Infectious Diseases 2017

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Scientific Tracks & Abstracts

Day 1

Chandra Shekar Pingili, J Infect Dis Ther 2017, 5:3 (Suppl)
DOI: 10.4172/2332-0877-C1-026

Neuro sarcoidosis masquerading as neuroborreliosis (lymes)

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Background: Medical syndromes often overlap in clinical presentations. Often there is one or more than underlying etiology responsible for the patient's Clinical presentation. We are reporting a patient who was admitted thrice with fevers and joint pains. Lymes IGG was positive. He was discharged home on doxycycline and prednisone suspecting gout. Second admission he was discharged to home on IV ceftriaxone. Patient however was re admitted twice within 3 weeks with cognitive impairment. Lymph node biopsy was positive for non caseating granulomas. Sarcoidosis was the final diagnosis.

Case Report: 74 year old white male was admitted with fever and multiple joint pains. Tmax was 100.5. WBC was 15 with normal CBC. LFTs were elevated. Rest of the labs was normal. Lymes IGG was positive. He underwent extensive rheumatologic and virological evaluation. Sonogram of the abdomen was negative. He responded to IV Ceftriaxone and was discharged home on Doxycycline for 3 weeks and Prednisone taper for a week .He was readmitted within 2 weeks with weakness and confusion. After ruling out multiple etiologies he was discharged home on IV Ceftriaxone suspecting Neuroborreliosis. But he was re admitted with worsening mentation in a week. This time he was diagnosed as case of neurosarcoidosis. He responded dramatically to IV steroids, methotrexate and one dose of infliximab. Patient continues to follow up with the clinic and is now at his base line with no recurrence.

Conclusion: He is one patient where an underlying disabling pathology was missed twice. He is a case of systemic and neurosarcoidosis masquerading as neuroborreliosis. Rarely is a clinical encounter so perplexing.

Biography

Chandra Shekar Pingili is a Director, Division of infectious diseases, Sacred Heart and Saint Joseph Hospitals. Associate Professor of Medicine, University of Wisconsin Madison at Eau Claire, Wisconsin. Actively involved in teaching family medicine residency program and nursing staff. Director of Infectious Diseases at LE Phillips Rehab Center, Eau Claire and Chippewa Falls. Chief Infectious Disease adviser to the Clearwater Care Center, Eau Claire, WI. Chief Infectious Disease adviser to the Dove Health and Rehab Center, Chippewa Falls, WI. Director of Infectious Diseases at Indian Head Medical Center.

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Nichola Ashby, J Infect Dis Ther 2017, 5:3 (Suppl)
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Student nurses, stigma and infectious diseases: A mixed methods study

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Individuals or groups will form impressions of another based upon a series of traits, which may be relied upon when forming behavior pattern towards others. These traits will depict the reception individuals received within healthcare and may depend upon learnt and inherited 'perceived' ideals affecting the working and personal relationships experienced by healthcare workers with a positive diagnosis of infection, predisposing stigma responses to others. A longitudinal exploratory study was undertaken over three years investigating the potential existence of stigmatizing values from student nurses towards positively diagnosed healthcare workers with Pulmonary Tuberculosis (PTB), Human Immunodeficiency Virus (HIV), *Methicillin-resistant Staphylococcus aureus* (MRSA), Hepatitis C and Diabetes type-2, was undertaken. The mixed methods used to analyze data provided an interpretive exploration of the stigmatizing attitudes and values of 482 student nurses undertaking an education program. Interpretation of the findings explored the participants' views at course commencement, midpoint and completion considering variables of education (theoretical and clinical), personal and professional influences. Principle component analysis of the data provided components for three ANOVA's and the within-subjects repeated measures showed little significance between disease groups. Further qualitative data was analyzed to provide interpretation of these results demonstrating the presence of stigma. Therefore, the study recommends the implementation of a longitudinal education model for all healthcare workers, considering disease processes and influencing factors psychologically, socially and physically, which will provide opportunities to reduce the existence of stigmatization for positively diagnosed healthcare workers.

Biography

Nichola Ashby is an Assistant Professor of the University of Nottingham, School of Health Sciences, UK. As a Nurse, she is the lead within the School for Critical Care and Major Trauma. She undertook her PhD at the University of Birmingham and looked at stigma and iatrogenic disease, focusing on healthcare workers attitudes and values towards others within the profession. Her research interests are the perceptions, values and attitudes of healthcare workers towards sepsis and infection. She works actively within national policy development for critical care and major trauma and is a Clinical Expert for the National Institute of Clinical Excellence. She is also a steering group Committee Member for the Royal College of Nursing Critical Care and in Flight Nursing.

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Notes:

Guozheng Wang et al., J Infect Dis Ther 2017, 5:3 (Suppl)
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Roles and mechanisms of DAMPs in sepsis

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Statement of the Problem: The most common pathological change in critical illness is multiple organ failure, which often leads to death. However, the underlying mechanisms are not fully understood. Recently, the secondary hit by cell breakdown products causes great attention.

Methodology & Theoretical Orientation: Both septic animal models and patients with sepsis were investigated. Circulating histones released after cell death, the most abundant damage-associated molecular pattern (DAMPs), were detected and their association with organ injury markers was analyzed. Intervention with anti-histone reagents was carried out to confirm the cause-effect relationship.

