keynote Forum

10:10-10:55

Title: Development of an IT platform for the broad availability of molecular precision oncology
Dirk Hempel, Steinbeishochschule Berlin, Germany

Session Introduction

Sessions on: Medical Biotechnology | Food and Nutrition Biotechnology | Bacteriology

10:55-11:25
Title: Personalized tissues and organs replacement – A peek into the future
Asaf Toker, Matricelf, Israel

11:25-11:55
Title: Evaluating the effect of vacuum storage and storage conditions on the quality traits of fresh oregano (*Origanumsyriacum*)
Samer Mudalal, An-Najah National University, Jordan

11:55-12:25
Title: Probiotic lactobacilli and their bacteriocin combined with antibiotics display synergy against MDR pathogenic bacteria
Shyamapada Mandal, University of Gour Banga, India

12:25-12:55
Title: Next generation sequencing, in vivo pathogenicity study and prevalence of multidrug-resistance efflux pump genes oqxAB-encoding plasmid carrying *Escherichia coli*
Andes LAU, University of Hong Kong, Hong Kong

Lunch Break 12:55-13:30

Sessions on: Autoimmune Diseases | Diagnosis & treatment of microbial infections | Medical & Industrial Biotechnology

13:30-14:00
Title: Immuno-informatics design of a multimeric epitope peptide based vaccine targeting SARS-CoV-2 spike glycoprotein
Onyeka S. Chukwudozie, University of Lagos, Nigeria

14:00-14:30	**Title: Case report: Primary laryngeal cryptococcosis in an immunocompetent person** **Beenish Syed,** Liaquat National Hospital, Karachi
14:30-15:00	**Title: Association of DNA methylation in peripheral blood with diagnosis and treatment of gynaecological cancers** **Karunyadevi J,** Bharathiar University, India
15:00-15:30	**Title: Sequence comparison of PKS gene with wide spectrum antibiotic metabolite – Insilco approach for industrial applications** **Janani B,** Bharathiar University, India
Poster Presentation	
15:30-16:00	**Title: Linking the metabolic pathways of *Escherichia coli* with virulence by altering glucose availability, inhibiting the acetyl-CoA carboxylase gene accA with asRNA, and through the quantification of luxS** **Tatiana Hillman,** TheLAB INC., USA
Thanks Giving & Closing Ceremony	

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Dirk Hempel

Steinbeishochschule, Berlin, Germany

OncoVision: Development of an IT platform for the broad availability of molecular precision oncology

The OnkoVision project is the development of an AI-based molecular biological decision-making platform for various cancer diseases i.e. gastrointestinal tumors. The gastrointestinal tumors include colorectal carcinomas, liver carcinomas, carcinomas of the liver with hepatocellular carcinomas as well as bile duct carcinomas and carcinomas of the pancreas. The project's clinical partners have excellent expertise in the diagnosis and therapy of these diseases and are all members of certified colon, liver and pancreas cancer centers.

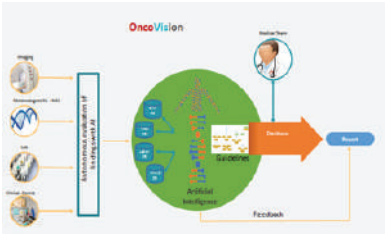
One part of the project consists of taking GI tumors as an example for the molecular genetic real world data of the patients treated in our network with regard to the somatic genetic alterations found, such as gene mutations, gene fusions, copy number variations (CNV), miRNA, lncRNA, DNA methylation, tumor mutational burdens and MSI as well regarding protein expression of tumors (Evaluate PDL1, ERBB2) and compare it with the sectional imaging and the clinical courses under the given therapy.

The planned platform is to automatically evaluate the existing data sets using AI, for example to identify and validate new prognostic and predictive biomarkers.

The relevant publications are also to be matched in the context of an AI-based database for the genetic generations found.

In addition, OnkoVision will be used in the group as a part of virtual molecular tumor boards. The existing network of the research project can be used for this. It will be examined to what extent the platform enables the broad availability of molecular tumor boards.

Due to the composition of the project group from university and non-university partners who have worked together in the past, existing logistical and organizational structures can be used. It can be assumed that this provides the best conditions for the group to achieve reliable results.



Biography

Dirk Hempel has studied human medicine at Rostock and LMU Munich. He got License to practice medicine in Munich. He completed Fellow ship training as an internist and further training as internal oncologist / hematologist at the Central Clinic Augsburg, II. Medical Clinic. He wrote a examination for hematologist / internal oncologist in Munich. He is Head of the Steinbeis Transfer Institute for Clinical Hemato-oncology at the Steinbeis University Berlin. He was appointed as junior professor at the Steinbeis University Berlin. He was the Chief Physician and Head of the Hematology Department at Helios Amper Clinic Dachau.

dirk.hempel@gmail.com

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Scientific Tracks & Abstracts

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Sessions

Medical Biotechnology | Food and Nutrition Biotechnology | Bacteriology

Session Introduction

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Asaf Toker, Matricelf, Israel

Title: **Evaluating the effect of vacuum storage and storage conditions on the quality traits of fresh oregano (*Origanumsyriacum*)**

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Title: **Probiotic lactobacilli and their bacteriocin combined with antibiotics display synergy against MDR pathogenic bacteria.**

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Title: **Immuno-informatics design of a multimeric epitope peptide based vaccine targeting SARS-CoV-2 spike glycoprotein**

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Title: **Sequence comparison of PKS gene with wide spectrum antibiotic metabolite – Insilco approach for industrial applications**

Janani B, Bharathiar University, India

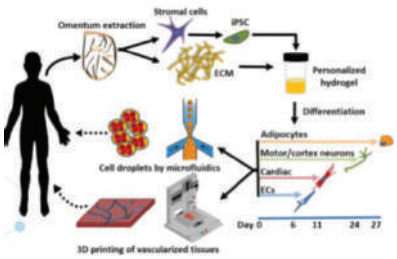
Personalized tissues and organs replacement – A peek into the future

Asaf Toker
Matricelf, Israel

Matricelf developed a technology that enables the production of autologous engineered tissue composed of matrix and cells derived from patients Omentum biopsy. The platform showed remarkable pre-clinical results for several medical conditions.

