Beyond Sciences Initiative

4th International Remote Conference: Science & Society

February 9 & 10, 2019.

PARTICIPANT BOOKLET

CANCER

CHRONIC DISEASES

GLOBAL HEALTH

BIOTECHNOLOGY

Thank you to our sponsors:

TRINITY COLLEGE
IN THE UNIVERSITY OF TORONTO

BioLegend®

HARVARD
INFECTIOUS DISEASES CONSORTIUM

Immunology
UNIVERSITY OF TORONTO

Janice Wright LL.B.

Beyond Sciences Initiative

Contents

Welcome Address

Dear Colleagues and Friends,

It is with pleasure that we extend a warm welcome to all participants of the 4th International Remote Conference: Science and Society, hosted by the Beyond Sciences Initiative (BSI).

This meeting will connect research scientists, educators and trainees around the globe - representatives from over 58 different countries. We look forward to hearing about scientific advances from our local and international colleagues, including the social, cultural and political contexts in which they conduct their academic activities.

Our scientific program is once again notably interdisciplinary and comprehensive, with specific foci on global health, cancer, chronic diseases and biotechnology. Our goal is to enable high caliber discussions surrounding research and community activities in order to foster international collaboration.

On behalf of members of Organizing Committees from BSI chapters around the globe, we thank you for your participation in our 4th International Remote Conference. We anticipate that this Conference will provide the impetus for ongoing collaboration and networking.

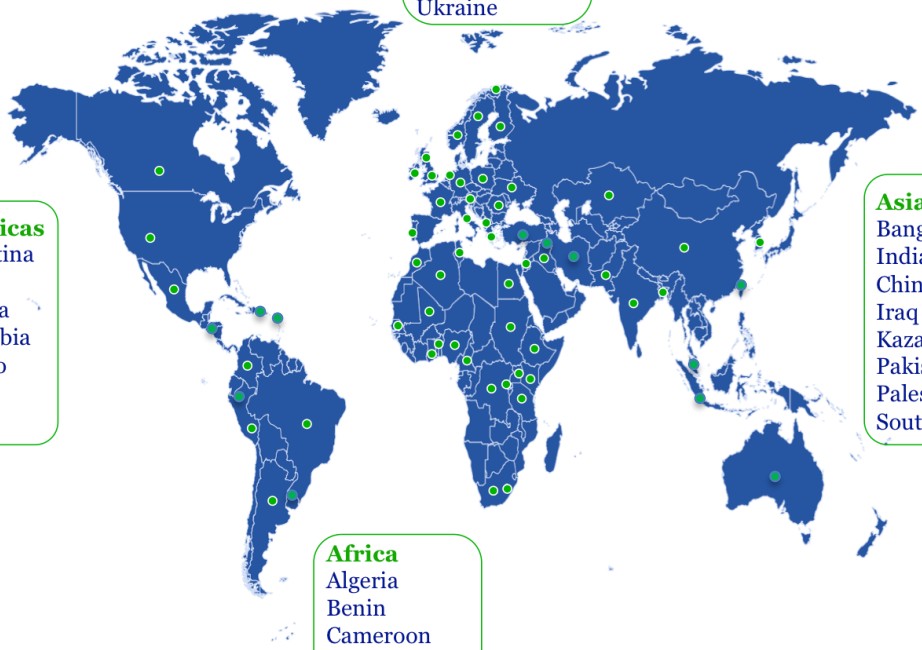
Sincerely Yours,

The BSI Executive Team

Welcome to Our Global Participants

Europe
Albania
Austria
England
Finland
France
Germany
Greece
Ireland
Italy
Norway
Poland
Portugal
Romania
Scotland
Sweden
The Netherlands
Ukraine

Cyprus
Turkey



Bolivia
Dominican Republic
Ecuador
Honduras
Puerto Rico
St. Kitts
Trinidad and Tobago
Uruguay
Venezuela

Americas
Argentina
Brazil
Canada
Colombia
Mexico
Peru
USA

Asia
Bangladesh
India
China
Iraq
Kazakhstan
Pakistan
Palestine
South Korea

Australia
Indonesia
Iran
Israel
Lebanon
Malaysia
Nepal
Philipines
Sri Lanka
Taiwan
Vietnam

Africa
Algeria
Benin
Cameroon
Congo
Egypt
Ethiopia
Ghana
Kenya
Lesotho
Mali
Morocco
Nigeria
Rwanda
Senegal
South Africa
Sudan
Tanzania
Tunisia
Uganda

Beyond Sciences Initiative

Keynote Speakers

Dr. Stephanie Dougan, Assistant Professor, Cancer Immunology and Virology, Dana Farber Cancer Institute, Harvard Medical School, USA. Stephanie Dougan received her PhD in Immunology from Harvard University where she studied lipid antigen presentation by CD1d and NKT cell development. She then undertook a postdoctoral fellowship with Hidde Ploegh at Whitehead Institute, where she employed somatic cell nuclear transfer and embryo manipulations for the purpose of generating transnuclear and CRISPR genome-modified mice. Dr. Dougan joined the faculty at Harvard Medical School and Dana-Farber Cancer Institute in 2014, where her lab uses unique mouse models to study the immune response to tumors. She is particularly interested in tumors that do not induce a CD8 T cell response at baseline, and has been using pancreatic cancer as a model to develop new immunotherapies for non-T cell infiltrated tumors. Dr. Dougan is a Pew-Stewart Scholar in Cancer Research, a Bill and Melinda Gates Global Health Innovation Scholar, a Melanoma Research Alliance Young Investigator, and received a Pathway to Leadership Award from the Pancreatic Cancer Action Network and AACR.

Dr. Thumbi Ndung'u is the Deputy Director (Science) and a Max Planck Research Group Leader at the Africa Health Research Institute (AHRI) in Durban, South Africa. He is Professor and Victor Daitz Chair in HIV/TB Research at the Nelson R. Mandela School of Medicine, University of KwaZulu-Natal. He holds the South African Research Chair in Systems Biology of HIV/AIDS. He is an Adjunct Professor of Immunology and Infectious Diseases at the Harvard T.H. Chan School of Public Health. He is the Program Director of the Sub-Saharan African Network for TB/HIV Research Excellence (SANTHE), a research and capacity building initiative funded by the Wellcome Trust. He graduated with a Bachelor of Veterinary Medicine degree from the University of Nairobi, Kenya, and obtained a PhD in Biological Sciences in Public Health from Harvard University, United States. He was a Postdoctoral Fellow in Virology at Harvard Medical School. He is a member of the Academy of Science of South Africa and a fellow of the African Academy of Sciences. Dr. Ndung'u is on the advisory board of the Global Health and Vaccination Research Programme (GLOBVAC), The Research Council of Norway, and is a member of the External Advisory Board of the HIV Vaccine Trials Network (HVTN).
His research interests are host-pathogen interactions, particularly immune mechanisms of HIV and TB control. He is leading a multidisciplinary team of researchers working in the fields of HIV and TB immunopathogenesis, vaccine development and immune-based HIV functional cure strategies. Dr. Ndung'u also has a special interest in capacity building for biomedical research in Africa.

Keynote Speakers

Dana Philpott is a Professor in the Department of Immunology, Co-Director of the Host-Microbiome Research Network at the University of Toronto and holds a Canada Research Chair in Microbe-Host Interactions in Intestinal Homeostasis. Dr. Philpott undertook her post-doctoral training and then held a Group leader position at the Institute Pasteur in Paris, France. She was recruited to the University of Toronto in 2006. Her research employs animal models of inflammatory bowel disease and considers how innate immunity and the microbiome shape immune homeostasis within the intestine. Dr. Philpott was a Howard Hughes International Scholar (2006-2011) and received the Canadian Society for Immunology Investigator Award (2015) and the Canadian Association of Gastroenterology Research Excellence Award (2017).

Eleanor M. Riley is Professor of Immunology and Infectious Diseases, Director of The Roslin Institute, & Dean for Research, Royal (Dick) School of Veterinary Studies, University of Edinburgh, UK

After graduating from Bristol University with degrees in Cellular Pathology and Veterinary Science, Dr. Riley interned in veterinary pathology at Cornell University and then obtained her PhD in Immunology and Parasitology from the University of Liverpool, UK. After 5 years at the Medical Research Council (MRC) Laboratories in The Gambia, Dr. Riley moved to the University of Edinburgh as a Wellcome Trust Senior Research Fellow, prior to her appointment as Chair of Immunology at the London School of Hygiene and Tropical Medicine in 1998. In September 2017, Dr.Riley moved to the University of Edinburgh to take up the role of Director of the Roslin Institute in the College of Medicine and Veterinary Medicine. Dr. Riley's research focuses on mechanisms of immunity to malaria, how the immune response can contribute to disease, how immunity affects the distribution and transmission of the parasite and how malaria infection affects resistance to other infections. In addition, Dr. Riley has a long-standing interest in the biology of natural killer (NK) cells and their role in resistance to infection. Dr. Riley is a fellow of the Academy of Medical Sciences and has previously served as Strategy Panel Chair at BBSRC and as Deputy Chair of the MRC Infections and Immunity Board. She has recently been appointed to the Governing Council of the MRC.

Online Conference Program: Day 1 (Saturday, Feb. 9, 2019)

Time (EST)	Topic	Speaker
7:00 – 7:15 am	**Opening Ceremony – Introduction and Welcome from BSI**	**Dr. Eleanor Fish,** Univ. of Toronto, Canada
Scientific Session 1: Global Health, Infectious Diseases		
7:15–7:50 am	**Keynote – Malaria and salmonella: it's a neutrophil problem**	**Dr. Eleanor Riley,** Roslin Institute, Scotland
7:55–8:10 am	**Characterization of novel bacteriophages with therapeutic potential against *Staph. aureus***	**Joseph Michael O. Odour,** U. Helsinki and U. Nairobi, Finland/Kenya
8:15–8:30 am	**Assessment of Meningitis causing bacteria at the Kumasi Central Prison**	**Emmanuel Amewu,** KNUST, Ghana
8:35–8:50 am	**Prevalence of intestinal helminth parasitic infections and associated risk factors among students in Tepi Town, South West Ethiopia**	**Esmael Belachew,** Addis Ababa University, Ethiopia
8:55–9:10 am	**Identification of ARV resistance mutations outside of the drug-target gene**	**Phuong Pham,** NIH, USA
9:10–9:25 am	**Global governance of drug quality: examining the disbanding of the WHO International Medical Products Anti-Counterfeiting Taskforce (IMPACT)**	**Dr. Aria Ilyad Ahmad,** World Health Organization, Switzerland
9:25–9:40 am	**HotDoc: HIV and stigma**	**Atiyya tul Munim, Ian Omoyo, Amara Daniels** Moi University, Kenya
9:40–9:45 am	**Break**	
Scientific Session 2: Global Health, Chronic and Infectious Diseases		
9:45–10:20 am	**Keynote – Prospects and challenges of HIV functional cure following treatment of acute infection**	**Dr. Thumbi Ndung'u,** Univ. of KwaZulu-Natal South Africa
10:25–10:40 am	**Interspecies interactions induce antimicrobial activity**	**Dr. Gleb Pishchany,** Harvard Medical School, USA
10:45-11:00 am	**Reactivation of CMV in patients with sepsis: association of immunological mediators, lab. parameters and clinical manifestations**	**Taylon Felipe Silva,** State University of Londrina, Brazil
11:05–11:20 am	**Immunophenotypic assessment of natural killer cells in chronic rhinosinusitis with and without nasal polyps**	**Patrycja Popowicz,** Poznan Univ. of Medical Sciences, Poland
11:25–11:40 am	**Contribution of TCF7L2- (C/T), KLF14- (C/T) and PPAR-γ2- (C/G) gene polymorphisms in the predisposition to type 2 diabetes in a Cameroonian population**	**Dr. Guewo Fokeng Magellan,** University of Yaounde, Cameroon
11:45-12:00 pm	**Interleukin-33 promotes type 1 cytokine responses in human natural killer cells**	**Dr. David Ohayon,** Cincinnati Children's Hospital, USA
12:05-12:20 pm	**Re-entrant waves demonstrated in human induced stem cell derived cardiomyocytes (hiPSC-CMs)**	**Adrienne Caldwell,** McGill University, Canada
12:20-12:45 pm	**HotDoc: BSI Nairobi at Kabete Rehab Centre** **Hot Doc: Life of a dentistry student from PUMS**	**Esther Anyango** Univ. of Nairobi, Kenya **Jakub Szczupak,** PUMS, Poland

Online Conference Program: Day 2 (Sunday, Feb. 10, 2019)