Findings: Circulating histones were dramatically elevated in both animal models and septic patients. Their levels were strongly associated with the severity of organ injury, particularly lung and cardiac injury. Using anti-histone scFv or non-anticoagulant heparin could significantly reduce organ injury as well as mortality rates. In addition, histones binding prothrombin initialized coagulation and significantly contribute to dysregulated coagulation leading to disseminated intravascular coagulation (DIC). Extracellular histones could interrupt integrity of cell membrane and cause calcium influx to damage cells, stimulate cytokine release and cause cardiac arrhythmia.

Conclusion & Significance: DMAPs, particularly histones, play critical roles in sepsis, including inflammation, coagulation activation, and multiple organ injury. This lays a foundation for future anti-histone intervention to reduce the unacceptably high mortality rates of sepsis.

Biography

Guozheng Wang is a Reader in University of Liverpool, UK, focuses on critical care medicine, particularly sepsis, using molecular and cellular approach, animal models and clinical investigation to understand the molecular mechanisms, develop diagnostic and therapeutic tools.

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Hua Zhu, J Infect Dis Ther 2017, 5:3 (Suppl)
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Varicella-zoster virus tissue tropisms and neuro attenuated vaccine development

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Varicella zoster virus (VZV) infection causes two distinct, but related diseases: varicella (chickenpox) following primary infection and zoster (shingles) after reactivation of latent VZV. VZV reactivation causes serious neurological diseases such as, post herpetic neuralgia, myelitis, stroke and giant cell arteritis especially in the elderly. The factors involved in neuronal invasion and establishment of latency are still elusive. In our previous work, we employed a VZV BAC system in order to characterize a comprehensive library of VZV single ORF deletion mutants. We reported 18 ORFs to be fully dispensable in melanoma cells, which we postulated to encode elements responsible for specific tissue tropism. We now demonstrate that screening of these 18 dispensable gene mutants in differentiated neurons led to the identification of ORF7 as a neurotropic factor. This finding adds to our previous report that ORF7 is also a skin tropic factor. ORF7 is a virion component localized to the golgi compartment in infected cells, whose deletion causes loss of polykaryon formation *in vitro* and severely impairs viral spread in human nervous tissue *ex vivo*. Molecular mechanism of ORF7 in tissue tropism and pathogenesis are under investigation. Furthermore, ORF7 is required for VZV replication in xenografts of human skin and dorsal root ganglia in a SCID-hu mouse model. We showed that an ORF7 deletion virus is able to infect dendritic cells, which in turn can infect T cells. This unique set of characteristics lends an ORF7 deletion mutant the potential to become an excellent VZV vaccine candidate. This neuro attenuated vaccine would cause neither the primary chickenpox nor the secondary herpes zoster diseases. Finally, given that ORF7 is essential for VZV initial infection of neurons and replication therein, it may also be a critical trigger of reactivation from latency.

Biography

Hua Zhu has obtained his PhD degree from Columbia University and completed his Post-doctoral studies from Princeton University. He has been working on herpesviruses for over 20 years. He started with studying human cytomegalovirus (HCMV) immediate-early gene function. He performed pioneer works on global cellular transcriptional responses to viral infection using differential display and gene chip technology. One important discovery from these studies is how HCMV infection activates large numbers of interferon-stimulated genes. Later, he applied the bacterial artificial chromosome (BAC) technology to study HCMV and varicella zoster virus (VZV) gene function, tropism and pathogenesis. He is one of the first to construct for HCMV and VZV BACs. He also used humanized mouse model and luciferase assay to study viral replication *in vivo*. He was first to discover VZV neurotropic factor which leads to a novel neuro-attenuated VZV vaccine candidate developed. He has published over 70 research articles, reviews and book chapters.

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Chris Whiteley, J Infect Dis Ther 2017, 5:3 (Suppl)
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In vivo, in vitro interaction of silver nanoparticles with leucine amino peptidase from human and *Plasmodium falciparum*

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Statement of the Problem: There is increasing requirement for the development of new drug protocols against malaria, a fatal disease caused by the lethal parasite *Plasmodium falciparum*. Leucine aminopeptidase (PfLAP) of *Plasmodium falciparum* is being pursued as a promising target for the discovery of novel antimalarials.

Methodology: *Pf*LAP and HsLAP were expressed in *Escherichia coli*, and AgNPs (3-10 nm) characterized by ultra-violet spectroscopy and transmission electron microscopy. The effects of silver nanoparticles (AgNPs) against *P. falciparum* leucine amino-peptidase (PfLAP) and the human homolog (HsLAP) were compared.

Findings: PfLAP indicated a K_m of 694 µM towards leucine-*p*-nitroanilide and a V_{max} of 57.9 µmol.ml^{-1}. min^{-1} while *Hs*LAP had a Km of 1.6 mM and V_{max} of 119.6 µmol.ml-1.min-1. On interaction with AgNPs (670 nM) PfLAP was selectively inhibited (57.1 %; K_i=610 nM) relative to HsLAP (10.8 %; K_i=5.22 µM). The viability of *P. falciparum* parasites was decreased when exposed to silver nanoparticles, with an IC_{50} value of 6.96 µM, compared to an IC_{50} value of 647.7 µM for human HeLa cells.