The company recently licensed the technology that enabled scientist at Tel Aviv university that 3D printed a human heart from human cells and matrix for the first time in human history.

The company plans to conduct its first human clinical trial for Acute Spinal Cord Injury (SCI) early in 2023.



Biography

Toker is a seasoned CEO with a proven track record in the biotechnology and healthcare industries. He possesses strong business development skills with prior experience in medical devices, R&D, and Life Sciences. Dr. Toker is a pediatrician and also has a degree in Health Systems Management and MSc in Biotechnology Engineering from Ben Gurion University of the Negev. Dr Toker served in several executive positions in the private and public healthcare system and served as a director in several biotechnology and medical device companies.

asaf@matricelf.com

Evaluating the effect of vacuum storage and storage conditions on the quality traits of fresh oregano (*Origanum syriacum*)

Samer Mudalal and Doaa Kanan
An-Najah National University, Jordan

Origanum syriacum L. (common names: zaatar, bible hyssop, Syrian oregano, Lebanon oregano) is considered one the most commonly used aromatic herbs in the mediterranean diet. The objective of this study to evaluate the effect of vacuum packaging and storage conditions on the shelf life of fresh leaves of Origanum syriacum by employing. In this study, 132 samples of fresh oregano have been prepared in vacuum packs and divided into four treatments (n=33/treatments). The treatments were labeled as A (fresh oregano100%), B (fresh oregano 63.2%, fresh onion 15%, olive oil 20%, NaCl 1.8%), C (fresh oregano 61.91%, fresh onion 15%, olive oil 20%, NaCl 1.8%, sumac powder 1.29%), and D (Fresh oregano 59.2%, 15% Fresh onion, 20% oil, 1.8% salt, 4% lactic Acid, ultimate pH 4.4). The potential growth of Clostridium botulinum by using Clostridium sporogenes DSM795 as a surrogate microbe has been assessed. Moreover, color traits (L*a*b*), microbiological counts (aerobic, anaerobic, and psychrotrophic as well as yeast and molds), and pH- values have been evaluated during the storage period (42 days). Both spot and spreading agar journey methods showed that groups B and D could resist the growth of Clostridium sporogenes DSM 795. It was found that lactic acid was the most effective ingredient against aerobic, anaerobic, and psychrotrophic bacteria if compared to sumac and onion. On another hand, Group C showed significantly ($p<0.05$) the lowest L* and b*-values if compared with other groups. In conclusion, there is a possibility to extend the shelf life of fresh oregano by employing hurdle technology (vacuum packaging combined with natural additives).

Keywords: Oregano, color traits, Clostridium sporogenes, vacuum, sumac

Biography

Samer Mudalal got his Ph.D. in Fo od science and Biotechnology from Bologna University, Italy. Currently, he is assistant professor at Department of Nutrition and Food Technology. He has more than 25 publications in food science and biotechnology field. He was awarded several research grants. He worked as quality control, production, and R& D Manager in different sectors in food industries.

samer.mudalal@najah.edu

Probiotic lactobacilli and their bacteriocin combined with antibiotics display synergy against MDR pathogenic bacteria

Shyamapada Mandal
University of Gour Banga, India

The LAB (lactic acid bacteria) especially that belong to the genus Lactobacillus are good probiotics and such microorganisms have the capacity to antagonize the pathogenic bacterial growth. This communication states the probiotic features of some indigenous Lactobacillus spp. procured from different locally available sources: L. fermentum LMEM10 and L. gasseri LMEM12 (from commercially available curd), L. animalis LMEM11 and L. plantarum LMEM15 (from homemade curd), and L. acidophilus LMEM13 and L. rhamnosus LMEM14 (from commercial probiotic sachet), and their antibacterial activity (alone and in combination with antibiotics) against gram-positive (Staphylococcus aureus and Listeria monocytogenes) and gram-negative (Salmonella enterica serovar Typhi, Pseudomonas aeruginosa and Escherichia coli) multidrug resistant (MDR) bacterial pathogens. The lactobacilli having probiotics attributes displayed excellent antibacterial activity, and combined with antibiotics had synergistic interaction (in terms of growth inhibitory index). Bacteriocin isolated from such probiotic lactobacilli also displayed antibacterial activity against gram-negative as well as gram-positive MDR pathogenic bacteria. Following checker-board agar dilution, LAB bacteriocin combined with antibiotics had synergistic interaction (in terms of fractional inhibitory concentration index) against MDR pathogens. Thus, locally available LAB are good probiotics secreting antibacterial bacteriocin, and might be useful as naturally available biotherapeutics in mitigating bacterial antibiotic resistances.

Audience Take Away

- This speech helps understand the effective probiotics attributes of natural lactic acid bacteria.
- This research shed lights on the synergism between bacteriocin/probiotic LAB and antibiotics against MDR pathogens.
- This study underlines the need of application of LAB probiotics in mitigating antibacterial resistance of pathogenic bacteria.

Biography

Shyamapada Mandal is currently employed at Gurudas College,Kolkata,west bengal,India. Dr. Shyamapada Mandal has research interest in the field of Immunology and Microbiology. Publications in Antibiotic resistance of Salmonella enterica serovar Typhi in Kolkata, India, and in vitro experiments on effect of combined chemotherapy.

sam.micro11@ugb.ac

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Next generation sequencing, in vivo pathogenicity study and prevalence of multidrug-resistance efflux pump genes oqxAB-encoding plasmid carrying *Escherichia coli*

Andes LAU
University of Hong Kong, Hong Kong

Background: Multidrug-resistant efflux pump genes *oqxAB*-encoding plasmids are disseminated among Enterobacteriaceae in animal and human. Giving its high presence and the multidrug resisting nature of *oqxAB*, thorough understanding and constant monitoring of oqxAB-encoding plasmid carrying *E. coli* is necessary.