Time (EST)	Topic	Speaker
Scientific Session 3: Bioinformatics/ Biotechnology		
7:00–7:35 am	**Keynote – The gut microbiome regulates immunity**	**Dr. Dana Philpott,** University of Toronto, Canada
7:40–7:55 am	**Resistance to protease inhibitor in Nigerian HIV-1 isolates**	**Elijah K. Oladipo** Adeleke University, Nigeria
8:00–8:15 am	**Screening *in vitro* targets related to diabetes in herbal extracts from Peru: Identification of active compounds in *hypericum laricifolium Juss*. by offline HPLC**	**Yanymee N. Guillen Quispe,** Hallym University, South Korea
8:20–8:35 am	**Computer-aided skin cancer detection: a novel image processing technique**	**Aimoldir Aldabergen** Suleyman Demirel University, Kazakhstan
8:40–8:55 am	**Progenitor T cells for thymic regeneration and as a platform for genetically engineered T cells**	**Ashton Trotman-Grant** Sunnybrook Research Inst., Canada
8:55–9:10 am	**Comprehensive assessment of large scale patient derived xenografts data**	**Dr. Arvind Mer** University Health Network, Canada
9:15–9:30 am	**Toward computer-made artificial antibiotics**	**Dr. Cesar de la Fuente** MIT, USA
9:35–9:50 am	**HotDoc: Blue Roots Med Tech Accelerator**	**Dr. Helina Kassahun** St. Paul's Hospital, Ethiopia
9:50–10:00 am	**Break**	
Scientific Session 4: Cancer		
10:00-10:35 am	**Keynote – Generating immunity to recalcitrant cancers**	**Dr. Stephanie Dougan** Harvard Medical School and DFCI, USA
10:40-10:55 am	**Loss of IL-10/STAT3 signaling aggravates CD8+ T-cell exhaustion and impedes control of chronic lymphocytic leukemia**	**Dr. Bola Hanna** Harvard Medical School USA/Germany
11:00–11:15 am	**Human cytolytic fusion proteins targeting CSPG4 for the treatment of triple-negative breast cancer**	**Neelakshi Mungra** University of Cape Town, South Africa
11:20 –11:35 am	**The impact of coxibs on Wnt/β-catenin pathway, cell cycle and apoptosis in GBM cells**	**Nastassia Kruhlenia** Poznan Univ. of Medical Sciences, Poland
11:40–11:55 am	**Restoration of microRNA-34a expression decreases cell viability and promotes apoptosis in T-cell acute lymphoblastic leukemia cell line**	**Shiva Najjary** University of Maragheh, Iran
12:00–12:15 pm	**Synergistic checkpoint blockade and cytokine therapy increases γδ T-cell mediated cytotoxicity in murine hepatocellular carcinoma**	**Rutvij Khanolkar** University of Toronto, Canada
12:20–12:45 pm	**HotDoc: Period poverty at Kakuma Refugee Camp** **HotDoc: Reproductive health and education for street adolescents and women in Eldoret, Kenya**	**Bahati E. Hategekimana** **Pavanraj Chana, Atiyya tul Munim** Moi University, Kenya

Instructions for Conference Participants

Quick Instructions

1. Register to join the conference: http://www.beyondsciences.org/conference2019/ .
2. All registrants (**participants & presenters**) will receive an email invitation by **Monday February 4th,** with details of how to join the conference on the conference days. If you have registered but have not received an invitation by this date, please e-mail beyondsciencesinitiative@gmail.com.
3. The invitation email will include the details of the event as well as the option to *accept* or *decline*. Click *Accept* once you are ready to join the conference. Note that the conference "room" will not only start to exist/ be available at the time of the first talk on each day.
4. Enter your name and email address to complete your conference registration. This acts as your "login" for the platform. No additional passwords or info are required.
5. Once you have successfully joined the conference, you may access various features such as the live *chat* and the *status update* (accessed by clicking the smiley icon).

Detailed Instructions

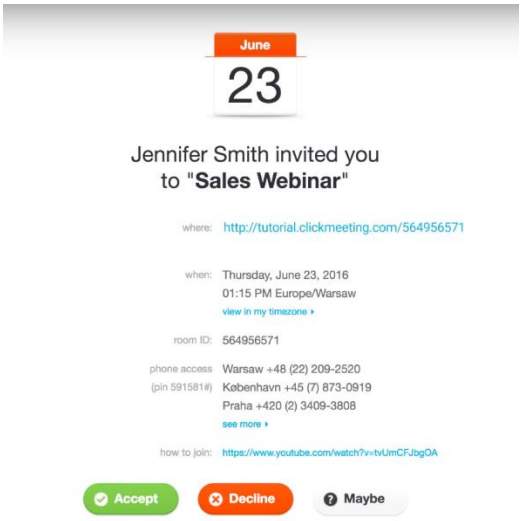
Before the Conference

1. Be sure to have the following up-to-date:
   - Adobe Flash Player
   - Web browser (we have tested Chrome & Firefox)
2. All registrants (**participants & presenters**) will receive an email invitation by **Sunday January 21st, 2019** with details of how to join the conference for the days they have registered. If you have registered but have not received an invitation by this date, please e-mail beyondsciencesinitiative@gmail.com.

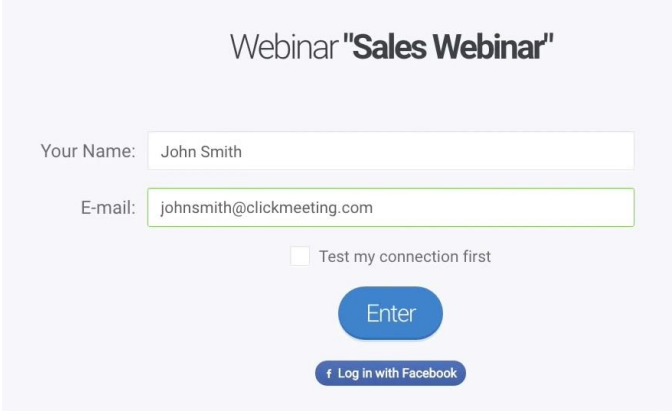
Joining the Conference

1. The email invitation will include details of the event as well as the option to *accept* or *decline*. Choosing *accept* will let us know that you are attending the event and will provide you with a link to the event.

Instructions for Conference Participants



2. Upon clicking this link (on the appropriate conference date) you will be prompted to enter your name and email address to complete your conference registration. You also have the option of testing your connection via the "Test my connection first" checkbox, which might prompt you to download any additional plugins required to utilize the Clickmeeting platform.

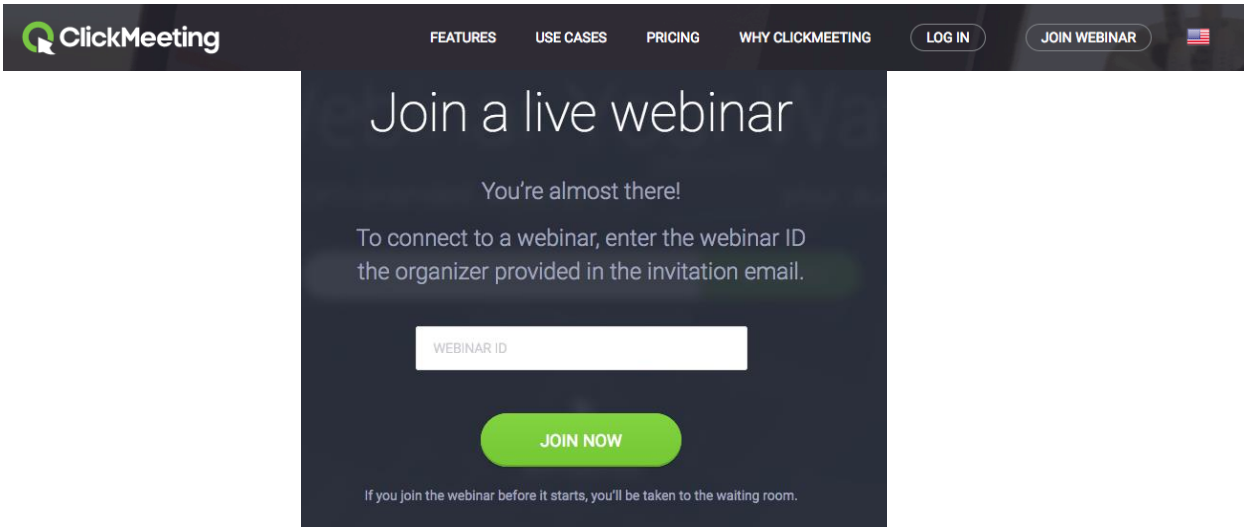


3. Alternatively, you may choose to login via your Facebook account.

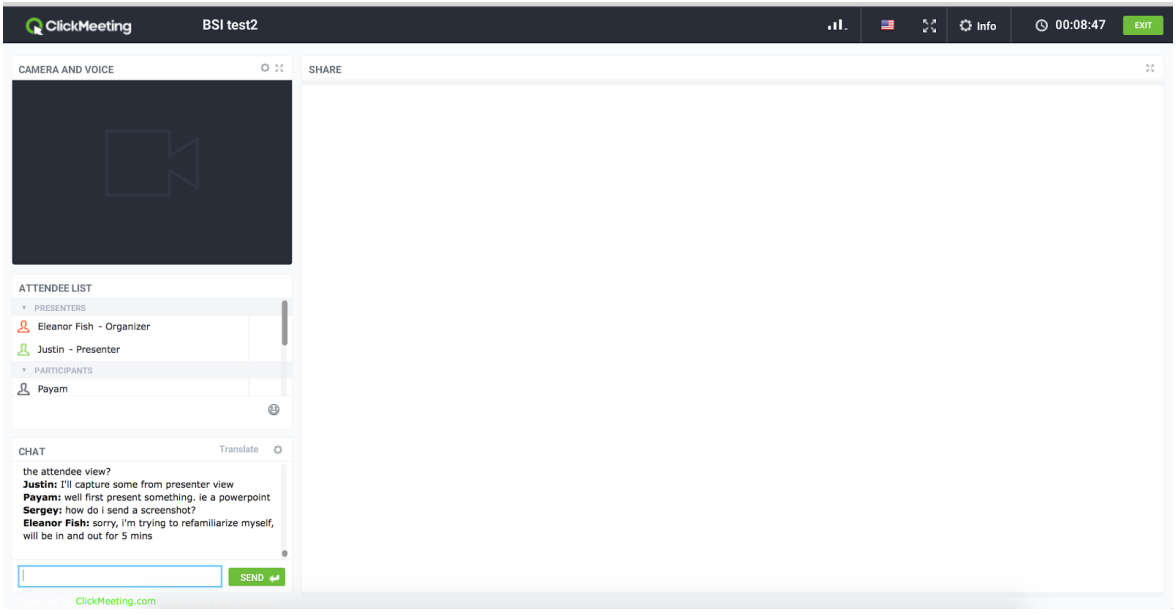
4. For further clarification on the previous three steps, please view the following Youtube video that illustrates the login procedure: https://www.youtube.com/watch?v=N5fp1G4BuZ4

Instructions for Conference Participants

5. For last minute access on conference days, we will be providing a *WEBINAR ID* on our website which may be used to access the conference. First, visit the Clickmeeting website, clickmeeting.com, then clicking the "JOIN WEBINAR" button on the top right of the page, and finally enter the *WEBINAR ID*.



6. Once logged in, you should have a view like this:

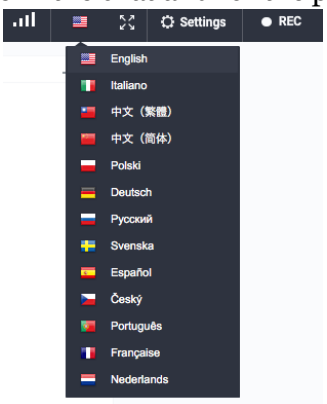


Instructions for Conference Participants

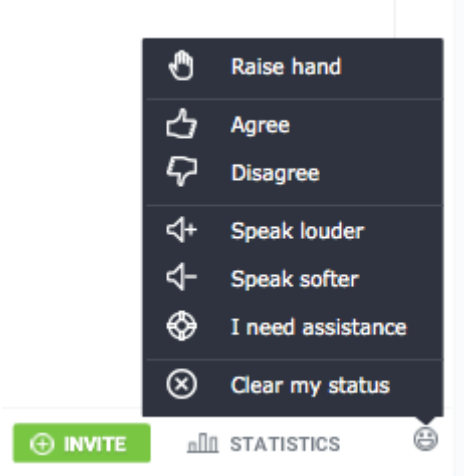
During the Conference

1. During the conference, the *chat* box in the bottom right corner may be used to share your thoughts, or to pose questions for the presenters.

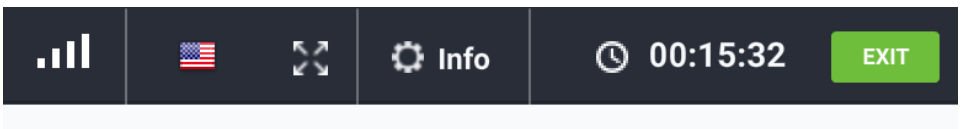
2. The interface language may be toggled by clicking the *flag icon* and choosing a language from the resultant drop-down menu. Note, however, that English will be the primary conversational language in the chat and for the presentations.



3. The grey *smiley* icon may be selected to indicate your status. For example, there exists a *Speak louder* status, which communicates a clear message to the presenter.



4. At any time during the presentation, you may choose to exit via the green *Exit* button. Note that you may access the presentation again, later, via the same link.