Conclusion & Significance: Structural differences between the enzyme variants, particularly the orientation and distance of surface Met^{349} in PfLAP and Met^{306} in HsLAP to the zinc binding sites were significant and may allow for selective targeting of *Pf*LAP by AgNPs.

Biography

Chris Whiteley is an Emeritus Professor of Biochemistry at Rhodes University, Grahamstown, South Africa and distinguished Research Professor at National Taiwan University Science & Technology, Visiting International Professor in Enzymology at School of Bioscience & BioEngineering of South China University Technology, Guangzhou, PRC. He served as Visiting Research Scientist at the Department of Chemical Engineering, National Taiwan University, Taipei, Taiwan in 2004 and as Visiting Professor of Biochemistry at Institute of Biomedical Technology, Veterans General Hospital, Yang Ming University, Taipei, Taiwan. He also worked as Visiting Professor of Enzymology & Organic Synthesis at Oregon State University, Corvallis, Oregon, USA and Visiting Professor of Organic Synthesis at University British Columbia, Vancouver, Canada. He is the Executive Member of Royal Chemical Society (London), MRSC (C. Chem), South African Chemical Institute (SACI). He has published 6 chapters in books and has 110 peer-reviewed papers on Biomedical Enzymology and Nanomaterials.

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Hamoud Khalid Alshaya et al., J Infect Dis Ther 2017, 5:3 (Suppl)
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Isolation and characterization of bacterial species from patients with dental caries and caries-free subjects

Hamoud Khalid Alshaya, Khalid Sukhail G Alshammari, Saleh Ahmed Alogla, Carlo L Nazareno, Mohammad Abdulaziz Saud AlJameel and **Ashfaque Hossain**
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Background: The oral cavity harbours a large number of bacterial species as normal flora existing as biofilm. Dental disease such as dental caries results when there is a shift in the balance of bacteria towards pathogenic species within these biofilms.

Objective: The objective of this study was to isolation, identification and characterization of oral bacterial species of patients with dental caries and caries-free healthy control subjects.

Materials & Methods: A standard bacteriological procedures were followed in the isolation of bacteria. The identification of bacteria was carried out using Matrix-Associated Laser Desorption Ionisation–Time of Flight–Mass Spectrometry (MALDI–TOF–MS) (Bruker MALDI Biotyper system). The characterization of bacteria involved in the determination of biofilm forming potential and assessment of synergistic antimicrobial action of manuka honey and gentamicin against the oral species.

Results: A total of 13 bacterial species were isolated from 35 orals samples (10 from patients with dental caries); of which 7 bacterial species have been isolated for the first time in Saudi Arabia. The Streptococcus spp. exhibited varied biofilm-forming potential and response to synergistic antimicrobial activity of manuka honey and gentamicin.

Conclusion: The isolation of 7 bacterial species for the first time from dental caries and caries-free subjects in Saudi Arabia warrants a larger prevalence study involving molecular and phenotypic tests to assess their role in health and disease in Saudi population.

Biography

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Notes:

Ting Li et al., J Infect Dis Ther 2017, 5:3 (Suppl)
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Baofukang suppository promotes the repair of vaginal epithelial cells in response to *Candida albicans*

Ting Li, Xiaoxi Niu, Xu Zhang, Suxia Wang and **Zhaohui Liu**
Peking University First Hospital, China

Statement of the Problem: Vulvovaginal candidiasis (VVC) is an opportunistic fungal infection predominantly caused by *Candida albicans* affecting a significant number of women of reproductive age. The Chinese medicine, the Baofukang suppository is widely used in the clinic for its antimicrobial activity and is therefore of great interest as a potential antifungal drug for the prevention of VVC.

Methodology & Theoretical Orientation: We evaluated the cytotoxic activity of the Baofukang suppository using the VK2/E6E7 vaginal epithelial cell (VEC) line. An ELISA analysis was made to evaluate three kinds of cytokines (Th1, Th2 and Th17 types) and non-B IgG in the supernatants. SEM was conducted to observe ultrastructural changes of VECs.

Findings: When treated with the Baofukang suppository, all of the immunocompetent cytokines and chemokines (e.g., IL-2, IL-4, IL-6, IL-8, and IL-17) by infected VK2/E6E7 cells was statistically up-regulated ($P<0.05$), except IL-4 (11.70±1.82 vs. 14.88±4.72, $P=0.343$) compared to the infected control cells. The secretion of non-B IgG also exhibited the same trend. Our scanning electron microscopy results revealed that C. albicans can invade VECs by both induced endocytosis and active penetration. The Baofukang suppository could effectively inhibit the adhesion, hyphal formation, and proliferation, as well as notably restore the vaginal epithelial cell morphology, viability, and enhance the local immune function of the VECs.

Conclusion & Significance: These preliminary results suggest promising antimicrobial properties of the Baofukang suppository, which may be efficacious as an antifungal therapy candidate via up-regulating Th1 cellular immunity, the Th17-axis of the innate immune response, and the secretion of vaginal epithelial-derived IgG. These combined effects collectively restore the immune function of the infected VECs against *Candida albicans in vitro*.

Biography

Ting Li has her expertise in female genital tract infection diseases.