Methodology: Characterisation and next generation sequencing of 43 *oqxAB*carrying E. coli were performed, all isolates were originated from human and livestock from China and Hong Kong. NGS analysis of these 43 isolates was performed with five addition oqxAB-encoding plasmid sequences extracted from Genbank. In vivo pathogenicity study of *oqxAB*-encoding plasmid was performed using *E. coli* J53 transconjugants containing *oqxAB* plasmid and Galleria mellonella larvae as study model. In the period of September 2019 to September 2020, 36 fresh chicken meat samples and 100 chicken swab samples were screened for *oqxAB*-carrying *E. coli.*

Findings: According to analysis, there are 27 IncFII F18 plasmids, 12 F16 plasmids, six F33 plasmids, two F24 plasmids, and one F14 plasmid among the 48 plasmids. Plasmids of same Inc group encoded similar set of virulence factors and antibiotic resistance genes, which F18 and F24 plasmids presented the most virulence factors. Co-existence of *blaCTX-M*, fosA3, and *oqxAB* genes was observed in all F33 plasmids and one F18 plasmid, while F16 plasmids encode lesser resistance genes compare to others. in-vivopathogenicity study suggested all *oqxAB*-encoded plasmids caused significant health deterioration, but no significant increase in death rate. 25 *oqxAB*-carrying *E. coli* strains were isolated from the 36 fresh chicken meat samples, while only 7 *oqxAB*-carrying E. coli strains were isolated from the 100 chicken swab samples.

Conclusion: Our data suggests high correlation between plasmids identified from China and Hong Kong, and *oqxAB* plasmid increases pathogenicity of host bacteria. Future aspect: Further NGS will be performed with newly isolated *oqxAB*-carrying *E. coli*, and environmental sampling will be commenced.

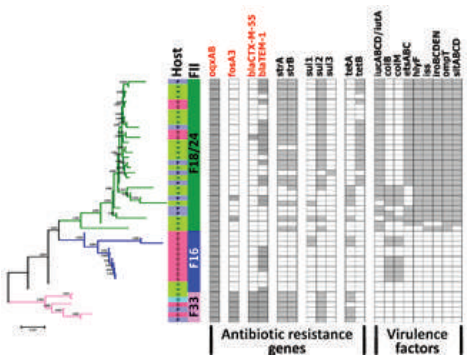

Fig. 1 Neighbor joining phylogenetic tree of the 48 plasmids sequences

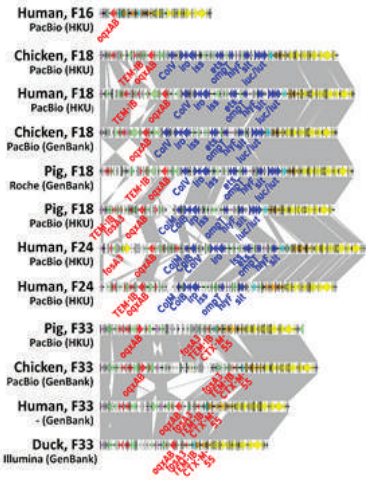

Fig. 2 Linear alignment of PacBio sequenced plasmids and GenBank obtained plasmids

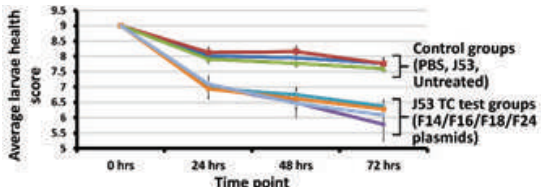

Fig. 3 Line graph showing average larvae health score of each test group over a period of 72 hours

Biography

A young microbiologist who graduated in B.Sc. Biomedical Science and M.Sc. Medical Microbiology, currently a PhD candidate in Department of Microbiology, University of Hong Kong. He focuses his time and effort on antibiotic resistance bacteria, mainly on *oqxAB* carrying *Escherichia coli*. In order to gain a thoroughly understanding, he employed *in vivo, in vitro*, and in silico approaches in his study. He first used *Galleria mellonella* larvae as pathogenicity model in the department, and very likely to be the first in the university. He is continue working on this topic, and currently focuses on determining the environmental reservoir and prevalence of the *oqxAB* carrying *Escherichia coli*, by performing a community-wide surface sampling. In conclusion, he is a scientist in his early stage of career, working his best to achieve as much as he can.

andesl@connect.hku.hk

Sessions

Autoimmune Diseases | Diagnosis & treatment of microbial infections | Medical & Industrial Biotechnology

Session Introduction

Title: **Immuno-informatics design of a multimeric epitope peptide based vaccine targeting SARSCoV- 2 spike glycoprotein**

Onyeka S. Chukwudozie, University of Lagos, Nigeria

Title: **Case report: Primary laryngeal cryptococcosis in an immunocompetent person**

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Immuno-informatics design of a multimeric epitope peptide based vaccine targeting SARS-CoV-2 spike glycoprotein

Onyeka S. Chukwudozie
University of Lagos, Nigeria

Developing an efficacious vaccine to SARS-CoV-2 infection is critical to stem COVID-19 fatalities and providing the global community with immune protection. We have used a bioinformatic approach to aid in the design of an epitope peptide-based vaccine against the spike protein of the virus. Five antigenic B cell epitopes with viable antigenicity and 27 discontinuous B cell epitopes were mapped out structurally in the spike protein for antibody recognition. We identified eight CD8+ T cell 9-mers along with 12 CD4+ T cell 14-15-mer as promising candidate epitopes putatively restricted by a large number of MHC-I and II alleles respectively. We used this information to construct an in silico chimeric peptide vaccine whose translational rate was highly expressed when cloned in pET28a (+) vector. The vaccine construct was predicted to elicit high antigenicity and cell-mediated immunity when given as a homologous prime-boost, with triggering of toll-like receptor 5 by the adjuvant linker. The vaccine was characterized by an increase in IgM and IgG and an array of Th1 and Th2 cytokines. Upon in silico challenge with SARS-CoV-2, there was a decrease in antigen levels using our immune simulations. We therefore propose that potential vaccine designs consider this approach.