BEYOND SCIENCES INITIATIVE

4TH INTERNATIONAL REMOTE CONFERENCE: SCIENCE & SOCIETY

PRESENTER ABSTRACTS

SS1-2: Global Health, Infectious Diseases

Timeslot: 7:55 – 8:10 am

Presenter: Joseph Ochieng' Odour[1,2]
Institution: University of Nairobi, KAVI Institute of Clinical Research, University of Helsinki, Helsinki Finland/Nairobi, Kenya
Co-Authors: Ermir Kadija[4], Saija Kiljun[1], Marianne W. Mureithi[2], Atunga Nyachieo[3], Mikael Skurnik[1, 5]

[1] Department of Bacteriology and Immunology, Medicum, and Research Programs Unit, Immunobiology, University of Helsinki-Finland,
[2] KAVI-Institute of Clinical Research, University of Nairobi-Kenya,
[3] Institute of Primate Research (IPR), Nairobi-Kenya,
[4] University "Luigj Gurakuqi", Shkoder-Albania,
[5] Division of Clinical Microbiology, Helsinki University Hospital, HUSLAB, Helsinki, Finland

Characterization of novel bacteriophages with therapeutic potential against Staphylococcus aureus

Background: Emergence of multi-drug resistant S. aureus is a threat to the public health and global economy. The bacterium is infectious to livestock, pets and humans; with ability to rapidly acquire drug resistance and infections may have high mortality rate. The development of new antibiotics has recently declined to a standstill as many pharmaceutical companies consider it non-profitable. Bacteriophages (phages) are viruses of bacteria and have been used as antibacterial agents for a century in Eastern Europe but ignored in other parts of the world. Use of phages for bioremediation and therapy is considered as a promising alternative as they are environmental friendly and safe. In this study we describe two novel lytic Staphylococcus phages; Stab20 and Stab21.
Methodology: Phages Stab20 and Stab21 were isolated from sewage and wastewater samples of the city of Tirana, Albania, following a standard double agar layer method. A sausage-fermenting S. xylosus strain was used as host bacteria. The morphology, genome, burst size, physico-chemical properties and host range of the phages were then determined.
Results: Transmission electron microscopy and genome analysis showed that Stab20 and Stab21 are novel myovirus phages with genome sizes of 153338 bp and 153797 bp respectively. They are stable at 39 °C, pH range of 5.4 – 9.4, 25 – 50 µJ/cm2 UV radiation and at 50% chloroform. These phages have a burst size is >80. The phages were effective against MRSA and MSSA isolates originating from major hospitals in Helsinki even though they were originally isolated from Albania.
Conclusion: These results suggest that both phages could be potential candidates to be included in phage cocktails for therapeutic and biocontrol purpose.

References

1. Founou, R. C., Founou, L. L. & Essack, S. Y. Clinical and economic impact of antibiotic resistance in developing countries: A systematic review and meta-analysis. PLoS ONE 12, (2017).
2. Busche, T. et al. Comparative secretome analyses of human and zoonotic Staphylococcus aureus isolates of CC8, CC22 and CC398. Mol. Cell. Proteomics mcp.RA118.001036 (2018). doi:10.1074/mcp.RA118.001036
3. Fernandes, P. & Martens, E. Antibiotics in late clinical development. Biochem. Pharmacol. 133, 152–163 (2017).
4. Meaden, S. & Koskella, B. Exploring the risks of phage application in the environment. Front. Microbiol. 4, (2013).

SS1-3: Global Health, Infectious Diseases

Timeslot: 8:15 – 8:30 am

Presenter: Emmanuel Amewu[1]
Institution: Kwame Nkrumah University of Science and Technology, Kumasi, Ghana
Co-Authors: Cynthia K. Adu-Asiamah[1,2], Samuel Terkper Ahuno[1,2], Alexander Kwarteng[1,2]

[1] Department of Biochemistry and Biotechnology, KNUST, Kumasi, Ghana,
[2] Kumasi Centre for Collaborative Research in Tropical Medicine, KNUST, Kumasi, Ghana.

Assessment of Meningitis causing bacteria at the Kumasi Central Prison

Background: Meningitis is an inflammation of the meninges. Asymptomatic colonization of the pharynx and nasopharynx has been identified as the most important risk factor for subsequent invasive disease by several bacterial pathogens. While prisons in Ghana are known to be overpopulated, in addition to other significant challenges with health implications, and thus poses a high risk for transmission of infectious diseases, such as meningitis, colonization of meningitis-causing bacterial remains to be fully characterized

Methods: To this end, a cross-sectional study was conducted with 205 volunteers at the Kumasi Central Prison to assess the pharyngeal carriage and association with years of incarceration. The pharyngeal swabs were plated on CNA agar for isolation of Group A and B streptococcus, Staphylococcus aureus and Streptococcus pneumoniae, and GC agar for the isolation Neisseria species. Positive colonies were sub-cultured for further processing, which included Strept grouping for Group A and B streptococcus, catalase and optochin tests for S. pneumoniae and S. aureus (catalase only), oxidase tests and gram staining for Neisseria spp.

Results: We observed a total carriage of 51.7%, where Neisseria spp. were highest, followed by S. aureus and S. pneumoniae. There was an inverse association between carriage and years of incarceration. Fischer Exact Test showed no significant association between carriage and the following variables years of incarceration (p= 0.914), gender (p= 0.838), knowledge of meningitis (p= 0.728) and nasal congestion (p= 0.469).

Conclusion: Taken together, we showed high carriage of meningitis-causing bacteria among inmates in the Kumasi Central Prisons and a higher carriage among inmates who have been in prison for fewer years. There is the need for further studies to assess the nasopharyngeal colonization of inmates in other prisons and the development of health policies which includes vaccination of at risk inmates.

SS1-4: Global Health, Infectious Diseases

Timeslot: 8:35 – 8:50am

Presenter: Esmael Belachew [1]
Institution: Addis Ababa University, Addis Ababa, Ethiopia.
Co-Authors: Esmael Besufikad Belachew[1], Dagnew Bitew Tarko[1], Yilkal Messelu Wallie[1]

[1] Department of Biology, College of Natural and Computational Sciences, Mizan-Tepi University, Tepi, Ethiopia

Prevalence of intestinal helminthic parasitic infections and associated risk Factors among students in Tepi Town, South West Ethiopia

Intestinal *helminthic* parasites are responsible for considerable morbidity and occasional mortality among infected population all over the world. Their prevalence and specific risk factors was not clearly confirmed especially in African countries including Ethiopia. Based on this fact, the present study was conducted to determine the prevalence and associated risk factors of intestinal *helminthic* infection among students in Tepi town, south west Ethiopia. To conduct this research, we were used a cross-sectional study design. Stool samples were collected from all enrolled students and wet mount and formalin-ether sedimentation concentration procedures were used for each helminthes examination. A total of 380 study participants were included in the study, out of which 94 (24.7%) were positive for intestinal helminthic parasites. The commonest helminthes isolated in this study was *Ascaris lumbricoides* (9.2%) followed by *Trichuris trichiura* (5.8%). Hookworm and Schistosoma mansoni infection were more prevalent among males than females. The binary logistic regression result showed that sex, cleanness of the finger nails, school, family size, protective shoe, and religion were significantly associated with intestinal helminthic infection. The overall prevalence rate of helminthes observed in the present study was 24.7%. The commonest helminthes was A. *lumbricoides* (9.2%) followed by T. *trichiura* (5.8%). General health educations among those risky groups are highly recommended in order to reduce its prevalence and to formulate appropriate intervention.

SS1-5: Global Health, Infectious Diseases

Timeslot: 8:55 – 9:10am

Presenter: Phuong Pham
Institution: National Institutes of Health, Frederick, MD, USA.
Co-Authors: Rachel Van Duyne[1], Eric O. Freed[1]

[1] Virus-Cell Interaction Section, HIV Dynamics and Replication Program, NCI-Frederick, Frederick, MD, USA

Identification of ARV-resistance mutations outside of the drug-target gene

Background: Resistance to antiretrovirals (ARVs) continues to impair the overall quality of life for some HIV-infected individuals, despite the effectiveness of combination antiretroviral therapy (cART). The goal of this study was to explore the ability of HIV-1 to escape inhibition by ARVs in vitro by acquiring resistance mutations outside of the drug-target gene.

Methods: We propagated HIV-1 in T-cell lines and measured virus replication kinetics in the presence or absence of low (sub-IC50) concentrations of ARVs, testing at least one representative of each class of inhibitor. We selected for viral escape mutants exhibiting at least partial resistance to ARVs as indicated by efficient replication in the presence of the inhibitors. A number of analyses were then performed to validate the ability of the selected mutations to confer ARV resistance.

Results: Long-term passage of wild-type virus in the presence of ARVs led to the selection of ARV-escape mutants lacking changes in the target gene, but instead containing substitutions in the envelope (Env) glycoprotein and occasionally in Vpu. We have now identified a panel of partially ARV-resistant NL4-3 Env mutants that arose in the presence of protease, reverse transcriptase, and integrase inhibitors. Mutations were selected in the context of two different T-cell lines, Jurkat and CEM12D7, that favor cell-cell and cell-free transmission, respectively. Remarkably, the same ARV-resistant Env mutant was selected in both cell lines. We extended our analyses to a transmitted-founder, subtype C virus, CH185_TF, which acquired a mutation in Env when propagated in the presence of Dolutegravir (DTG). These data demonstrate that ARV-resistant Env mutants arise in the context of three different T-cell lines and two viral subtypes with different coreceptor tropism. Finally, we found that several of the Env mutation positions are highly conserved within and across HIV-1 clades but that these mutations do appear in patient isolates.

Conclusions: These results demonstrate that mutations in Env can contribute to HIV drug resistance in vitro. A combination of in vitro selections and in vivo analyses is ongoing and may establish a role for Env mutations in ARV resistance in patients and help guide the development of more effective therapies.

SS1-6: Global Health, Infectious Diseases

Timeslot: 9:10 – 9:25am

Presenter: Dr. Aria Ilyad Ahmad
Institution: World Health Organization, Geneva, Switzerland and Institute for Global Health Research, York University, Toronto, Canada.

Global Governance of Drug Quality: Examining the Disbanding of the WHO International Medical Products Anti-Counterfeiting Taskforce (IMPACT)

The globalization of pharmaceutical supply chains has introduced new challenges in ensuring the safety and quality of medicines. To support health systems, particularly in low- and middle-income countries, the World Health Organization (WHO) in 2006 established the International Medical Product Anti-Counterfeiting Taskforce (IMPACT). Despite unanimous initial support from Member States, the activities of the IMPACT were controversially suspended in 2010, and the Taskforce was ultimately disbanded at the 2012 World Health Assembly. Informed by historical and sociological institutionalism, this thesis examines why the IMPACT was disbanded. To this end, I propose a causal mechanism with three interrelated factors based on ideas, interests and institutions. In the first instance, I argue that framing the problem as "counterfeit medicines" invoked the structural and normative domains of intellectual property rights, undermining the public health mandate of the IMPACT, and by extension of the WHO (ideas). Establishing a 'Taskforce' moreover delegated agenda- and priority-setting authority away from Member States, including the accountability mechanisms of the WHO's governing bodies (institutions). Lastly and relatedly, the prevalent role of non-state actors, notably from the pharmaceutical industry and law enforcement agencies, furthermore contributed to a perceived subversion of the IMPACT's public health activities (interests). In other words, I argue that the disbanding of the Taskforce by the World Health Assembly represented a reassertion of the WHO's public health mandate, as well as an effort by Member States to reclaim priority- and agenda-setting authority. This was particularly evident in the abandonment of the "counterfeit" terminology and introduction of an institutionally innovative 'Member State Mechanism' following the disbanding of the IMPACT in 2012. The findings of this case studies have notable implications in global health governance. In addition to illustrating the importance of appropriate problem framing, the story also highlights the contestation of priority- and agenda-setting power within and across institutions, and the explanatory capacity of neo-institutionalist theory in examining how norms and values are contested within inter-governmental organizations.

SS2-2: Global Health, Chronic and Infectious Diseases

Timeslot: 10:25 – 10:40am

Presenter: Dr. Pishchany, Gleb[1]
Institution: Harvard Medical School, Boston, USA.
Co-Authors: Emily Mevers[2], Sula Ndousse-Fetter[1], Dennis J. Horvath Jr.[3], Camila R. Paludo[1,2,4], Eduardo A. Silva-Junior[2,4], Sergey Koren[5], Eric P. Skaar[3], Jon Clardy[2], and Roberto Kolter[1]

[1] Department of Microbiology and Immunobiology, Harvard Medical School, Boston, USA
[2] Department of Biological Chemistry and Molecular Pharmacology, Harvard Medical School, Boston, USA
[3] Department of Pathology, Microbiology, and Immunology, Vanderbilt University Medical Center, Nashville, USA
[4] School of Pharmaceutical Sciences of Ribeirão Preto, University of São Paulo, Ribeirão Preto, São Paulo, Brazil
[5] Genome Informatics Section, Computational and Statistical Genomics Branch, National Human Genome Research Institute, National Institutes of Health, Bethesda, USA

Interspecies interactions induce antimicrobial activity

Background: The rapid emergence of antibiotic-resistant pathogenic bacteria has accelerated the search for new antibiotics. Actinomycetes have been a fruitful source of antimicrobials, however in the past decades the antibiotic pipeline has run dry. Compounded by rapid acquisition of resistance by pathogenic bacteria, acceleration of antibiotic discovery is critical for public health. Traditionally, antibiotics have been harvested from pure cultures consisting of a single species growing under nutrient rich conditions. In contrast, in the environment, bacteria constantly compete and interact with their neighbors tailoring their behavior.