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V Kattel et al., J Infect Dis Ther 2017, 5:3 (Suppl)
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Immunological non responder's as real or virtual phenomenon

V Kattel, B Pradhan, P Karki, S Rijal, SK Sharma, S Pandey, B Khanal and **Y Agrawal**
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Statement of the Problem: HIV and Hepatitis C viral Infection (HCV) have same mode of transmission. A subset of HIV people on antiretroviral therapy (ART) achieves virological suppression but poor recovery of CD4 cell termed as immunological non-responders. It has been recommended to start HCV treatment in HIV coinfection if CD4 cells are more than 200/ml. Immunological non-responders could be a challenge to initiate HCV treatment especially in limited resources setting.

Case Description: A 24 years intravenous drug abuser male with HCV for last 3 years presented as HIV positive (CD4 - 186/ml) on July 2008. Despite ZDV/3TC/EFV for six months he did not achieve immunological recovery but his viral load was below 400copies/ml. On September 2009 he was presented with fever and constitutional symptoms for two weeks. On examination he was pale, icteric and had hepatospleenomegaly. Investigation revealed that pancytopenia, transaminitis, hepatospleenomegaly, sterile blood culture, normal chest X ray, sputum for acid fast bacilli and PCR for mycobacterium tuberculi negative, negative rK-39, malaria negative. He had CD4 of 156/ml, HIV viral load 72 copies/ml HCV RNA 15600copies/ml. Bone marrow aspiration revealed 3+ Leishmania Donovani (LD) bodies. ARV regimen was changed to TDF/3TC/EFV and tablet Miltefosine 50 mg twice a day for 28 days was initiated. He improved clinically and parasitologically. On April 2010 his second infection of Visceral Leishmaniasis (VL) was treated with injection amphoteracin B. On March 2011 and August 2012 he had third and fourth episode of VL infection and was treated with amphoteracin B plus miltefosine and liposomal amphoteracin B respectively. However the fourth episode was continued with secondary prophylaxis for six months with immunological recovery (CD4 756/ml). On April 2015 his HCV was treated with 12 weeks sofosbuvir and daclatasvir with rapid viral and sustained viral response.

Significance: Immunological non responders might be virtual phenomena.

Biography

V Kattel is the Faculty Member of Internal Medicine and Incharge of Tropical and Infectious Disease Unit at Referral Hospital and Medical School BPKIHS, Nepal. He has been involved in training more than 300 Nepalese Medical Doctors working at remote part of the country on infectious diseases of Nepal as a national expert. He has contributed for the development of national guidelines on outbreak potential infectious disease of Nepal, Management of Kala Azar in Nepal. His fields of interest are HIV/AIDS, acute undifferentiated fever and sepsis.

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Infectious Diseases 2017

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Scientific Tracks & Abstracts

Day 2

Benjamin Lelouvier, J Infect Dis Ther 2017, 5:3 (Suppl)
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Analysis of blood microbiome by highly sensitive 16S metagenomic sequencing: A new tool for diagnosis

Benjamin Lelouvier
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Diagnosis and treatment of bloodstream infection (BSI) will greatly benefit from sensitive and exhaustive molecular methods to detect bacterial DNA in blood, such as quantitative PCR (qPCR) and metagenomics sequencing. Such approaches are already studied with the aim of reducing the turnaround time and increasing the sensitivity of the microbiota detection in suspected BSI. However, this type of molecular diagnosis is greatly complicated by the presence of human DNA and PCR inhibitors in blood, as well as bacterial DNA contaminants present in the environment, reagents and consumables, which dramatically hamper the signal to noise ratio of qPCR and sequencing pipelines. In the course of our investigations into the role of tissue microbiota in cardiometabolic diseases we developed specific optimized pipelines of qPCR and 16S targeted metagenomic sequencing to analyze blood bacterial DNA, despite the technical difficulties associated with this sample type. Using these molecular tools we have demonstrated the existence of a highly diversified blood micro biome in healthy human donors and shown the association between changes in the blood microbiome and liver fibrosis in obese patients. These assays were primarily designed to analyze bacterial DNA in blood and tissue of healthy donors and patients with no infectious disease, and therefore their signal to noise ratios are high and they are also capable of detecting BSI in patients with high sensitivity and at early stages of infection.

Biography

Benjamin Lelouvier received his PhD in Cellular and Molecular Neurobiology from the University Pierre et Marie Curie, Paris VI, France, in 2007. After a Postdoctoral Fellowship at the National Institutes of Health (USA), he joined Vaiomer in 2012. As cellular and molecular biology Group Leader and Head of biomarkers discovery, he developed with his group the molecular tools (16S qPCR and 16S metagenomics sequencing) to study specifically the blood and tissue microbiomes, before becoming Chief Scientific Officer of Vaiomer in 2016. The study of tissue and blood microbiota allows Vaiomer to link intestinal dysbiosis and tissular inflammation for the development of biomarkers and therapeutics in the fields of cardiometabolic diseases, neurodegenerative disorders and chronic infection

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Notes:

Alvarez-Maya Ikuri et al., J Infect Dis Ther 2017, 5:3 (Suppl)
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Whole genome sequencing analysis from bacterial DNA: An attempt to *Mycobacterium tuberculosis* complete genome sequencing

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Statement of the Problem: Tuberculosis is a bacterial disease caused by *Mycobacterium tuberculosis*. This bacterium is known for a high rate of drug resistance, and then tuberculosis is considered a worldwide public disease with high health and economic impact. Statistics in Mexico show that the incidence increases 15% every year, being a major problem due to the persistence. We aim to sequence the complete genome of *Mycobacterium tuberculosis* and subsequently perform bioinformatics analysis to determine possible molecular changes.