Figure 1: In silico cloning of the final vaccine construct into pET28a (+) expression vector where the red part indicates the coding gene for the vaccine surrounded between EagI-NotI (166) and SAlI (1838) while the vector backbone has shown in a black circle. MCS represents the multiple cloning site.

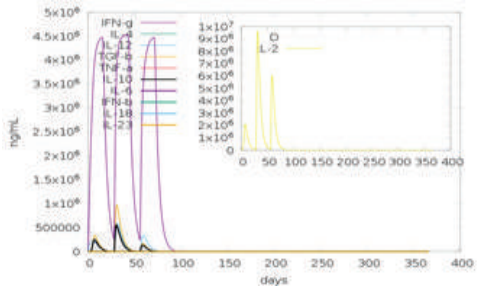

Figure 2: Concentration of cytokines and interleukins. D in the inset plot is danger signal

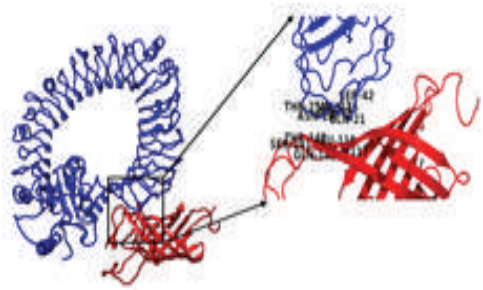

Figure 3: The molecular interaction of the vaccine and TLR5 receptor. The vaccine chain is highlighted in red and the toll like receptor in blue.

Biography

Onyeka Chukwudozie is a young researcher in the field of bioinformatics, computational biology, and immunology. He obtained a first-class degree in Cell Biology and Genetics, before his huge diversion into computational modeling of biomolecules for disease studies. He has published in several international reputable journals and won awards and fellowships. Given his expertise, he has vast experience in viral studies, where he has adequately studied the genomics, transcriptomics, and proteomics characterizations of viruses such as Ebola, Lassa, and the current coronavirus. At the age of 23, he had his first sole author publication, where he adopted and applied sophisticated computational pipelines in deciphering the Ebola virus host-pathogen relationships. He has won several international awards and travel fellowships to present his prestigious research works.

solomononyeka84@gmail.com

Case report: Primary laryngeal cryptococcosis in an immunocompetent person

Beenish Syed, Sadia Amir and **Siddiqa Saeed**
Liaquat National Hospital, Karachi

Statement of the Problem/Background: *Cryptococcus spisencapsulated* yeast, found in the environment and bird excrement. Cryptococcal infections are uncommon in immunocompetent patients and Primary Laryngeal cryptococcosis is a rare condition. Inhaled corticosteroiduse is the most common predisposing factor, causing localized immunosuppression and disruption of laryngeal mucosal barrier. We present here a case of Primary Laryngeal Cryptococcosis in a patient on prolonged inhaled steroids.

Case discussion/report: A 71 year's old male, known case of hypertension and asthma presented with complaints of hoarseness of voice for 5 months, progressively increasing, painless and ultimately leading to aphonia.He was taking inhaled corticosteroids for last 15 years. Physical examination showed no swelling or enlarged lymph nodes in the neck and oropharynx was also normal on gross examination. Patient was evaluated with fibreoptic laryngoscopy (FOL) which showed bilateral irregular thickened, swollen vocal cords with granulation tissue. Histopathology showed:Rounded narrow based budding yeast with thick capsule on PASD stain suggestive of *Cryptococcus*. HIV serology was negative. Serum cryptococcal antigen titers were raised (1:4). Patient was started on oral Fluconazole 400 mg once daily. Dose of inhaled steroids was reduced. Patient responded to the treatment with improvement in his voice after 4 weeksand cryptococcal antigen titers were reduced to 1:1. No neurological involvement was found on further investigations.

Conclusion: Use of inhaled steroids for prolonged periods is a significant risk factor for laryngeal cryptococcal infection. Fiberoptic larnygoscopy and histopathological examination with appropriate staining enables accurate diagnosis. Treatment with oral antifungal agents, most commonly high dose oral fluconazole is shown to be effective. Prolonged duration with minimum of 6-8 weeks is generally required. Surgical treatment may be necessary if indicated. No guidelines exist in literature whether these patients should be followed clinically or with repeat FOL to document resolution of lesions.