Methods: In an effort to recapitulate the natural environment, we generated a nine-strain actinomycete community and used 16S rDNA sequencing to deconvolute the stochastic production of antimicrobial activity. Activity-guided purification followed by mass spectrometry and NMR analysis was used to characterize the small-molecule antibiotic. Genetic approaches and animal experiments were used to identify the molecular target of the purified molecule and its potential use as a therapeutic agent.

Results: When grown in the presence of other bacteria Amycolatopsis sp. AA4 produces an antibiotic we named amycomicin. Amycomicin is a highly modified fatty acid containing an epoxide isonitrile warhead and is a potent and specific inhibitor of Staphylococcus aureus. Amycomicin targets an essential enzyme (FabH) in fatty acid biosynthesis and reduces S. aureus infection in a mouse skin-infection model.

Conclusions: The discovery of amycomicin demonstrates the utility of screening complex communities against specific targets to discover small molecule antibiotics..

SS2-3: Global Health, Chronic and Infectious Diseases

Timeslot: 10:45–11:00am

Presenter: Taylon Felipe Silva
Institution: State University of Londrina, Londrina, Brazil
Co-Authors: Virginia Marcia Concato[1], Fernanda Tomiotto-Pellissier[1], Manoela Daiele Gonçalves[2], Eliandro Reis Tavares[3], Lucy Megumi Yamauchi Lioni[3], Cintia Magalhães Carvalho Grion[4], Andréa Name Colado Simão[5], Milena Menegazzo Miranda-Sapla[1], Idessania Narazeth Costa[1], Wander Rogério Pavanelli[1], Ivete Conchon-Costa[1]

[1] Laboratory of Immunoparasitology of neglected diseases and cancer - LIDNC, Department of Pathological Sciences, Center of Biological Sciences, State University of Londrina, Paraná, Brazil.
[2] Department of Chemistry, Center of Exact Sciences, State University of Londrina, Paraná, Brazil.
[3] Department of Microbiology, Center of Biological Sciences. State University of Londrina, Paraná, Brazil.
[4] Department of Clinical Medicine, Health Sciences Center, State University of Londrina, Paraná, Brazil.
[5] Department of Pathology, Clinical Analysis and Toxicology, State University of Londrina, Paraná, Brazil.

Reactivation of cytomegalovirus in patients with sepsis: association of immunological mediators, laboratory parameters and clinical manifestations

Background: Sepsis is a pathological syndrome with biochemical abnormalities induced by infection. It is defined as an organic dysfunction with imminent threat to life triggered by a dysregulated host response to an infection. Human Cytomegalovirus (CMV) is a double-stranded DNA virus that can be transmitted by various bodily secretions and fluids. The CMV reactivation has been widely associated with bacterial sepsis, and probably results from the inflammatory process characteristic of this condition, having been described as a factor of worse clinical prognosis, with a significant increase in morbidity and mortality, being directly associated with severe organ dysfunction and hemodynamic imbalance.

Methods: Cohort study conducted with septic patients at the University Hospital of Londrina, Brazil. Anti-CMV IgG and IgM was quantified by ELISA assay. Viral load were determined using real-time PCR technique. Plasma cytokines were quantified by cytometric bead array technique and nitric oxide by Griess method with cadmium. All analyzes were performed on the seventh day after the diagnosis of sepsis. Statistical significance was set at $p<0.05$ for all analyzes.

Results: The overall occurrence of cytomegalovirus reactivation in the cohort was 17.58%. Was observed an increase in plasma levels of NO ($p<0.001$), reduction of percetage of free days of mechanical ventilation ($p=0.008$) and arterial pH (0.036), as well as changes in variables related to coagulation factors, such as reduction of platelet count ($p=0.008$) and increase of activated partial thromboplastin time ($p=0.002$) in the reactivated group when compared with non-reactivated group. There was also a significant increase in plasma of IL-10 ($p<0.001$), creatinine ($p<0.001$), urea ($p=0.027$) and reduction of 24-hour urine output ($p<0.001$). In addition, IL-10 levels ($r=0.910/p<0.001$), creatinine ($r=0.652/p=0.056$) and 24-hour urine output ($r=-0.763/p=0.010$) correlated with the load viral, demonstrating an association between the reactivation process and kidney failure present in sepsis. The reactivated group still had 2.1 times the risk of developing septic shock (RR 2.1; 95% CI 1.4 to 3.1; $p=0.012$) and an increase in the mortality rates with 28 ($p=0.026$) and 180 days ($p=0.039$).

Conclusion: CMV reactivation may increase mortality rates among septic patients; our data suggest that IL-10 and NO are involved in this process.

SS2-4: Global Health, Chronic and Infectious Diseases

Timeslot: 11:05–11:20am

Presenter: Patrycja Popowicz
Institution: Poznan University of Medical Sciences, Poznan, Poland.
Co-Authors: Karolina Wasicka[1], Mariusz Kaczmarek[2], Patrycja Popowicz[3], Jadzia Tin-Tsen Chou[3], Malgorzata Leszczynska[4]

[1] Immunology Research Group, Medical University in Poznan, Poznan, PL
[2] Immunology Department, Poznan University of Medical Sciences, Poznan, PL
[3] Otolaryngology Research Group, Poznan University of Medical Sciences, Poznan, PL
[4] Otolaryngology and Laryngeal Oncology Department, Poznan University of Medical Sciences, Poznan PL

Immunophenotypic assessment of natural killer cells in chronic rhinosinusitis with and without nasal polyps

Background: Due to the broad spectrum of symptoms and its multi-factorial morbidity, chronic rhinosinusitis (CRS) is difficult to treat, and is a significant economic problem. CRS is an inflammatory process of the mucous membranes of the nasal cavity and paranasal sinuses lasting at least 12 consecutive weeks, with two co-occurring symptoms, e.g. presence of secretions in the nasal cavity, feeling of obstruction, facial pain or olfactory disorders. There are two types of CRS: CRS with and CRS without polyps and both differ in regards to its inflammatory reaction profile. In the physiological state, natural killer (NK) cells are involved in both the innate and acquired immune response. However, their function may be limited under pathological conditions, which may play a significant role in the pathogenesis of polyp formation.

Aim: The aim was to determine the participation of NK cells, and their activity and involvement in the course of CRS. The above goal was determined by evaluating the percentage of NK cells in polyps, mucous membranes of the mesh cells and nasal turbinates, and peripheral blood of patients with CRS. The degree of NK cell maturity in the tissue and peripheral blood was also investigated.

Methods: Material was obtained from 49 patients with CRS (36 with nasal polyps, 13 without polyps) who underwent endoscopic nasal and sinus surgery and from 15 patients with nasal septum deviation and hypertrophic rhinitis as control samples. Immunophenotypic identification of NK cells was evaluated using a flow cytometer to determine the level of expression of selected functional receptors.

Results: The results did not show any significant differences in the percentage of NK cells within the analyzed groups. Significant differences were present within the degree of maturation of NK cells between the examined groups and tissues. A lower expression of the receptors was identified compared to the control.

Conclusions: These findings demonstrate the involvement of NK cells in the inflammatory process of CRS. The different expression of receptors in the analyzed groups may indicate the presence of a modifying agent. Disorders of the maturation process and lower expression of receptors activating function of NK cells may be an important element of the etiopathogenesis of chronic rhinosinusitis with and without polyps.

SS2-5: Global Health, Chronic and Infectious Diseases

Timeslot: 11:25–11:40am

Presenter: Dr. Guewo Fokeng Magellan[1,2]
Institution: University of Yaounde, Yaoundé, Cameroon
Co-Authors: Eugene Sobngwi[2,3,4], Barbara Atogho Tiedeu[1,2], Jean-Claude Mbanya[2,3,4], Wilfred Fon Mbacham[1,2]

[1] Department of Biochemistry, Faculty of Science, University of Yaoundé I, Yaoundé, Cameroon
[2] The Biotechnology Center, University of Yaoundé I, Nkolbisson, Yaoundé, Cameroon
[3] Department of Internal Medicine and Specialties, Faculty of Medicine and Biomedical Sciences, University of Yaoundé I, Yaoundé, Cameroon
[4] National Obesity Center, Diabetes, Endocrinology and Metabolic Diseases, Yaoundé Central Hospital, Yaoundé, Cameroon

Contribution of TCF7L2-rs7903146(C/T), KLF14-rs4731702(C/T) and PPAR-γ2-rs1801282(C/G) gene polymorphisms in the predisposition to type 2 diabetes in a Cameroonian population

Background: The aim of this study was to investigate the implication of KLF14 rs4731702(C/T), TCF7L2 rs7903146(C/T) and PPAR-γ2 rs1801282(C/G) gene polymorphisms in the predisposition to T2D in a Cameroonian population.

Methods: This case-control study included 198 T2DM patients and 182 healthy normoglycemic controls. They were all unrelated, of Cameroonian origin, and adults aged 18 years old and above. Demographic, clinical and biological data were collected, and biochemical explorations were performed using enzymatic colorimetric methods. The genotyping of KLF14 rs4731702(C/T), TCF7L2 rs7903146(C/T) and PPAR-γ2 rs1801282(C/G) gene polymorphisms was done by the Polymerase Chain Reaction and Restriction Fragment Length Polymorphism (PCR-RFLP).

Results: The metabolic profile of the patients with T2D was in poorer shape than that of the control group. The KLF14 rs4731702(C/T) gene polymorphism was strongly associated with T2D (OR=5.857; p<0.0001) in this Cameroonian population, and not dependent on any specific T2D phenotype. The combined effect of the rs4731702(C/T) of the KLF14 gene, the rs7903146(C/T) of the TCF7L2 gene and the rs1801282(C/G) of the PPAR-γ2 gene showed that individuals with the TTrs4731702 and TTrs7903146 (OR=5.167 and p=0.0125) genotypic combination, like individuals with the TTrs4731702 and CCrs1801282 combination (OR=9.203 and p=0.0003), and more interestingly those presenting the TTrs4731702_CTrs7903146_ CCrs1801282 combination (100%), stand a greater risk of developing T2D.

Conclusion: The KLF14 rs4731702(C/T) gene polymorphism and certain genotypic combinations of KLF14 rs4731702(C/T), TCF7L2 rs7903146(C/T) and PPAR-γ2 rs1801282(C/G) gene polymorphisms may predispose this population to T2D.

SS2-6: Global Health, Chronic and Infectious Diseases

Timeslot: 11:45–12:00 pm

Presenter: Dr. David Ohayon[2]
Institution: College of Medicine, University of Cincinnati, Cincinnati, OH
Co-Authors: Ayad Ali[1,2,3], Pablo C. Alarcon[2,3], Durga Krishnamurthy[1], Andrew R. Osterburg[5], Michael Borchers[5], Stephen N. Waggoner[1,2,3,6]

[1]Center for Autoimmune Genomics and Etiology, Cincinnati Children's Hospital Medical Center
[2]Medical Scientist Training Program
[3]Graduate Program in Immunology
[4]Division of Pulmonary, Critical Care, and Sleep Medicine
[5]Department of Internal Medicine
[6]Department of Pediatrics, University of Cincinnati College of Medicine, Cincinnati, OH

Interleukin-33 promotes type 1 cytokine responses in human natural killer cells

Interleukin-33 promotes type 1 cytokine responses in human natural killer cellsInterleukin-33 (IL-33) mediates type 2 cytokine responses in CD4 T cells, granulocytes, and innate immune lymphocytes. Although type 1 (IL-12) and type 2 cytokines are classically thought to counterbalance one another, a combination of IL-12 and IL-33 paradoxically promotes high-level expression of type 1 effector cytokines (e.g. IFN-g and TNFa) by human natural killer (NK) cells. Mechanistically, IL-33 stimulates potent mitogen-activated protein kinase (MAPK) p38 in human NK cells, but has no apparent impact on IL-12-induced phosphorylation of signal transducer and activator of transcription 4 (STAT4). Notably, pharmacological inhibition of p38 MAPK significantly reduced IFN-g and TNF-a release by IL-12 and IL-33 stimulated NK cells. Additionally, IL-33 triggered high expression of IFN-g independently of IL-12 stimulation when combined with the type 2 cytokines IL-4 or IL-27. The altered sensitivity of NK cells to type 1 and 2 cytokines in the presence of IL-33 may have important consequences in diseases associated with mixed cytokine milieus, including cases of severe asthma exacerbated by respiratory viral infection.

S2-7: Global Health, Chronic and Infectious Diseases

Timeslot: 12:05–12:20 pm

Presenter: Adrienne Caldwell
Institution: McGill University, Montreal, Canada
Co-Authors: Miguel Romero Sepúlveda[1], Gil Bub[1], Alvin Shrier[1]

[1] McGill University Department of Physiology, Montreal QE, Canada.