Methodology & Theoretical Orientation: The complete genome of a Laboratory *Mycobacterium tuberculosis* strain H37Rv was sequenced using Next-Generation Sequencing (NGS) on the Illumina MiSeq platform. Genome DNA (gDNA) library was constructed using Nextera XT (Illumina) protocol. DNA was fragmented, tagged and selected by size, then sequenced by Illumina MiSeq-NGS platform. For bioinformatics, all sequences with adaptor contamination, duplicate reads or unknown nucleotides were removed by trimmomatic. Clean-filtered reads were mapped to the reference genome from GenBank (AL123456.3) by BWA software. Finally SAMTools software was used for SNP calling, since a resistance anti-tuberculous drug has been associated with SNPs in particular genes.

Findings: Phred quality score in DNA sequencing was calculate (Q45) then this score was assigned to each nucleotide in the generated sequences. The P value was obtained (3.162e-005) and indicated that the genotype GC is very likely to be the true genotype in the sequenced sample. Preliminary results shown that there is a single nucleotide variant (SNV) from G to C at position 3982 in the strain of *Mycobacterium tuberculosis*.

Conclusion & Significance: Mapping between Laboratory strain H37Rv and GeneBank H37Rv (ID 20829) shown at least one SNP in the position 3982. However, this result must to be confirmed using a higher depth reading and a further exhaustive analysis.

Biography

Alvarez-Maya Ikuri is a Researcher at the Center for Research and Assistance in Technology and Design of the State of Jalisco. She holds a Post-doctoral degree in Neurobiology Department, NRC in University of Alabama at Birmingham UAB, Alabama, and USA; and in Department of Virology, Children's Hospital of Eastern Ontario CHEO, Ottawa, Canada. She has published in several indexed journals, attended more than 30 national and international congresses, and has contributed to the training of students in different levels of postgraduation. Her research interest is focused mainly on molecular diagnosis of infectious diseases.

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Prashant Mule, J Infect Dis Ther 2017, 5:3 (Suppl)
DOI: 10.4172/2332-0877-C1-026

In-house real time PCR for the diagnosis and prognostication of invasive fungal infections in a tertiary care cancer hospital

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Introduction: Invasive fungal infections (IFI) have emerged as an important cause of morbidity and mortality in cancer patients. Aggressive chemotherapeutic protocols for treatment resulting in prolonged and profound neutropenia, are the most important contributory factors. Patients with hematological malignancies and those undergoing bone marrow transplantation are at high risk of invasive mycoses and an increase in morbidity and mortality. Blood culture lacks the sensitivity but with the availibility of molecular techniques, the diagnosis of systemic fungal infections has signifacantly improved.

Objectives: To evaluate an in-house real-time PCR for the diagnosis of IFI. To correlate the results of PCR with the EORTC classification of invasive fungal infections (IFI).

Methods: 3 ml of whole blood is collected from patients with suspected invasive fungal infections. Extraction is performed and DNA is detected using SYBR green PCR. The panfungal PCR using primers NL1 and 260R targeting a region of the ribosomal gene followed by species specific hybridization with probes for *Candida* species as well as *Aspergillus* species.

Results: A total of 80 in patients were included in the study from August 2015 to December 2015 at Tata Memorial Hospital. 52 patients had haematological malignancies and 28 patients belonged to the surgical disease management group (DMG). They were classified by the EORTC criteria as proven, possible and probable cases of IFI of the 80 patients, 49 were positive for yeast DNA and 3 were positive for *Aspergillus* DNA.

Discussion: Fungal infections, in neutropenic patients with malignancies do not show characteristic signs and symptoms, making accurate diagnosis difficult. Early recognition is crucial, as the progression of invasive disease from detection to death is typically less than 14 days. Empirical treatment with antifungal agents is initiated in high-risk patients with suspected fungal infection. This is associated with high toxicity and high cost.

Conclusions: The SYBR green real time PCR was useful and sensitive indicator for the detection of fungal DNA. The SYBR Green PCR is found to be a reproducile assay and it is validated for patients with Candidemia.

Biography

Prashant Mule has completed his MD in Microbiology from the Department of Microbiology, Tata Memorial Hospital, Mumbai, India in 2016. Presently, he is working as a Senior Resident in the Department of Microbiology. His areas of interests are Mycology, Molecular Microbiology, Virology and prevention of health care associated infections. He has worked on the evaluation of in house real time PCR for the diagnosis and prognostication of invasive fungal infections in a tertiary care cancer institute in Mumbai.