Biography

Beenish Syed is an Infectious Disease specialist based in Karachi, Pakistan. She did her post-graduate training in Internal Medicine (FCPS) in 2014 and then in Infectious Diseases (FCPS) in 2017. She is currently working as Assistant Professor and Infectious Diseases Consultant at Liaquat National Hospital, Karachi, one of the leading undergraduate and post-graduate training institutes in Karachi, Pakistan. She is an integral part of Infection Control and Antimicrobial Stewardship committee at her institute.

bnishsyed@yahoo.com

Association of DNA methylation In peripheral blood With diagnosis and treatment of gynaecological cancers

Karunyadevi Jairaman, Janani Balraj, Vidhya Kalieswaran and **Angayarkanni Jayaraman**
Bharathiar University, India

Epigenetic changes such as DNA methylation act to regulate gene expression in normal mammalian development. Much more of the genome is generally subjected to undermethylation rather than overmethylation. The relationship of DNA methylation to tumorigenesis is important to be considered in the light of cancer therapies involving decreasing DNA methylation. All women are at risk of gynaecological cancers and probability increases with age. When gynaecological cancers are found early, treatment is more effective. Cancers of the female reproductive tract and breast has a high incidence among Indian women. Aberrant DNA methylation at CpG islands, often in close proximity to transcription start sites, is associated with the epigenetic regulation of genes through altered transcription factor binding and chromatin structure. The CpG islands display tumour-specific patterns of aberrant methylation, whereas selected CpG islands have been reported to show stage-specific patterns of aberrant methylation. Loss or altered expression of certain genes has been associated with the pathogenesis of a variety of cancers. As cancer cells cannot live without oxygen they send out signals such as angiogenic factors to encourage new blood vessels. The blood collected from cancer patients can have biomarkers and it can be further screened which will be non-invasive method to screen cancer at initial stage instead of biopsy method. Therefore the aim of the present study is to investigate the methylation status and significance of such genes in gynaecological cancers and to determine the association between gene promotor methylation with clinico-pathologic features. Overall This study is to identify a novel epigenetic biomarker for gynaecological cancer.

Key words: Epigenetic, Methylation, CpG islands, Gynaecological, Angiogenic, Biomarker

Biography

J.karunyadevi is a PhD Research Scholar of Cancer Therapeutics laboratory in the Department of Microbial Biotechnology at BharathiarUniversity, India.

karuns2112@gmail.com

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Janani Balraj, Santhosh Manikandan K, Karunyadevi Jairaman, Vidhya Kalieswaran and **Angayarkanni Jayaraman**
Bharathiar University, India

Actinobacteria has its own brand in the field of life sciences for its metabolites and its by-products. The metabolites from actinobacteria isolated from various sources has predominant role in various industries especially in pharmaceutical industries. Polyketides have been proved to be one potent anticancer drug and it is still under development to enhance its potential for various needs. Polyketides are present in various organisms but still, from actinobacteria has some novelty in it. Tracking the role and the applications of polyketides from actinobacteria could reveal novel conceptual strategies for our needs. In the scenario of 21st century bioinformatics tools have been a time saving and most valuable in drug discovery and its elucidation. Polyketide synthase gene from various actinobacterial strains were selected and subjected to homological verification. There are three different PKS gene was widely seen and among the three different variant, PKS II gene was widely noted among actinobacterial strains. The antibiotic metabolite from the potent strain was mapped with the PKS gene cluster to study the structural variations. Further the variations among the structural comparisons traced, the genetic profile of the PKS gene was noted which in turn studied further to use this potent strain as a biotransforming organism for industrial scale up process.

Key words: Antimetabolites, Polyketide synthase, Biotransformation.

Biography

Janani got her B.Sc. Biotechnology Degree at P.S.G. College of Arts & Science, India. She did her M.Sc Industrial Biotechnology at Bharathiar University, India. She has undergone training for Mushroom Cultivation and Vermicompost, Tamil nadu agricultural university, India. She is the Project Assistant under DST-SERC project at Bharathiar University, India.

jananibiotech12@gmail.com

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Poster

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Linking the metabolic pathways of *Escherichia coli* with virulence by altering glucose availability, inhibiting the acetyl-CoA carboxylase gene *accA* with asRNA, and through the quantification of *luxS*

Tatiana Hillman
TheLAB, Inc., United States

The present study determines to confirm a link between the metabolic pathways of bacteria and virulence. Commensal bacteria convert ingested D-glucose into short-chain fatty acids and long- chain fatty acids. The long-chain fatty acids are produced for plasma membrane and biofilm construction. The genetic activity of accA produces the acetyl-CoA carboxylase enzyme needed for long-chain fatty acid elongation. In this study, Luria broth liquid cultures of Escherichia coli were enhanced with Dglucose. The 15 mM glucose sample yielded 4,210 ng/µL of accA as compared to 196 ng/µL for the control. The gene accA was inhibited with antisense RNA with a qPCR gene copy number of 63. The inhibition of accA suppressed the expression of the luxS gene. The luxS gene is vital for transferring intercellular quorum-sensing signals through its increasing the synthesis of autoinducer-2. Bacterial cells that expressed antisense inhibition of accA were more susceptible to antibiotics. The purpose of the study is to advocate for an antibiotic design that targets bacterial metabolic genes and enzymes. An antibiotic design that inhibits bacterial metabolism may help to overcome the issue of bacterial antibiotic resistance..

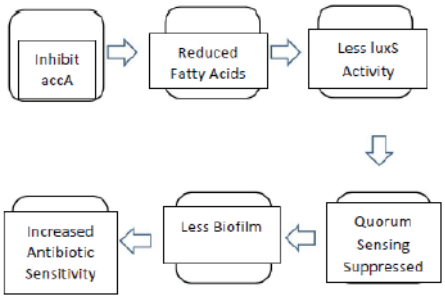

Figure 1: The flowchart shows the effects of inhibiting a bacterial metabolic gene, accA. Inhibiting accA reduces long chain fatty acid formation, suppresses luxS, which then lowers dissemination of quorum sensing signals. The luxS gene is responsible for releasing QS signals in the form of autoinducer-2 that controls biofilm formation and other virulent factors. Suppressing luxS lessens the consistency of biofilm. As a result, the antibiotic sensitivity was increased in mutant E. coli cells that expressed accA inhibition

Biography

Tatiana Hillman conducts research as an independent scientist for the biotechnology company, TheLAB INC., located in Los Angeles, California. She has expertise in the study of synthetic biology and genetic engineering. Her research focuses on the microbiome and its link to our overall health. She is interested in finding and discovering more complex and specific networks within the microbiome of the large gastrointestinal tract. In the future, she hopes to demonstrate the immense potential of genetically rewiring these intricate gut microbiome networks that may improve many health conditions.