Re-entrant waves demonstrated in human induced stem cell derived cardiomyocytes (Hipsc-Cms)

Background: Re-entrant ventricular arrhythmias are a leading cause of mortality worldwide, and patients with previous myocardial infarctions (MI) are at particularly high risk of developing re-entrant rhythms. Anatomical cardiac re-entry occurs when an impulse propagates in a circuit around an in-excitable obstacle instead of terminating at the heart's apex. Simulations using the FitzHugh-Nagumo model suggest that a previously unreported mechanism may be responsible for arrhythmia generation around obstacles with a second excitable pathway. Based on these simulations, we propose that asymmetry in the location of the pace making site leads to a higher propensity for arrhythmia generation. This investigation has implication in the health care field as a further understanding of arrhythmia generation mechanism will lead to more precise treatment options available to clinicians.

Methods: The robustness of this mechanism was investigated in a bioengineered human tissue model system. The model system used was a monolayer of human induced pluripotent stem cells (iPSCs) that had been differentiated into cardiomyocytes, and sensitized to light by expression of Channelrhodopsin-2 (ChR2). By inscribing light sensitivity into tissue, precise stimulations of the tissue can be applied in various locations around the ring. Additionally, tissue can be partially depolarized, resulting in an increase in conduction velocity when an action potential triggering stimulation is applied.

Results: Experiments were conducted by varying the stimulus location/ frequency and the size/shape of the stimulus applied. This resulted in varying degrees of entrainment of the cardiac tissue and therefore diverse types of behaviours were observed in the model system.

Conclusion: Experiments demonstrate that asymmetries in stimulation location or local conduction velocity are key factors in arrhythmia induction.

SS3-2: Bioinformatics/Biotechnology

Timeslot: 7:40 – 7:55am

Presenter: Elijah K. Oladipo[1,2]
Institution: Ladoke Akintola University of Technology; Adeleke University, Ogbomoso, Ede, Nigeria

Co-Authors: Awoyelu E.H.[2], Oyawoye O.M.[1] , Oluremi A.S.[3], Oloke J.K[2].

[1]Department of Microbiology, Laboratory of Molecular Biology and Bioinformatics, Adeleke University, P.M.B. 250, Ede, Osun State, Nigeria.
[2]Department of Pure and Applied Biology (Microbiology Unit), Ladoke Akintola University Technology, P.M.B. 4000, Ogbomoso, Oyo State, Nigeria.
[3]Department of Biomedical Sciences, Ladoke Akintola University Technology, P.M.B. 4000, Ogbomoso, Oyo State, Nigeria.

Resistance to protease inhibitor in Nigerian HIV-1 isolates

Background: The changes in drug prescription is as a result of the development of mutations in HIV-1 protease which stops the activity of the anti-retroviral drugs. Drug resistance represents a significant challenge in treatment of AIDS. Computational analysis could provide a more general assessment of drug resistance and could be made available to clinicians through the available sequences in databases. Hence, this study investigates genetic diversity and the presence of protease inhibitors in HIV-1 from Nigeria.

Methods: Several nucleotide sequences of HIV-1 from Nigeria were obtained from NCBI database till 2018 and were analyzed. The analysis was performed using Stanford Genotyping Resistance Interpretation Algorithm available at http://sierra2.stanford.edu/sierra/servlet/JSierra and IAS-USA 2015 Drug Resistance Interpretation list.

Results: From computational approach the results show that the major sub-types of HIV-1 circulating in Nigeria are G, A+G, and CRF02_AG. No major resistance mutation was observed in the study. Accessory resistance mutations such as L10F, 184L, L89V and L89T were detected from this study. This study has revealed the types of circulating protease inhibitor resistance in Nigeria.

Conclusion: These findings suggest the importance of addressing drug resistance in the HIV treatment as observed in Nigeria and strengthening the intervention of drug adherence hereby preventing switching line of treatment.

SS3-3: Bioinformatics/Biotechnology

Timeslot: 8:00 – 8:15am

Presenter: Yanymee Nimesia Guillen Quispe[1]
Institution: Hallym University, South Korea

Co-Authors: Seung Hwan Hwang[1], Zhiqiang Wang[1,2], Guanglei Zuo[1], Soon Sung Lim[1,3,4]

[1] Department of Food Science and Nutrition, Hallym University, 1 Hallymdeahak-gil, Chuncheon 24252, Korea
[2] College of Public Health, Hebei University, Baoding 071002, China
[3] Institute of Natural Medicine, Hallym University, 1 Hallymdeahak-gil, Chuncheon 24252, Korea
[4] Institute of Korean Nutrition, Hallym University, 1 Hallymdeahak-gil, Chuncheon 24252, Korea

***Screening in vitro* targets related to diabetes in herbal extracts from Peru:i of active compounds in *Hypericum laricifolium Juss.* by offline high-performance liquid chromatography**

Background: According to the World Health Organization (WHO), the prevalence of diabetes continues to increase at an alarming rate. Globally, an estimated 346 million people are living with diabetes, figures that are predicted to have a severe impact on human health by 2025. Therapy for Diabetes mellitus (DM) relies on several approaches, many of which comprise drug targets for type 2 diabetes. Moreover, various efforts have been made to obtain other effective and safe enzyme inhibitors from plant extracts to control diabetes. There are different targets related to diabetes and its complications such as α-glucosidase, aldose reductase (AR), and free radicals.

Methods: This study investigates in vitro targets related to diabetes in 30 herbal extracts from Peru, for the first time, using α-glucosidase, aldose reductase (AR) inhibitory assays and 2,2-diphenyl-1-picrylhydrazyl (DPPH) and 2,2′-azino-bis(3-ethylbenzothiazoline-6-sulfonic acid) (ABTS) scavenging assays. Subsequently, an ultrafiltration method and offline DPPH- high-performance liquid chromatography (HPLC) and ABTS-HPLC assays to screen active compounds for Hypericum laricifolium Juss. (HL).

Results: Of the 30 herbal extracts assayed, only 23 crude extracts exhibited inhibition at 500 μg/mL in the α-glucosidase inhibition assay and AR inhibition assay. A total of 13 extracts presented relatively high antioxidant capacities (>50%). Among the 30 herbal extracts, Hypericum laricifolium Juss. (HL) was the herb which showed more than 50% inhibition in all assays, presenting 97.2 ± 2.0%, 56.9 ± 5.6%, 81.9 ± 2.5%, and 58.8 ± 4.6% inhibition for the α-glucosidase, AR, DPPH, and ABTS assays, respectively. Finally, six bioactive compounds, namely, protocatechuic acid, chlorogenic acid, caffeic acid, kaempferol 3-O-glucuronide, quercetin, and kaempferol were identified in HL by offline high-performance liquid chromatography (HPLC). Quercetin exhibited the strongest inhibition in all enzyme assays and the strongest antioxidant activity.

Conclusions: In this study, the results suggest that HL shows great potential for the complementary treatment of diabetes and its complications.

SS3-4: Bioinformatics/Biotechnology

Timeslot: 8:20 – 8:35am

Presenter: Aimoldir Aldabergen[2]
Institution: Suleyman Demirel University, Kaskelen, Almaty, Kazakhstan
Co-Authors: Kynabay Bakdaulet[2], Zhappasova Ainur[2], Amirgaliyev Yedilkhan[1,3] (supervisor) and Shamiluulu Shahriar[2] (supervisor)

[1] Institute of Information Technologies,
[2] Department of Computer Science, Suleyman Demirel University, Kaskelen, Kazakhstan, 040900
[3] Institute of Information and Computing Technologies (IICT), Almaty, Kazakhstan

Computer-aided skin cancer detection: novel image processing techniques.

Background: Early stage detection of skin cancer will reduce patient mortality and can be realized by using computer- aided techniques. Automatic skin cancer diagnosis is a major challenge in medical image processing. This work presents a novel approach for automated skin cancer diagnosis by implementing machine learning and computer vision techniques and methods.

Methods: To extract the features from the lesion, several filters and other necessary methods were implemented: RGB to Gray conversion, histogram equalization, Wiener or Gaussian filter. To remove noise from the image, Otsu thresholding that segments the lesion from the entire image, boundary tracing algorithm, algorithm for finding the center of mass and the supervised learning algorithms for classification of the images were implemented. To provide distinguishing quantitative measures for automatic diagnosis of cancer two supervised machine learning algorithms were trained: K-nearest neighbors (KNN) and Support Vector Machine (SVM).

Results: Overall performance of the approaches were good. KNN model and SVM showed precision of ~ 73% and 98% respectively. However, because of the limited amount of available data, there was considerable amount of bias and overfitting.

Conclusions: Results of the research work demonstrate that skin cancer detection through computer-aided techniques is possible and can be applied in real life. However, for the further researches it is preferable to collect more data and create more automated and developed system.The system makes possible to detect skin cancer in real-time and will be very efficient and comfortable. From the second hand it is a new approach of treating skin cancer and not only makes doctors work more efficient, but also save both patients and doctors resources.

SS3-5: Bioinformatics/Biotechnology

Timeslot: 8: 40 – 8:55am

Presenter: Ashton Trotman-Grant[1,2]
Institution: Sunnybrook Research Institute, Toronto, Canada
Co-Author: Mahmood Mohtashami[2], Joshua De Sousa Casal[1,2], Patrick Brauer[2], Juan Carlos Zúñiga Pflücker[1,2]

[1] Department of Immunology, University of Toronto, Canada
[2] Biological Sciences, Sunnybrook Research Institute, University of Toronto, Canada

Progenitor T Cells for thymic regeneration and as a platform for genetically-engineered T Cells

Current cancer therapies requiring hematopoietic stem cell transplantation are followed by a period of immunodeficiency in patients. The majority of hematopoietic cells are restored within weeks following transplantation, however, the restoration of T-cells is a slow process that requires the development of T-cell progenitors in the thymus. Using the OP9-DL cell-based co-culture system, we have identified a progenitor-T (proT) subset that, upon adoptive transfer into immunodeficient mice, is able to engraft the thymus, restore its architecture and ultimately restore its capacity to be seeded by progenitors and give rise to T-cells. As OP9-DL cells are mouse-derived, and thus not yet approved for clinical use, we sought to develop a cell-free approach that is amenable to scale up in suspension culture. Our strategy uses an artificial Notch signaling system, wherein DL4-Fc is immobilized to beads. These DL4-beads, along with the requisite cytokines, are able to produce pro-T and T cells from CD34+ cells sourced from human cord blood, mobilized peripheral blood and induced pluripotent stem cells-derived hematopoietic progenitor cells. Using this system, we aim to investigate the mechanism by which proT cells regenerate the thymus at single-cell resolution.

SS3-6: Bioinformatics/Biotechnology

Timeslot: 8:55 – 9:10am

Presenter: Dr. Arvind Mer[1,2]
Institution: University Health Network, University of Toronto
Co-Authors: Wail Ba-alawi[1,2], Petr Smirnov[1,2], Yi Xiao Wang[1,2], Ben Brew[3], Janosch Ortmann[4], Ming-Sound Tsao[1,2], David Cescon[1], Anna Goldenberg[3,5,6], Benjamin Haibe-Kains[1,2,3,5,7]

[1] Princess Margaret Cancer Centre, University Health Network, Toronto, Ontario, Canada
[2] Department of Medical Biophysics, University of Toronto, Toronto, Ontario, Canada
[3] Hospital for Sick Children, Toronto, Ontario, Canada
[4] Département de management et technologie, Université du Québec à Montréal, Canada
[5] Department of Computer Science, University of Toronto, Toronto, Ontario, Canada
[6] Vector Institute, Toronto, Ontario, Canada
[7] Ontario Institute for Cancer Research, Toronto, Ontario, Canada"

Comprehensive assessment of large scale patient derived xenografts data

One of the key challenges in cancer precision medicine is finding robust biomarkers of drug response. Patient-derived tumor xenografts (PDXs) have emerged as reliable preclinical models since they better recapitulate tumor response to chemo- and targeted therapies. However, the lack of standard tools poses a challenge in the analysis of PDXs with molecular and pharmacological profiles. Efficient storage, access and analysis is key to the realization of the full potential of PDX pharmacogenomic data. We have developed Xeva (XEnograft Visualization & Analysis), an open-source software package for processing, visualization and integrative analysis of a compendium of in vivo pharmacogenomic datasets. The Xeva package follows the PDX minimum information (PDX-MI) standards and can handle both replicate-based and 1x1x1 experimental designs. We used Xeva to characterize the variability of gene expression and pathway activity across passages. We found that only a few genes and pathways have passage specific alterations (median intraclass correlation of 0.53 for genes and positive enrichment score for 92.5% pathways). For example, activity of the mRNA 3'-end processing and elongation arrest and recovery pathways were strongly affected by model passaging (gene set enrichment analysis false discovery rate [FDR] <5%). We then leveraged our platform to link the drug response and the pathways whose activity is consistent across passages by mining the Novartis PDX Encyclopedia (PDXE) data containing 1,075 PDXs spanning 5 tissue types and 62 anticancer drugs. We identified 87 pathways significantly associated with response to 51 drugs (FDR < 5%), including associations such as erlotinib response and signaling by EGFR in cancer pathways and MAP kinase activation in TLR cascade and binimetinib response. Among the significant pathway-drug associations, we found novel biomarkers based on gene expressions, Copy Number Aberrations (CNAs) and mutations predictive of drug response (concordance index > 0.60; FDR < 0.05). Xeva provides a flexible platform for integrative analysis of preclinical in vivo pharmacogenomics data to identify biomarkers predictive of drug response, a major step toward precision oncology.