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Notes:

Pavithra S et al., J Infect Dis Ther 2017, 5:3 (Suppl)
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Epidemiology of hepatitis C virus in Chennai, south India during the year 2014

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Hepatitis C Virus (HCV) is known to cause serious complications such as chronic liver cirrhosis, liver failure and hepatocellular carcinoma. Globally 3% of the population is affected by HCV infection. Tamil Nadu, a southern state of India; accounts for 0.5% of this disease. The present study aims at analyzing the prevalence of HCV infection in different age groups in the population of Tamil Nadu. The samples were received and collected from primary health care, private and government hospitals. A total of 751 HCV susceptible samples were screened for anti-HCV antibodies by ELISA. Among the 751 samples, 41 samples were positive, which was further confirmed by polymerase chain reaction. Our study revealed that pediatric age groups 1-5 and 6-12 were predominantly affected by HCV, with high incidence among males. The statistical analysis student t-test was performed and the distribution was significant across groups. In addition, other epidemiological parameters were also analyzed as a part of this study.

Biography

Pavithra S is a Visiting Scholar in Genetics and Stem Cell Laboratory at University of Pacific, San Francisco, where she is currently researching the effect of Folic Acid in ameliorating hypoxia induced stem cell changes, and its correlation to non-syndromic craniofacial cleft lip and palate. She obtained her medical degree from India, at the culmination of which she was awarded the "Best Outgoing Student" for her academic excellence and research interests. She worked in the Department of Internal Medicine where she treated patients and organized medical camps in rural and underserved areas. She plans to continue her research and provide healthcare as a Physician in the US.

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Notes:

Valentin Trofimov et al., J Infect Dis Ther 2017, 5:3 (Suppl)
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Dual targeting of the host-pathogen interface: Bacterial release and selective cytotoxicity

Valentin Trofimov, Nathalie Deboosere, Okryul Song, Joana Costa-Gouveia, Arnaud Machelart and **Priscille Brodin**
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A critical feature of the Mycobacterium tuberculosis bacillus is its ability to survive within macrophages, making these host cells an ideal niche for persisting microbes. Identifying inhibitors of *M. tuberculosis* intracellular growth from large chemical library has long been hampered by labor-cumbersome techniques. We thus developed a phenotypic cell-based assay relying on automated confocal fluorescence microscopy and adapted it for the high throughput screen of compounds that interfere with the multiplication of *M. tuberculosis* within macrophages. The current project is an early drug discovery that uses alternative drug screening strategies and targets previously unexplored biological activities during tuberculosis (TB) infection. The aim of the project is to establish a novel approach within the host pathogen interaction paradigm. The approach is based on identification of the drugs and cellular pathways that trigger active bacterial release form its host into the extracellular space or by specific killing of infected host cells. Both of these strategies can prevent the infection from spreading. Such drugs and pathways might also facilitate the boosting of the immune response and enhance the effect of other conventional antitubercular compounds. To reach our goal we established a high though put assay that uses a host-pathogen system based on human cultivated macrophages and Mycobacterium tuberculosis H37Rv to test the activity of the drugs at the single cell level. Screening will be followed by drug synergy studies with the use of known antitubercular compounds. Subsequently, studying the drug mechanisms of action will be performed with cultivated macrophages.

Biography

Valentin Trofimov has his expertise in high-content and high-throughput drug screening. He aims to help eradication of the threat of tuberculosis worldwide. Tuberculosis (TB) results in the death of millions of people every year. There is a growing threat because of the emergence of multidrug resistant strains. In order to achieve that goal, new effective drugs and efficient TB therapies need to be discovered. He focuses his effort on early drug discovery with a close look at host-pathogen interactions, since in vivo activities, such as intracellular host defense mechanisms, are largely overlooked in drug research.

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Notes:

Osadolor Ebhuoma et al., J Infect Dis Ther 2017, 5:3 (Suppl)
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Socio-economic determinants of malaria transmission risk in KwaZulu-Natal, South Africa: A Bayesian inference approach

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Low socio-economic status (SES) has been suggested to sustain malaria transmission which in turn can propel the cycle of poverty. Thus, a deep understanding of the SES that influences malaria risk is vital because it will guide towards creating policy and strategies that will concurrently help combat malaria transmission, improve socio-economic conditions and strengthen the malaria elimination campaign in KwaZulu-Natal (KZN), South Africa (SA). The main purpose of this study is to assess the relationship between SES and malaria incidence in KZN, SA, using the Bayesian inference approach. Database of demographic/socioeconomic information and clinically confirmed malaria case data aggregated at the local municipality level for 2011 were obtained from statistics SA and the malaria control program of KZN, SA respectively. We used the 2011 dataset (SES and malaria incidence) for this study because it completely covered the study area. The association between SES and malaria incidence was evaluated by employing the Bayesian multiple regression model to obtain the posterior samples via a Markov chain Monte Carlo (MCMC) methodology. The obtained posterior samples reveal that, significant association existed between malaria disease and low SES such as illiteracy, unemployment, no toilet facilities and no electricity at 95% CI. Lack of toilet facilities (OR =20.2; 95% CI = -36.82, 76.0) exhibited the strongest association with malaria disease, followed by lack of electricity (OR=5.252; 95% CI = -52.40, 62.32). This study suggests low SES potentially sustains malaria transmission and burden. As an implication, poverty alleviation and malaria intervention resources should be incorporated side by side into the socioeconomic framework to attain zero malaria transmission. Therefore, the relevant policy makers and departments should stimulate additional sustainable developmental approach that combines both improved malaria intervention resources and socioeconomic conditions, which in turn, will help strengthen the malaria elimination goals in KZN, SA.