thillman@usc.edu

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Molecular typing Of *Azadiracha indica* And *Ocimum gratissimum* resistant pathogenic isolates from Sabe in Oke-Ogun

Adeoti Olatunde
The Oke- Ogun Polytechnic Saki, Nigeria

The aim of this study was present the molecular typing of bacteria which were resistant to extract of the leaves of Ocimum gratissimum and Azadirachta indica and to investigate whether there was any relationship between non-sensitivity to antibiotics and plant extract to the test organisms. Four solvents used were Ethanol, N-Hexane, Water, Ethanol and Water combined in five different concentrations. The soil was serially diluted and isolates subjected to biochemical tests and subsequently to Polymerase Chain Reaction (PCR) and Sanger sequencing method. Two Gram negative bacteria; Pseudomonas aeruginosa (KF530797) and Pseudomonas monteilii (KJ676707) identified were subjected to BLAST from NCBI database. The two plant extracts were tested on Escherichia coli and Salmonella spp which was earlier isolated from milk and water respectively. There was no zone of inhibition as observed in all concentrations of plant extract except a noticeable clear zone of inhibition against synthetic antibiotics in the order of Ofloxacin and Gentamycin. Although suspected gene markers from the two soil isolate were suspected to be amplified around 1400bp. Conversely the two soil isolates could have conferred resistance genes on Escherichia coli and Salmonella spp through Horizontal-Gene-Transfer mechanism thereby rendering the two local plant extracts as unusable as antibacterial agents.

Keywords: Pseudomonas monteilii, BLAST, Antimicrobial, Horizontal-Gene -Transfer, Gene Markers. Abbreviations:

BLAST: Basic Local Alignment Sequence Tools

txy23m@yahoo.com

Graphene based nanocomposite and its application in biotechnology

Alexander Seifalian and **Mazaher Gholipourmalekabadi**
NanoRegMed Ltd, UK

The world advancing rapidly in the field of technology, a simple example is our mobile phone. However, when compared to healthcare, the diagnostic and treatment of diseases are still very poor, and surgery has not changed significantly compared with 50 years ago.

There is plenty of news in academia/media that everything could be diagnosed and cured, but in reality, the invention has been tested in rodents and has not moved to human. This is due to; the complexity of the medical devices developed in a university research environment, the lack of difficulty taking devices to the clinical setting, as well as the positive outcome obtained from in vitro and rodents may not transferable to human. Therefore, need going back to the drawing table and rethink to build medical devices that; commercially feasible, reliable, sensitive, repeatable and non-toxic and biocompatible.

The potential for using advanced/smart nanomaterial and consequent research to replace damaged tissues has also seen a quantum leap in the last decade. In 2010, two scientists in the UK isolated a single layer of carbon atoms on scotch tape. Graphene considers as a wonder material, it is the strongest material on the planet, an order of 100 times stronger than steel, super-elastic and conductive. The functionalized graphene oxide (FGO) is non-toxic and antibacterial. FGO has been used for drug and gene delivery, development of biosensor or in nanocomposite materials development of human organs.

a.seifalian@gmail.com

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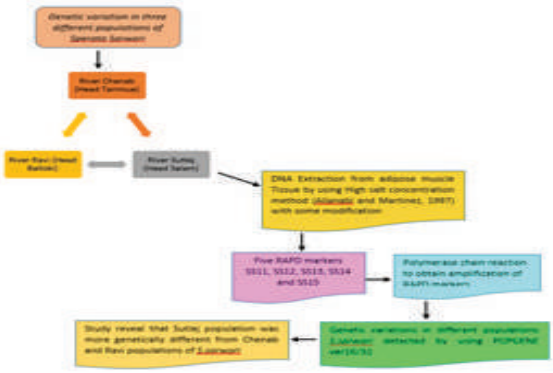
Genetic variations and phylogenetic relationship among different populations Of fresh water catfish Sapreta sarwari in Punjab Pakistan through RAPD PCR

Asma Aziz and Muhammad Ahmad Raza
Uhs, Pakistan

The Pakistan has geographic and geological diversity. The Indus drainage system consists of Indus river and its related rivers (Chenab, Jhelum, Ravi and Sutlej), and formed the largest drainage system of the Pakistan. The *S.sarwari* is one of the commercially important fish found in the Indus drainage system and its associated reservoir. The aim of the present study was to detect the genetic variations between the different populations of *S. sarwari* and their phylogenetic relationships among population of three different regions. The RAPD technique was used to determine the genetic variations in population of *S. sarwari* collected from three different rivers (Chenab, Ravi and Sutlej). Three populations of *S. sarwari* were collected from the selected areas of River Chenab, Ravi and Sutlej. Five RAPD markers (SS11, SS12, SS13, SS14 and SS15) were produced the 30 scorable bands ranged from 225-1750 bp. The highest polymorphism was found in River Chenab population (90%) and lowest polymorphism was observed in population of River Sutlej (76%). The genetic variability with total heterozygosis (Ht, 0.3522) reveled the lowest genetic variability (Gst, 0.135) with higher level of migration flow (Nm, 3.2033) that showed the movement of a individuals among the species. Cluster analysis showed the significant variation among the riverine populations of *S.sarwari*. The population of River Chenab and River Ravi were closely related while the population of River Sutlej was completely distinct from the other riverine populations of S.sarwari. In the present Study, it was concluded that the highest genetic flow decreased the inbreeding coefficient that help to conserve the population in their natural habitat..



asma.aziz53@yahoo.com

Adapationomen and responses at low pH in the metabolism of *Escherichia coli* in view of gene expressions