SS3-7: Bioinformatics/Biotechnology

Timeslot: 9:15 – 9:30am

Presenter: Dr. Cesar de la Fuente[1]
Institution: MIT, Cambridge, USA

[1] Department of Biological Engineering, MIT, Cambridge, USA

Toward computer-made artificial antibiotics

Proteins perform the cellular tasks required for life. The great variety of their biological activity is due in part to their vast combinatorial space: 20n, n being the number of amino acids present in any given peptide chain and 20 being the number of natural amino acid monomer building blocks. Yet we do not have the tools to properly engineer these diverse molecules. One approach is to start small: I will present foundational synthetic biology frameworks to rationally develop peptides, tiny proteins that display great sequence diversity but are more amenable than larger molecules to redesign and engineering. My approach is to expand nature's repertoire to build novel synthetic peptides with extremely useful properties. In addition, I will discuss novel tools for the discovery of novel antimicrobials in biological information, and synthetic biology approaches for building cell-based therapeutics. My overarching vision is to generate a peptide encyclopedia encompassing peptides that target every medically relevant microbe and to devise therapies that nature has not previously discovered. The synthetic computational biology tools and platforms that I am developing offer solutions to some of the most pressing unmet clinical challenges we face, including finding strategies for treating antibiotic-resistant infections.

SS4-2: Cancer

Timeslot: 10:40–10:55 am

Presenter: Hanna, Bola
Institution: Harvard Medical School, Boston, USA
Co-Authors: Murat Iskar[1], Philipp M. Rößner[1], Lauro Llao Cid[1], Lara Klett[2], Selcen Öztürk[1], Norman Mack[1], Verena Kalter[1], Dolors Colomer[3], Elías Campo[3], Stephan Stilgenbauer[4], Manfred Schmidt[5], Marc Zapatka[1], Richard Gabriel[5], Karsten Rippe[2], Markus Feuerer[6,7], Peter Lichter[1], and Martina Seiffert[1]

[1] Molecular Genetics, German Cancer Research Center (DKFZ), Heidelberg, Germany
[2] Chromatin Networks, German Cancer Research Center (DKFZ), Heidelberg, Germany
[3] Institut d'Investigacions Biomèdiques August Pi i Sunyer (IDIBAPS), Hematopathology Unit, Hospital Clinic, CIBERONC, Barcelona, Spain
[4] Internal Medicine III, University of Ulm, Ulm, Germany
[5] Translational Oncology, National Center for Tumor Diseases and German Cancer Research Center, Heidelberg, Germany
[6] Immune Tolerance, Tumor Immunology Program, German Cancer Research Center (DKFZ), Heidelberg, Germany
[7] Institute of Immunology, Regensburg Center for Interventional Immunology (RCI), University Regensburg and University Medical Center Regensburg, Regensburg, Germany

Loss of IL-10/STAT3 signaling aggravates CD8+ T-cell exhaustion and impedes control of chronic lymphocytic leukemia

Chronic antigenic stimulation in tumors drives T-cells into terminal differentiation or “exhaustion”. Here, we explore microenvironmental signals regulating this process and describe an unexpected mechanism of IL-10 preventing activation-induced exhaustion of tumor-reactive T-cells in chronic lymphocytic leukemia (CLL). Within CD8+ effector T-cells that control CLL progression, we identified a population of exhausted PD-1hi cells that accumulate in secondary lymphoid organs of CLL patients, and are transcriptionally distinct from PD-1int cells that maintain functional properties. We show that the balance between these two CD8+ T-cell subsets is regulated by IL-10R/STAT3 signaling. Using ATAC-seq, we observed that IL-10 receptor blockade alters chromatin accessibility and disrupts the cooperativity of NFAT and AP-1 in CD8+ T-cells leading to a dramatic loss of the PD-1int subset and an accumulation of dysfunctional PD-1hi cells. Accordingly, T-cell mediated control of CLL is compromised following IL-10 receptor blockade. We further show that loss of IL-10R/STAT3 signaling correlates with CD8+ T-cell terminal differentiation and poor survival in cancer patients. Taken together, these data demonstrate the central role of IL-10/STAT3 signaling in modulating chromatin states of CD8+ T-cells preventing their exhaustion, and suggest this mechanism as therapeutic target for cancer patients.

SS4-3: Cancer

Timeslot: 11:00– 11:15 am

Presenter: Neelakshi Mungra
Institution: University of Cape Town, Cape Town, South Africa
Co-Authors: S. Jordaan[1], S. Chetty[1] & S. Barth[1,2]

[1] Medical Biotechnology & Immunotherapy Unit, Faculty of Health Sciences, University of Cape Town, Cape Town 7700, South Africa
[2] South African Research Chair (SARChI) in Cancer Biotechnology, Department of Integrative Biomedical Sciences, Faculty of Health Sciences, University of Cape Town, Cape Town 7700, South Africa

Human cytolytic fusion proteins targeting CSPG4 for the treatment of triple-negative breast cancer

Background: Breast cancer, a disease characterized by the perpetual growth of malignant cells in the tissues of the breast, represents one of the most common forms of female malignancy of the 21st century. According to statistics, breast cancer is known as the second-leading cause of death in women and, on that account, it constitutes an alarming threat to global socioeconomic well-being. Conventional chemotherapeutic approaches for breast cancer face obstacles such as off-target toxicity and therapy-resistance. Human cytolytic fusion proteins (hCFPs) are targeted therapeutic agents composed of a disease-specific humanized antibody-based ligand recombinantly fused with a conditionally apoptosis-inducing human oligopeptide. They exhibit low off-target toxicity and can overcome tumor resistance depending on the biomarker selected. We generated hCFPs targeting chondroitin-sulphate proteoglycan (CSPG4), a biomarker of aggressive and treatment-resistant cancers, for treatment of triple-negative breast cancer (TNBC). These hCFPs are designed to bind to CSPG4-positive TNBC cells and deliver cytotoxic proteins intracellularly, where they induce tumor cell death by disrupting biosynthesis (angiogenin) or mitosis (microtubule-associated protein tau or MAP tau) in a compartment-dependent manner.

Methods: We designed recombinant hCFPs based on angiogenin and MAP tau as lead agents (designated CSPG4(scFv)-AngWT and CSPG4(scFv)-MAP tau), as well as a CSPG4-targeting SNAP-tag fusion protein (CSPG4(scFv)-SNAP) as a fluorescent mimic for binding. All fusion proteins were expressed in a transient secretory mammalian expression system and purified from the cell culture supernatant by ion metal affinity chromatography. Binding of CSPG4(scFv)-SNAP to CSPG4-positive and -negative TNBC cell lines was validated both quantitatively (by flow cytometry) and qualitatively (by confocal microscopy).

Results: Preliminary proof-of-concept data demonstrate that the CSPG4-targeting, fluorescently-labeled CSPG4(scFv)-SNAP binds effectively to CSPG4-positive TNBC cells.

Conclusions: While the binding specificities and cytotoxic activities of the angiogenin and MAP tau-based fusion proteins still need to be assessed, CSPG4(scFv)-SNAP represents a promising strategy to improve the diagnosis of TNBC tumours, thereby promoting the concept of precision medicine to existing health care frameworks.

SS4-4: Cancer

Timeslot: 11:20 – 11:35am

Presenter: Nastassia Kruhlenia
Institution: Poznan University of Medical Sciences, Poznan, Poland.
Co-Authors: Aleksandra Majchrzak-Celińska

[1] Department of Pharmaceutical Biochemistry, Poznan University of Medical Sciences.

The impact of coxibs on Wnt/β-catenin pathway, cell cycle and apoptosis in GBM cells

Background: Glioblastoma multiforme is the deadliest and the most common primary brain tumor in adults. Despite maximal surgical resection followed by combined adjuvant therapy, around 70% of patients are likely to suffer a tumor recurrence within 1 year of surgery. Increasing evidence indicates that the aberrant activation of Wnt/β-catenin pathway plays a key role in GBM development and progression. Wnt/β-catenin signaling can, therefore, be regarded as an important therapeutic target.
Coxibs are selective COX-2 inhibitors, which also exert COX-independent mechanisms on Wnt/β-catenin pathway. The most widely described as a potential anti-GBM therapeutic coxib in the literature is celecoxib. However, little is known about the possible use of other coxibs in GBM therapy.

Methods: In this study three GBM cell lines, A-172, T98G and U-138 MG were used. The impact of analyzed compounds on cell viability was determined using MTT assay. qPCR analysis of β-catenin (CTNNB1), Axin-2, C-Myc, CCND1, BIRC5 and NEDD9 was applied to determine the activity of Wnt/ β-catenin pathway. Downregulatory effect of coxibs on Wnt/β-catenin pathway was confirmed by means of Western blot. MGMT expression and promoter methylation level were determined using qPCR and MS-HRM, respectively. Apoptosis was detected based on caspase-3/7 activation, whereas cell cycle distribution was analyzed using propidium iodide staining; both assays were performed on Muse™ Cell Analyzer.

Results: This study shows that all analyzed coxibs reduced the viability of GBM cells in a dose-dependent manner. However, the most cytotoxic in all three cell lines were 2,5-dimethylcelecoxib and celecoxib. Analyzed coxibs were able to significantly downregulate β-catenin on both mRNA and transcript levels. Moreover, the reduction of MGMT expression was also observed, which was not accompanied by changes in DNA methylation level. Furthermore, this study shows that coxibs are also able to induce cell cycle arrest and apoptosis, but these phenomena were observed only in T98G cell line.

Conclusions: Not only celecoxib and 2,5-dimethylcelecoxib, which are the most widely described coxibs in the literature as beneficial in GBM therapy, but also etoricoxib, rofecoxib and valdecoxib should be further investigated and checked in clinical trials since all of them are potentially good anti-GBM therapeutics.

SS4-5: Cancer

Timeslot: 11:40– 11:55 am

Presenter: Shiva Najjary[1,2]
Institution: University of Maragheh, Maragheh, Iran.
Co-Authors: Reza Mohammadzadeh[1], Behzad Baradaran[2]

[1] Department of Cell and Molecular Biology, Faculty of Basic Science, University of Maragheh, Maragheh, Iran
[2] Immunology Research Center, Tabriz University of Medical Sciences, Tabriz, Iran"

Restoration of microRNA-34a expression decreases cell viability and promotes apoptosis in T-cell acute lymphoblastic leukemia cell line (Jurkat).

Background: T-cell acute lymphoblastic leukemia (T-ALL) is an aggressive lymphoid malignancy due to the oncogenic transformation of immature T-cell progenitors. The emergence of microRNAs as gene expression regulators identifies them as emerging diagnostic candidates and potential therapeutic targets. microRNAs play a crucial role in the progression of T-ALL by regulating proliferation and apoptosis through targeting major signaling pathways or transcription factors. miR-34a is a tumor suppressor with reduced expression levels in many cancers, including T-ALL. The purpose of the present study was to investigate the effect of miR-34a on induction of apoptosis in the jurkat cell line.

Methods: Jurkat cells which are related to T-cell acute lymphoblastic leukemia (T-ALL) were cultured in RPMI1640 medium supplemented with 10% fetal bovine serum (FBS) at 37˚C and 5% CO2. miR-34a mimic was transfected using jetPEI in vitro DNA transfection reagent and the expression of miR-34a was detected using quantitative real-time PCR. Cell viability of jurkat cells was detected using 3-(4, 5-dimethylthiazol-2-yl)- 2, 5-diphenyltetrazolium bromide (MTT) assay. Then, flow cytometry assay was exploited measure the percentage of apoptotic cells. Finally, Cell cycle assay was used to differentiate different phases of the cell cycle.

Results: qRT-PCR analyses showed that in Jurkat cells after transfection with miR-34a mimic at the concentration of 5nmol the expression of miR-34a mRNA was significantly increased compared to the control group. MTT assay results demonstrated that transfection by miR-34a at the concentration of 5nmol decreased the viability of jurkat cells and reduction in cell viability obeyed a dose-dependent course. According to the flow cytometry assay result, in the transfected cells, miR-34a mimic at the concentration of 5nmol was able to induce apoptosis the in Jurkat cell line. Data derived from cell cycle assay revealed that cell cycle arrest in cancer cells which have been under treatment of miR-34a occurred at G2/M phase.

Conclusions: Our results have obviously demonstrated that the miR-34a effectively decreased the viability of jurkat cells, induced apoptosis in this cell line, and therefore could serve as a potential therapeutic agent for the treatment of T-ALL as well as biomarkers for diagnosis of this cancer.