Biography

Osadolor Ebhuoma is a Doctoral student at the University of KwaZulu-Natal, South Africa, and teaches geographic information systems (GIS) and remote sensing. His research is aimed at developing spatial and temporal malaria transmission models in KZN, South Africa using malaria surveillance data, remote sensing derived climatic/environmental variables and socioeconomic factors. The expected outcome of his research will be the identification of determinants of malaria transmission in KwaZulu-Natal and the development of malaria forecast models and by applying time series and Bayesian models. His research interests include spatial epidemiology, GIS and remote sensing.

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Notes:

Saleh Ahmed Alogla et al., J Infect Dis Ther 2017, 5:3 (Suppl)
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Prevalence of *UMOD gene* mutation among Saudi patients with kidney failure

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Background: Mutations in the uromodulin (*UMOD*) *gene* lead to a dominant hereditary renal disease, which may ultimately result in kidney failure. Therefore, the aim of this study was to assess the burden of *UMOD* associated renal among Saudi patients with renal failure (RF).

Methodology: PCR amplification of 10 exons (forward and reverse) enclosed in the *UMOD gene* is done on the patient's genomic DNA of 103 Saudi patients with RF.

Results: Of the 103 patients, *UMOD gene* mutation was identified in 10/103 (9.7%).

v *UMOD gene* mutation is relatively prevalent among Saudi patients with RF. Further evaluation of different mutations in this *gene* is important for overall assessment of its role in RF among Saudi population.

Biography

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Notes:

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Scientific Tracks & Abstracts

Day 3

Steve Harakeh et al., J Infect Dis Ther 2017, 5:3 (Suppl)
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Microbiota in relation to obesity among healthy Saudi females

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Background: Obesity has been considered as one of the major modern global epidemics and a risk factor for both cardiovascular diseases (CVD) and diabetes. There is a rapid rise in the rate of overweight and obese people in the Kingdom of Saudi Arabia which has a tremendous impact on health and economic resources. Gut microbiota has lately been a major factor for many metabolic disorders and diseases, including obesity, diabetes, and CVD.

Objective: The aim of this research was to define those specific gut microbiota that are obesity-associated as determined based on mass index (BMI) among healthy Saudi females.

Methodology: 120 healthy females, below the age of 30, with different degrees of obesity were included in this study. All the participants had to fill out a questionnaire concerning their nutritional habits, health conditions and demographics. Their height, body weight, hip and waist circumference were measured and their BMI was determined accordingly. Stool samples were collected and genomic DNA was extracted from our study group. The DNA samples were sequenced using next generation sequencing (MiSeq), sequencing reads were trimmed, analyzed and filtered and assigned to taxonomic units.

Results: The results revealed the existence of different bacteriological groups including *Firmicutes*, *Actinomyces odontolyticus*, *Escherichia coli* and *Ruminococcus obeum* and others. Work is in progress to correlate the prevalence of those bacterial groups with BMI.

Conclusion & Recommendations: The data showed the presence of a variety of bacterial strains and microbiota populations among our study individuals. Bioinformatics data analysis will help to identify certain microbiota marker populations to be associated with different stages of obesity among the female Saudi population. Final goal is an early prediction of obesity and to target those patient groups to treat obesity.

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Notes:

Atul Ratra et al., J Infect Dis Ther 2017, 5:3 (Suppl)
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Non convulsive status epilepticus associated with ertapenem use

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Introduction: Carbapenems are broad spectrum beta-lactam antimicrobials especially useful in infections involving multi-drug resistant bacteria and nosocomial infections. Seizures involving carbapenems are a rare occurrence overall and usually reported with imipenem use rather than ertapenem. Neurotoxicity associated with ertapenem use in a renal transplant patient has not been previously reported. We report a rare case of nonconvulsive status epilepticus associated with the use of ertapenem in a renal transplant patient.

Case Description: A 67 year old Lebanese woman with a history of living-related right renal transplant in 1993 presented with progressively worsening altered mental status for the past three days. She had a baseline creatinin of 2.5 mg/dL at the time and was on chronic immunosuppressive therapy. Patient was discharged three days prior from an outside hospital with a diagnosis of a complicated urinary tract infection (UTI) from ESBL-producing *Escherichia coli* bacteria which was sensitive to gentamicin, carbapenems and amikacin. She was sent home on a 14 day course of intravenous ertapenem therapy. She had completed 7 days of ertapenem therapy at the time of presentation. Patient was continued on her home UTI treatment regimen with 500gm IV ertapenem daily upon admission. Next day of her admission, patient had a witnessed generalized tonic-clonic seizure. On the 3rd day of admission (10th day of ertapenem administration), patient developed nonconvulsive status epilepticus. Ertapenem was at that point discontinued. She remained in status epilepticus for the next 4 days and was monitored with continuous electroencephalography (EEG) in the intensive care unit. She was treated with IV Dilantin, phenobarbital and versed. She responded well to the treatment. Seizure activity eventually diminished over the next 48 hours with intermittent left temporal lobe spikes initially until complete resolution. Patient returned to baseline mentation 9 days after admission and was subsequently discharged to acute rehabilitation.