Chy Mohammad Monirul Hasan
University of Chittagong, Bangladesh

The major aims of biology to understanding life at a systems level. Escherichia coli is a metabolically versatile bacterium able to respond to changes in environmental factors availability. The effect of pH downshift on fermentation characteristics was investigated in a continuous culture of Escherichia coli at aerobic and micro-aerobic conditions. Regardless of oxygen availability, higher levels of acetate were associated with lower biomass yields and lower glucose consumption rates at pH 5.5 as compared to the observations made at pH 7.0. Observed gene expressions indicated that the down- regulation of the glucose uptake rate corresponded to the down-regulation of ptsG gene expression which in turn was caused by the up-regulation of mlc gene under the positive control of Crp. In accordance with up-regulation of arcA gene expression at acidic conditions, the expressions of TCA cycle-related genes such as icdA and gltA, and the respiratory chain gene cyoA were down-regulated, whereas cydB gene expression was up-regulated. Decreased activity of the TCA cycle caused more acetate formation at lower pH levels. Under micro-aerobic condition, higher levels of formate and lactate were produced at lower pH due to up-regulation of pflA, yfiD and ldhA genes. Meanwhile, lower levels of ethanol were produced due to the down-regulation of adhE gene at lower pH, as compared to the observation at neutral pH. The combined effect of pH and temperature on gene expression was also investigated and observed that decreases in the specific glucose consumption rate were associated with increases in the specific acetate production rate. This type of information is useful for the production of recombinant proteins, bio-molecules, simultaneous saccharification and fermentation (SSF) and strain improvement.

monirbiochem@cu.ac.bd

Prevalence, antimicrobial susceptibility pattern and associated risk factors for Salmonella species and Escherichia coli from raw meat at butchery houses in Mekelle, Tigray, Northern Ethiopia

Haftay Abraha Tadesse
Mekelle University, Ethiopia

Background: Salmonella species and Escherichia coli (E. coli) are important foodborne pathogens affecting humans and animals. They are among the most important causes of infection that are associated with the consumption of contaminated food. This study was aimed to determine the prevalence, antimicrobial susceptibility patterns and associated risk factors for Salmonella species and E. coli in raw meat from butchery houses of Mekelle, Northern Ethiopia.

Method: A cross-sectional study was conducted from January to December 2019. Socio-demographic data and risk factors were collected using a predesigned questionnaire. Meat samples were collected aseptically from the butchery houses and transported using icebox to Mekelle University, College of Veterinary Sciences for the isolation and identification of Salmonella species and E. coli. Antimicrobial susceptibility patterns were determined using Kirby disc diffusion method. Data obtained were cleaned and entered into Statistical Package for the Social Sciences version 22 and logistic regression models with odds ratio were calculated. P-value < 0.05 was considered as statistically significant.

Results: A total of 153 out of 384 (39.8%) of the meat specimens were found to be contaminated. The contamination of Salmonella species and E. coli were 15.6% (n=60) and 20.8%) (n=80), respectively. Mixed contamination (Salmonella species and E. coli) was observed in 13 (3.4 %) of the analyzed. Poor washing hands regularly (AOR = 8.37; 95% CI: 2.75-25.50) and not using gloves during meat handling (AOR=11. 28; 95% CI: (4.69 27.10) were associated with an overall bacterial contamination.

About 100% of the tested isolates were sensitive to ciprofloxacin, gentamicin, Co trimoxazole , sulphamethoxazole, ceftriaxone and trimethoprim and ciprofloxacin, gentamicin and norfloxacine of E. coli and Salmonella species, respectively while the resistance of amoxyclav_amoxicillin and erythromycin were both isolated bacteria species. The overall multidrug resistance pattern for Salmonella and E. coli were 51.4% (n=19) and 31.8% (14), respectively.

Conclusion: Of the 153 (153/384) contaminated raw meat, 60 (15.6%) and 80 (20.8%) were contaminated by Salmonella species and E. coli, respectively. Poor handwashing practice and not using glove during meat handling showed significant association with bacterial contamination. Multidrug-resistant showed in Salmonella species and E. coli were 19 (51.4%) and 14 (31.8%), respectively.

Keywords: Antimicrobial Susceptibility test, butchery houses, E. coli, raw meat, Salmonella species.

hiyab204011@gmail.com

Serum vitamin A and E, copper, zinc and selenium concentrations and their relationship with health outcomes in dromedary hospitalized camels (Camelus dromedarius)

Hany Hassan
University of Sadat City, Egypt

The goals of this study were to measure serum vitamin A (retinol) and E (α-tocopherol) and trace elements concentrations (copper, zinc and selenium) during diseases condition and to determine their association with hematological parameters and immune status of hospitalized camels. A total of 95 dromedary camels [healthy (n=65); hospitalized camels (n=30)] were included in this study. Vitamin A and E concentrations were significantly lower in hospitalized camels than apparently healthy ones (P<0.05). Hospitalized camels had lower concentrations of zinc and selenium compared to healthy camels (P<0.05). Vitamin E, copper, zinc and selenium concentrations were positively correlated with phagocytic activity in hospitalized camels (P<0.05). The likelihood of deficiency of vitamin A and E, zinc and selenium concentrations were significant in female hospitalized camels than males and in young age hospitalized camels < 6 years old compared to old ones (P<0.05). Decreased vitamin A and E and trace elements concentrations were associated with hospitalized camels' phagocytic activity and index. The prevalence of low vitamin A and E, zinc and selenium concentrations were frequent in female hospitalized camels and hospitalized camels of age < 6 years old suggesting severe oxidative stress.