SS4-6: Cancer

Timeslot: 12:00– 12:15 am

Presenter: Rutvij Khanolkar[1]
Institution: University of Toronto, Toronto, Canada.
Co-Authors: Huey Yee Teo[2,3], Song Yuan[2,3], Haiyan Liu[2,3]

[1] Department of Immunology, University of Toronto, Toronto, Canada
[2] Department of Microbiology and Immunology, National University of Singapore, Singapore
[3] Life Sciences Institute, National University of Singapore, Singapore

Synergistic checkpoint blockade and cytokine therapy increases γδ T-cell mediated cytotoxicity in murine hepatocellular carcinoma

Background: Hepatocellular carcinoma (HCC) is the most common form of primary liver cancer—constituting 90% of cases. Liver cancer rate has tripled since 1980, and 5-year survival remains poor at 17.6%. Current γδT-cell immunotherapies, while clinically safe, have low efficacy due to limited proliferation and longevity. Immune checkpoint inhibitors are an established mode of secondary treatment in HCC that decrease T-cell exhaustion and apoptosis, and prevent tumor cells from bypassing immune anti-cancer responses. We hypothesize that in response to cytokine stimulation and immune-checkpoint inhibitors, mouse γδT-cells will show increased cytotoxicity and proliferation, with decreased exhaustion and apoptosis.

Methods: γδT-cells were cultured using splenocytes harvested from TCRβ-knockout and C57BL/6 WT mice. Cells were treated with eight combination cytokine consisting of IL-12/15/18/21 as well as an IL-2 control group, and qPCR and Flow Cytometry were performed to identify changes in costimualtory molecules expression. Further flow cytometry was performed to determine expression levels of cytotoxic molecules in response to cytokine treatment. A delfia europium assay was used to establish the Effector-to-Target (E:T) ratio of cytokine activated γδ-Tcells that showed maximal cytotoxicity against A20 adenocarcinoma and Hepa1-6 HCC cell lines. A novel combinatorial treatment using PD-1/LAG-3 antagonistic mAb's and cytokine activated γδT-cells was tested through a CD107a degranulation assay.

Results: Cytokine stimulation increased cell-surface expression of anti-cancer molecules CD137 and OX-40, and lowered expression of pro-apoptotic PD-1. Four cytokine treatments, IL-12/18, IL-12/15/18, IL-12/18/21 and IL-12/15/18/21, were found to be effectively increase expression of FasL, TNF-a, IFNy, Perforin, and GranzymeB. The four cytokine treatments also increased CD107 degranulation when compared to the control while LAG-3/PD-1 antagonist combination alone increased degranulation.

Conclusion: Combination treatment provides a solution to the current challenges in γδT-cell immunotherapy by increasing cytotoxicity and proliferation of effector cells while decreasing apoptosis and exhaustion. The success of the combinatorial therapy in vitro establishes the rationale for in vivo studies using xenograft and orthotopic murine models.

BEYOND SCIENCES INITIATIVE

4TH INTERNATIONAL REMOTE CONFERENCE: SCIENCE & SOCIETY

PRE-RECORDED PRESENTER ABSTRACTS

To Access: http://www.beyondsciences.org/video/

Session Topic: Biotechnology

Presenter: Jacky Chow[1]
Institution: University of Calgary, Canada

Co-Authors: Janet Ronsky[1], Steven Boyd[2], Derek Lichti[3]

[1] Department of Medicine, Cumming School of Medicine, University of Calgary, Calgary, AB, Canada
[2] McCaig Institute for Bone and Joint Health, Cumming School of Medicine, University of Calgary, Calgary, AB, Canada
[3] Department of Geomatics Engineering, Schulich School of Engineering, University of Calgary, Calgary, AB, Canada

Minimizing geometric distortions in X-ray fluoroscopic imaging systems

Background: Fluoroscopy allows for non-invasive skeletal kinematic analysis by direct visualization of bone movement. To ensure accurate measurements, such systems need to be calibrated. In this research, a grey-box system identification framework was used to model the errors of a fluoroscopic imaging system by combining bundle adjustment with machine learning.

Methods: The imaging geometry of a fluoroscopic system can be approximated by a pinhole camera model. Under this assumption, the direction of X-rays should obey the collinearity condition, i.e. the object point, camera perspective center, and homologous image point lie on a straight line in 3D space. Any systematic deviation from this mathematical approximation can be identified using a robust bundle adjustment. A phantom with 503 targets was captured, producing two sets of X-ray imagery (dataset 1: 15 images, dataset 2: 75 images) to use for calibration. Reference measurements from a robotic arm were available for quality assessment. A distortion compensation function for the system was estimated using k-nearest-neighbour regression (self-tuned using 10-fold cross-validation) to improve the geometric accuracy.

Results: After calibration, the 3D mapping accuracy of the first and second dataset improved by 84% and 94% (i.e. errors reduced from 1.24 to 0.20 mm and from 0.83 to 0.05 mm), respectively. By smoothing the k-nearest-neighbour solution, the mapping error further reduced to 0.17 and 0.04 mm, respectively.

Conclusion: The proposed self-tuning calibration method can significantly reduce systematic errors in fluoroscopic imaging systems. The main benefit is that it can be performed on-site by a non-expert.

Session Topic: Biotechnology

Presenter: Yanymee Nimesia Guillen Quispe[1]
Institution: Hallym University, South Korea

Co-Authors: Seung Hwan Hwang[1], Zhiqiang Wang[1,2], Guanglei Zuo[1], Soon Sung Lim[1,3,4]

[1] Department of Food Science and Nutrition, Hallym University, 1 Hallymdeahak-gil, Chuncheon 24252, Korea
[2] College of Public Health, Hebei University, Baoding 071002, China
[3] Institute of Natural Medicine, Hallym University, 1 Hallymdeahak-gil, Chuncheon 24252, Korea
[4] Institute of Korean Nutrition, Hallym University, 1 Hallymdeahak-gil, Chuncheon 24252, Korea

***Screening in vitro* targets related to diabetes in herbal extracts from Peru:i of active compounds in *Hypericum laricifolium Juss.* by offline high-performance liquid chromatography**

Background: According to the World Health Organization (WHO), the prevalence of diabetes continues to increase at an alarming rate. Globally, an estimated 346 million people are living with diabetes, figures that are predicted to have a severe impact on human health by 2025. Therapy for Diabetes mellitus (DM) relies on several approaches, many of which comprise drug targets for type 2 diabetes. Moreover, various efforts have been made to obtain other effective and safe enzyme inhibitors from plant extracts to control diabetes. There are different targets related to diabetes and its complications such as α-glucosidase, aldose reductase (AR), and free radicals.

Methods: This study investigates in vitro targets related to diabetes in 30 herbal extracts from Peru, for the first time, using α-glucosidase, aldose reductase (AR) inhibitory assays and 2,2-diphenyl-1-picrylhydrazyl (DPPH) and 2,2′-azino-bis(3-ethylbenzothiazoline-6-sulfonic acid) (ABTS) scavenging assays. Subsequently, an ultrafiltration method and offline DPPH- high-performance liquid chromatography (HPLC) and ABTS-HPLC assays to screen active compounds for Hypericum laricifolium Juss. (HL).

Results: Of the 30 herbal extracts assayed, only 23 crude extracts exhibited inhibition at 500 μg/mL in the α-glucosidase inhibition assay and AR inhibition assay. A total of 13 extracts presented relatively high antioxidant capacities (>50%). Among the 30 herbal extracts, Hypericum laricifolium Juss. (HL) was the herb which showed more than 50% inhibition in all assays, presenting 97.2 ± 2.0%, 56.9 ± 5.6%, 81.9 ± 2.5%, and 58.8 ± 4.6% inhibition for the α-glucosidase, AR, DPPH, and ABTS assays, respectively. Finally, six bioactive compounds, namely, protocatechuic acid, chlorogenic acid, caffeic acid, kaempferol 3-O-glucuronide, quercetin, and kaempferol were identified in HL by offline high-performance liquid chromatography (HPLC). Quercetin exhibited the strongest inhibition in all enzyme assays and the strongest antioxidant activity.

Conclusions: In this study, the results suggest that HL shows great potential for the complementary treatment of diabetes and its complications.

Session Topic: Biotechnology

Presenter: Abiola Adeosun[1,2]
Institution: Federal University of Agriculture, Abeokuta, Nigeria

Co-Authors: Ighodaro O.M.[1], Akinloye O.A[2]

[1] Department of Biochemistry, Faculty of Basic Medical and Applied Sciences, Lead City University, Ibadan
[2] Department of Biochemistry, College of Biological Science, Federal University of Agriculture, Abeokuta.

New method For determining blood pressure in unanesthesized rats using non invasive contec 08A device with small cuff: a path to antihypertensive drug development in developing countries

Invasive method of determining blood pressure has been the commonly used method in animal model of hypertension study. Currently used non invasive blood pressure monitoring devices are very costly and unaffordable by researchers from developing or under developed countries. In our study, we designed a new method for determining blood pressure in animal model studies by using CONTEC 08A device with small cuff for rats. Ten male Wistar rats of 182-240 g body weight were randomly assigned to two groups (n=5/group). A group served as control (without treatment), the second group was administered dexamethasone (2mg/kg of body weight) supplemented with 4% table salt (NaCl) as drinking water to induce hypertension. Blood pressure was measured ten times in each rats of the two groups at baseline (day 0) and after 5 days. Reproducibility (S w) was calculated in each group. CONTEC 08A yielded good reproducibility in both hypertensive (SBP, S w = 6 mm Hg, DBP, S w = 10 mm Hg) and non hypertensive rats (SBP, S w = 3 mm Hg, DBP, S w = 6 mm Hg). Better reproducibility was obtained in non hypertensive rats. Consistency in data obtained showed that non invasive blood pressure monitoring using CONTEC 08A device with small cuff is effective, and recommendable for use in rat model study of hypertension.

Session Topic: Biotechnology

Presenter: Silvia Almeida Junior[1,2]
Institution: University of Franca, Sao Paulo, Brazil

Co-Authors: Nhaypi Iasmin Taveira Moreira[1], Fernanda Carolina da Silva,[1] Isabela de Castro Capoia[1], Inglity Lorrane da Silva Cruz[1], Danilo Cândido Bulgo[3] Rafaela Simei Pompolim[1]

[1] Research Group on Toxicology and Health Promotion (G.E.T.o.S) - Euro Anglo Franca, Franca, São Paulo, Brazil.
[2] Laboratory of Animal Science - Postgraduate Program in Animal Science, University of Franca, Franca, São Paulo, Brazil. [3] Postgraduate Program in Health Promotion, University of Franca, Franca, São Paulo, Brazil.

Use of plants by popular medicine in a medium-sized city in southeastern Brazil

Background: Brazil is a country with a rich diversity of flora, and despite the large number of plant species, there are few phytochemical studies and biological activities. The expression of this is the scientific research focused on university centers of great public and private institutions of the country. The use of popular medicine is already something millenarian and it brings great advances, being the plants of great interest in the pharmaceutical area because the discoveries of new drugs are promising. Faced with this, it is necessary ethnobotanical survey, as well as phytochemical studies, biological tests and their toxicological activities for safety analysis. The objective of this work is to evaluate the profile of plants used by people over 60 years of age, in a medium - sized city in southeastern Brazil.

Methods: Application of form to the local population and research in scientific bases.

Results: Among the surveys, the most cited ones due to their wide use were the “Capim cidreira” (Cymbopogon citratus), Camomila (Matricaria chamomilla), and Boldo (Peumus boldus). The lemon grass in its popular preparation, presents calming, hypnotic, analgesic, anti-inflammatory, antispasmodic, antihypertensive activities and through the essential oil, the plant has antibacterial, antifungal and antiparasitic activity. Chamomile has activity against flatulence, colic, hysteria, intermittent fever and strong anti-inflammatory, antiseptic and antioxidative activity. Boldo, a plant widely used in Latin America, presents great use related to gastric and hepatic problems. Plants are prepared through infusions or decoctions and are generally used fresh or dried aerial parts, filtered waters are used and are not sweetened and when they are, honey is used, in which it is widely used in folk medicine due to its already known biological activity.

Conclusion: Works such as this, of an exploratory nature, bring information about plants used in folk medicine beyond its already proven biological effect. It is of utmost importance to transmit scientific information to the community in an attempt to promote health and well-being for all. The work is in progress and shows promise within the region applied.

Session Topic: Biotechnology

Presenter: Avinash Kumar Singh
Institution: National Institute of Immunology, New Delhi, India

Co-Authors: Avinash Kumar Singh[1], Vijaykumar S. Pawale[1], Sreetama Das[2], Venkatareddy Dadireddy[2], Suryanarayanarao Ramakumar[2], and Rajendra P. Roy[1]

[1] National Institute of Immunology, Delhi, India
[2] Department of Physics, Indian Institute of Science, Bangalore, India

A tale of substrate recognition in two housekeeping sortases

Background: Cell wall anchoring of surface proteins in gram-positive bacteria is mediated by transpeptidase Sortase. In pathogenic bacteria sortases are potential drug targets, as many of the proteins that they display on the microbial surface play key roles in the infection process. Sortase enzymes are generally grouped into six classes(A-F) of which Class A sortase is considered as a housekeeping enzyme. The prototype Sortase A (SrtA) of Staphylococcus aureus recognizes a LPXTG pentapeptide motif in the C-terminal of sortase substrates, cleaves the T-G peptide bond and ligates Protein-LPXT to terminal aminoglycine branch of lipid II. The peptide ligation propensity of SrtA is very useful in protein engineering and semi-synthesis.