Discussion: Seizures due to ertapenem use are rare with a reported incidence of 1.8%. Ertapenem is thought to induce seizures and cause encephalopathy by binding to GABA receptors in the central nervous system and lowering the seizure threshold. Ertapenem is predominantly eliminated via renal excretion. Patients with reduced renal clearance are therefore at an increased risk of experiencing adverse events with ertapenem use. Our case highlights that ertapenem use can cause significant neurotoxicity in renal transplant patients and in patients with renal insufficiency. Seizure activity due to ertapenem if not identified early can progress to status epilepticus. Despite renal dose-adjustment, ertapenem has potential to cause seizures especially in such patients. Care must be taken in administration of ertapenem in patients with renal insufficiency and it must be stopped immediately if any clinical signs of neurotoxicity do occur.

Conclusion: Ertapenem has the potential to cause significant neurotoxicity and can induce status epilepticus in patients with prolonged use. Patients with renal insufficiency are especially vulnerable even after renal dose adjustments.

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Darshna Yagnik, J Infect Dis Ther 2017, 5:3 (Suppl)
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Apple cider vinegar (ACV®) displays potent antibiotic activity directly against *Escherichia coli and Candida albicans* and within *in vitro* monocytes exposed to microbes by inhibiting inflammatory cytokine secretion

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Introduction: Extraintestinal pathogenic Escherichia coli (E-coli) are the most frequent cause of blood borne, urinary tract and hospital acquired infections. *Candida albicans* infection can also pose a huge threat especially following transplantation and to immune compromised patients. Globally there has never been a more desperate time for novel anti-microbial agents to target microbes and multi drug resistance from bacterial or fungal associated infections.

Aim: The aim of this study was to investigate the potential anti-microbial effects of ACV®. We used microbial strains: *E. coli* strain 6571, *C. albicans* strain 90828 purchased from ATCC.

Methodology: We tested the effect of commercial ACV® directly on microbial cultures over a 24 hour period, measuring inhibition zones. We also looked at whether ACV® could have an anti-inflammatory effect *in vitro*. This was tested using human blood derived monocytes which were incubated with microbes and AVC®. The collected supernatants were analyzed for pro-inflammatory cytokine secretion by ELISA.

Results: When monocytes were cultured with both microbes they secreted TNFα and IL-1β. ACV® was able to significantly inhibit E-coli growth demonstrated by the results of direct co-culture with each of the microbial inoculums and ACV® in varying concentrations. The zone of inhibition with the addition of ACV® to each of the microbes varied dose dependently ACV® concentration. For *Candida albicans* undiluted ACV® had the strongest effect, whereas on E-coli cultures, the most potent effect was visible at lower dilutions including 1/1000 dilution of the neat solution ($p<0.05$). When monocytes were cultured with both microbes they secreted inflammatory cytokines (TNFα, IL-1β) ACV® was effective in significantly inhibiting inflammatory cytokine secretion in human peripheral blood monocytes cultured with *E. coli* and *Candida albicans*

Conclusion and significance: ACV® displayed potent anti-microbial and anti-inflammatory activity against *E. coli* and *Candida albicans*. We propose that ACV® could be potentially therapeutic in cases of antibiotic resistance and sepsis.

Biography

Darshna Yagnik is a Lecturer of Immunology and Biomedical Sciences at Middlesex University. Her research is based on human *in vitro* models of mononuclear cell differentiation and their role in inflammatory pathways and particularly the resolution phase of inflammation.

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Notes:

Safaa AbdElmoneim Mohamed Fadlelmoula et al., J Infect Dis Ther 2017, 5:3 (Suppl)
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Hepatitis B vaccination coverage rate and its barriers among nursing students as high risk group to percutaneous injuries Khartoum, Sudan 2016

Safaa AbdElmoneim Mohamed Fadlelmoula, Alshima Shihabaldeen Ali Siddig, Shahd Khalid Elkhalil, Safaa Jabber Allah and **Sanaa Hassan**
Sudan

Background: Hepatitis B is a global health problem which can cause lifelong infection, cirrhosis, liver cancer, liver failure, and death. According to WHO there is more than 350 million suffering from hepatitis B chronic infection worldwide. Sudan is a country with high HBV endemicity, according to CDC the prevalence of HBV chronic infection was reported to be(5% to 6%) in the general population , and 26% in the hospital outpatient. Hepatitis B is an important occupational hazard for health care personnel; however it can be prevented by the safe and effective vaccine with success rate of 95%. This study aimed to evaluate the hepatitis B vaccination coverage, barriers of complete vaccination, and immunization status after the vaccination among nursing students in Khartoum locality, as a high risk group to percutaneous injuries

Methods: Cross sectional institutional based study conducted among nursing students in three nursing schools in Khartoum locality with sample size of 261 using stratified random sampling. Data collection was carried out using pretested self-administered questionnaire.

Results: 80% of respondents were females and 12% were males with mean age of 22 years. More than 80% knew that percutaneous injuries carry the risk of HBV transmission, about 23% of the participant suffered a needle stick injuries, however Only 41% of the students were fully vaccinated and only 10% of them checked the anti-HBs Ag titer after vaccination. The major reasons reported by the participants were being busy and unavailability of the vaccine in a nearby facility where they searched.

Conclusion & Recommendations: The vaccination rate was found to be low, the awareness of importance of hepatitis B vaccination should be raised, complete hepatitis B vaccination should be provided to all nursing students, and good response to the vaccine should be evaluated before starting clinical training.

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