Keywords: Camel, Copper, Selenium, Vitamin, Zinc.

hanyhassan1959@gmail.com

Production of cellulose nanofiber from jute fiber via a facile chemical approach

Gulshan Kumar, Guru Gobind Singh and **Ritesh Kumar**
Indraprastha University, India

In present days, the use of cellulose nanofibers as a filler has grown rapidly due to its unique properties such as biocompatibility, renewability and low cost. In this work, we report a facile and cost-effective technique to extract cellulose nanofibers (CNFs) from jute fiber waste. Jute fibers were directly treated with HNO3-NaNO2 (JF/HNO3-NaNO2)mixtureas well as with NaOH and HNO3-NaNO2 (JF/NaOH/HNO3-NaNO2)mixture successively to extract CNFs. The resulting CNFs were characterized by TEM, UV-Visible spectroscopy, FT-IR, XRD and TGA/DTG. TEM measurement of CNFs obtained from alkali treated fiber further treated with HNO3-NaNO2 mixture had an average diameter of 7-9 nm. While, CNFs obtained from raw jute fibers directly treated with HNO3-NaNO2 mixture had an average diameter of 9-11nm. XRD analysis revealed that the CNFs obtained from alkali treated fibers have higher crystallinity of 63.9% compared to CNFs obtained from raw fibers of 55.5%, respectively. Furthermore, XRD results also revealed that the CNFs obtained from alkali treated fiber shows coexistence of cellulose I and cellulose II type structure, which would be useful for many potential applications.

Keywords: Jute fibers, cellulose nanofibers, morphology,crystallinity, nanocomposite, amorphous region.

gulshandhamija@ipu.ac.in

Studies on antibacterial activity of microbial strains isolated from soil samples

Roxana-MădălinaStoica
National Institute for Chemical-Pharmaceutical Research and Development – ICCF, Romania

Microbial production of secondary metabolites and especially those with therapeutic importance, such as "antibiotics", have been given significant attention worldwide regarding their role in the management of infectious disease. Nowadays, the antibiotic resistance is increasing dramatically and the discovery of new drugs from microbial sources represents a major challenge among the researches. Antibiotics are low molecular-weight molecules produced as secondary metabolites, mainly by microorganisms that live in the soil. Actinomycetes, mainly Streptomyces species, are well-known for bioactive compounds production.

The aim of our study was to investigate the ability of new microbial strains with potential of antibiotics production. The strains were preliminary isolate from soil samples and identified using MALDI-TOF mass-spectrometry as species which belong to the Streptomyces genus. Submerged fermentation was followed for the production of antibiotics and agar disc diffusion assay was done to determine the antimicrobial activity of the crude extract. The active metabolites were tested for antibiotic activity against two human pathogens, Escherichia coli ATCC 8739 and Staphylococcus aureus ATCC 6538 strains.

The results showed a good antibacterial activity with the diameter of inhibition zones more than 25 mm in the case of S. aureus, and more than 15 mm in the case of E.coli, respectively. In conclusion, the isolated strains can represent an important source of antimicrobial bioactive substances, which need to be further explored.

Keywords: Streptomyces, liquid cultures, microbial source, antibiotics.

roxym_stoica@yahoo.com

Detection Of Carbapenem resistant *Enterobacteriaecae* and the comparison Between phenotypic methods and multiplex PCR

Rubhana qadri
SKIMS Medical college, Srinagar

Background: Carbapenem resistant *Enterobacteriacea* (CRE) has created a remarkable health distress. Definitive detection of Carbapenemase producing CRE is the first step in combating this problem.

Objective: To detect and compare CP- CRE both by phenotypic and molecular methods.

Materials And Methods: A total of 52 carbapenem resistant clinical isolates were screened for the presence of carbapenemase genes by routine phenotypic methods like modified hodge test and combined disc test as well by multiplex PCR.

Results: Out of the total 52 meropenem resistant isolates, 35 were modified hodge test positive and 33 were combined disc test positive. 42 isolates were found harbouring one or more than one gene. blaKPC alone was present in 38 isolates, while as blaKPC with blaNDM were present in 1 isolate and blaKPC with blaIMP was seen in 1 isolate. blaNDM alone in 2 isoates, blaIMP and blaVIM alone in none of the isolates.

Conclusion: Accurate detection of carbapenemase producing genes by molecular methods overcomes the problem related to CRE.Though there is no signal method that is ideal for all situations.

Keywords: Modified hodge test, Combined disc test, Multiplex PCR, Carbapenem resistant *Enterobacteriaecae*.

rubhana.qadri@gmail.com

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Assessment of bacterial indoor air quality at Kebbi Medical Center, Kalgo, Kebbi State, Nigeria

Sule Sahabi Manga
Kebbi State University of Science and Technology, Nigeria

Indoor air quality is said to be an important determinant of human health and comfort. The indoor air quality in hospitals has become an important issue nowadays because of the infectious nature of disease agents such Corona virus (COVID -19) and Mycobacterium tubercullosis that may be transmitted through air droplets. Thus, the present study evaluated the indoor air bacterial quality within the study area. Plate settling method was adopted in sample collection in 150mm diameter petri dishes containing nutrient agar. A total of five samples each were collected from four different wards (i.e. Male medical ward, Female medical ward, Pediatrics ward, and Gynecology ward). After the exposure of the plates for 20 minutes, they were then incubated at 370C for 24-48 days. The bacteria isolated were characterized using relevant biochemical tests. The bacterial counts ranged from 1.40x102 to 1.85x103 cfu/AQ1. The bacteria identified included *S. aureus, Streptococus spp, Bacilus spp, Pseudermous aeruginosa , E. coli* and *proteins spp*. *S. aureus* was the most frequently occurred and the least was *E. coli*. All the indoor air environments studied harbored certain number of bacterial species which could be as a result of poor sanitation habits. Consequently, this could lead to the occurrence of nosocomial infections. The study therefore, suggest the frequent fumigation/sanitation of the hospital environment in order to safeguard the health of the populace.

Key words: Indoor, Quality, Sanitation, Bacteria, Infectious.

ssmanga2000@yahoo.com

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Email: contactus@pulsus.com

Address:

Pulsus

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Ph: +44-203-769-1778 | +44 330 808 0214

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