Methods: Here we describe the crystal structure and functional attributes of a new class of housekeeping sortase (SrtE) from Streptomyces avermitilis. SrtE prefers a LAXTG peptide substrate in contrast to LPXTG of SaSrtA. The crystal structure of SrtE, mutagenesis and biochemical experiments provide clues to the altered substrate specificity of SrtE.

Results: The results point to the role of a conserved Tyr residue (Tyr 112). Tyr 112 is conserved in all class E sortases despite the lack of high sequence identity between them. The mutation of Y112 to F112 resulted in 50-fold decrease in Ala specificity with no change in its specificity for the Pro-substrate. Interestingly mutation of the equivalent residue in SrtA (A104F) did not affect the specificity of SrtA.

Conclusions: In summary, cumulative results highlight Y112 residue of SavSrtE as a critical determinant of specificity. The significance of Y112 in substrate recognition is also borne out by the fact that evolved mutants of SaSrtA generated in the past with improved activity toward LAETG motif contained mutation of Y112 equivalent Ala104 residue. The retention of native-like Pro-specificity concomitant with several fold loss of Ala-specificity in a single Y112F mutant indicate some degree of natural divergence of LPXTG to LAXTG specificity in class E sortase. Furthermore, perturbation of activity by proximal mutations in the substrate binding cleft suggest that these residues may be contributing to the overall substrate recognition process in concert with the lead role of Y112. The studies pave the way for further selection of improved enzyme by directed evolution.

Session Topic: Cancer

Presenter: Azza Habel[1]
Institution: University Tunis El-Manar, Tunis, Tunisia

Co-Authors: Mariem Hadj Ahmed[1], Makni Lamia[1], Channoufi Badis[2], Besma Yacoubi-Loueslati[1], Mouna Stayoussef[1]

[1]El Manar University, Faculty of Sciences of Tunis, Laboratory of Mycology, Pathologies and Biomarkers (LR16ES05)
[2]Maternity and Neonatology Center, Tunis , Tunisia

Roles of environmental factors and cytokines in the development of ovarian cancer

Background: Ovarian cancer (OC) remains today a major public health problem in the world and especially in Tunisia, and this is due to its frequency and its high mortality rate.
In this work, we conducted an epidemiological and a case-control studies to investigate the involvement of environmentals factors and certain cytokines (IL-1β, IL-4, IL-8, IL-13 and IL-23) in the development of ovarian cancer.

Methods: The study comprises 35 patients with OC and 28 healthy cases and the cytokines assay was performed by the immuno-enzymatic amplification method (EASIA) or by the immunohistochemistry.

Results: The results speculate that obesity, early menarche may favour the occurrence of the disease while taking contraceptive pills could decrease the risk of developing the disease. The statistical study demonstrated a negative association between serum levels of IL-13, and IL-23 and OC, while the significant increase in IL-1β levels, IL-8, and a significant decrease of IL-4 could be implicated in the appearance of the disease. Advanced stages of OC are associated with low levels of IL-13. It has also been shown that IL-4 and IL-13 may be involved in recurrence of the disease and that high levels of IL-8 are positively correlated with resistance to treatment.

Conclusion: In conclusion, obesity, early menarche, and not taking contraceptive pills could increase the risk of developing the disease. IL-1β, IL-8 and IL-4 could be involved in the occurrence of OC; and increased levels of IL-8 are associated with the resistance to treatment.

Session Topic: Cancer

Presenter: Luciana Furtado[1]
Institution: University of Sao Paulo, Sao Paulo, Brazil

Co-Authors: Rafael de Felício[2], Daniela Barretto Barbosa Trivella[2], Leticia Veras Costa-Lotufo[1]

[1] Institute of Biomedical Sciences, University of São Paulo São Paulo, Brazil
[2] Brazilian Biosciences National Laboratory, National Center for Research in Energy and Material, São Paulo, Brazil

Evaluation of marine bacterial extract and fraction containing proteasome inhibitors in glioblastoma cell lines

Background: Marine microorganisms emerge as producers of compounds with peculiar chemical structure. A marine bacteria (BRA-346) isolated from ascidia, Euherdmania sp., showed a potentially cytotoxic extract. Studies carried out with this extract allowed identifying eponemycins compounds belonging of the proteasome inhibitors class. These substances are used clinically in the treatment of multiple myeloma, but have been tested with promising results in glioblastomas. This cancer represents an invasive malignant brain tumor where a deregulation of important signaling pathways related to DNA repair and apoptosis leads to chemoresistance.

Methods: The BRA346 extract was tested on HCT-116 cell lines by the MTT assay. The proteasome inhibition evaluation consisted of the application of extract in purified and crystallized yeast proteasome. The extract was then fractionated and two fractions showed close inhibition of 100% of the catalytic site chymotrypsin (ChTL) of the proteasome. To identify the molecule that binds to the catalytic subunit, the molecular networking of these two fractions was made and it was possible to highlight the mass 343.1 m/z. The fragmentation spectrum this mass was compared with GNPS bank that corroborate with eponemycin derivatives, which in turn are known proteasome inhibitors.

Results: BRA-346 is a marine Streptomyces sp. and its extract presents IC50 value of 30 ng/mL in HCT-116 cell line and its most active fraction showed IC50 values of 0.4; 0.5 and 0.9 μg/mL, for respectively the HOG, T98G and U87MG cell lines. A target-directed assay of BRA346 extract inhibited the chymotrypsin-like (ChTL) catalytic subunit of the yeast proteasome, with IC50 value of 0.4 μg/mL. Mass-spectrometry based dereplication and X-Ray protein crystallography of the crude extract and derived chromatographic fractions pointed TMC-86A (1-N-deacyl,1-N-butanoyl-Eponemycin) as the natural product responsible for proteasome inhibition. TMC-86A is a peptide epoxyketone, known as a proteasome inhibitor, which was previously isolated form terrestrial Streptomyces but has also been found in marine bacteria, which the marine environment as a promising source of anticancer molecules.

Conclusions: We conclude that the BRA-346 marine bacterium is a producer of proteasome inhibitors compounds of the class of eponemycins that responsible for the cytotoxic activity against tumor cell lines.

Session Topic: Chronic Diseases

Presenter: Anees Bahji[1,2]
Institution: Queen's University, Kingston, Canada

[1] Department of Psychiatry, Queen's University, Kingston, ON, Canada
[2] Department of Public Health Sciences, Queen's University, Kingston, ON, Canada

Hospital-based interventions for individuals with opioid use disorder: a scoping systematic review

Background: Various strategies, such as methadone-maintenance and buprenorphine therapies, have been proposed for the community-based treatment of individuals with severe opioid use disorder (OUD). However, research on the effectiveness of hospital-based interventions for individuals with OUD has been more limited.
Objectives: To systematically evaluate outcomes of hospital-based interventions in individuals with OUD.

Methods: Searches were conducted (up to October 2018) in the MEDLINE, CINAHL, Embase, PsycINFO, and Cochrane Central Register of Controlled Trials databases. Furthermore, relevant journals were searched by hand. References from identified studies were examined. Randomized and non-randomized intervention trials were considered. Trial quality was assessed according to the Cochrane Risk of Bias Tool.

Results: 22 of 354 retrieved papers met inclusion criteria. A total of 3604 individuals were included in the review, and 2 papers involved only children <5 years old. Papers were of average quality and all but eight had been published during the previous 10 years, 9 of which were from the United States. Study interventions were organized into three broad categories: detoxification programs (n = 7), prevention programs (n = 11), neonatal programs (n = 2), and combination programs (n = 2). Both interventions and outcome measures varied widely between studies. Overall findings demonstrate the effectiveness of the interventions considered.

Conclusions:T is evidence for the positive effects of hospital-based interventions for individuals for opioid use disorder. The effectiveness of these interventions aligns with community-based interventions for individuals with OUD, strengthening the importance of continuity of care across multiple settings of care. Moreover, it is important that knowledge translation, research, and debate extend to the medical community in order to ensure clinically effective care provision for these individuals.

Session Topic: Chronic Diseases

Presenter: Matthew Hacker Teper[1]
Institution: McGill University, Montreal, Canada

Co-Authors: Isabelle Vedel[1], Xin Yang[1], Eva Margo-Dermer [1], Catherine Hudon[2]

[1]Department of Family Medicine, McGill University, Montreal, Canada
[2]Department of Family and Emergency Medicine, Université de Sherbrooke, Sherbrooke, Canada

Modern management of chronic disease? Understanding barriers and facilitators to conducting case management (CM) in primary care

Background: In response to an aging global population with increased chronic illness, case management (CM) has emerged as a powerful innovation to address complex patient needs. CM is defined as the collaborative process of assessment, planning, facilitation, care coordination, evaluation and advocacy for the options and services required to meet patient needs. Despite impressive and established benefits of CM for the care of vulnerable and chronically ill patients, implementation of CM has been challenging worldwide. The remains a dearth of synthesis of evidence surrounding the barriers and facilitators to conducting CM, especially in primary care settings.

Methods: We conducted a systematic review and thematic synthesis of qualitative data. Studies from around the world were collected via searches in three electronic databases (MEDLINE, CINAHL, Embase). Titles, abstracts and full texts were screened for relevance to the research question. Included studies were assessed for quality, and a sensitivity analysis was conducted. Results from included articles were synthesized according to the protocol of Thomas and Harden (2008).

Results: Of the 1952 records initially located, 19 studies, originating from six countries, met our inclusion criteria. Nine factors (barriers and/or facilitators) affecting the ability of primary care teams to conduct case management were identified: “Family Context”, “Stable Policy and Available Resources”, “Physician Buy-in and Understanding of the Case Manager Role”, “Team Communication Practices”, “Adequate Training in Technology”, “Relationships with Physicians”, “Relationships with Patients”, “Time Pressure and Workload”, and “Autonomy of Case Manager”. A schematic representation, designed to situate these factors relative to one another, and to demonstrate the relationships between factors, is advanced.

Conclusions: This systematic review and thematic synthesis identifies and validates a wide range of factors that influence a primary care teams’ capacity to conduct CM. Understanding these factors may allow for the development of policy- or clinic-level interventions to improve case management function and, by extension, to provide better care for chronically ill patients. This understanding is especially timely, given the global push to address chronic illness and complex patient needs in primary care. Findings are pertinent to health services researchers, healthcare professionals and policy makers.

Session Topic: Chronic Diseases

Presenter: Miguel Romero Sepulveda[1]
Institution: McGill University, Montreal, Canada

Co-Authors: B. Adrienne Caldwell[1], Alvin Shrier[1], Gil Bub[1]

[1] Department of Physiology, McGill University, Canada

Conduction velocity manipulation of cardiac monolayers using optogenetics

Background: Cardiac arrhythmias are characterized by atypical heart rates or rhythms that can often be related to the formation of a spiral wave, after its initiation a spiral can persist, break up into multiple waves, or disappear. These various modes of dynamic behavior have been documented theoretically and experimentally by different groups, however, the transitions within the dynamical behavior of the system is poorly understood.

Methods: Stem cells were differentiated into cardiomyocytes are cultured to form a beating monolayer, viral infection using an adenovirus to express ChR2 when exposed to a blue light stimulus was performed. Cardiac optogenetics involves the use of light to control cells that express light-sensitive ion channels. Cardiac monolayers are preferred since blue light has a depth penetration limit of about 1mm, and the relative thinness of our experimental preparation allows us to fully excite the tissue.
Image Acquisition. Monolayers are excited with the use of an adapted projector, video recordings of wave propagation and their behavior would be collected from a high speed sCMOS camera mounted to a custom darkfield microscope, using software that has been developed by the laboratory supervisor Dr. Gil Bub.

Results: Test conducted in our lab using cardiomyocytes responsive to blue light stimulus patterned with spatial frequencies over the tissue resulted in a series of recordings showing variations in conduction velocity and overall wave propagation, promoting wave-breaks that induced spiral wave formation.

Conclusions: Heterogeneities are intrinsic in any physiological system; hence noise is an inherent characteristic of the studied media. The collected data allow us to shed some knowledge regarding the effects of noise in the cardiac system, its relation to spiral wave formation, and behavior, which can correlate to cardiac pathologies and may lead to new technologies to improve their treatment.

Session Topic: Chronic Diseases

Presenter: Elaine Liu[1]
Institution: University of Western Ontario, London, Canada

Co-Authors: Sara Ndombele[1], Charles Yin[1], and Bryan Heit[1]

[1] Department of Microbiology and Immunology, Schulich School of Medicine & Dentistry, University of Western Ontario, London, Canada

Differential antigen presentation following efferocytosis

Background: Efferocytosis is the engulfment and removal of dying cells by phagocytes. Although this process shares a common degradative pathway with pathogen phagocytosis, efferocytosis is immunosuppressive, suggesting that these processes differentially sort antigens. Dysregulated efferocytosis has been implicated in autoimmune disease, potentially via inappropriate presentation of apoptotic cell-derived antigens. Despite its importance in initiating appropriate immune responses, whether apoptotic cell-derived antigens are ultimately presented following efferocytosis and the effects of toll-like receptor (TLR) signaling on antigen presentation remains unclear. We hypothesize that phagocytosis and efferocytosis drive differential antigen presentation, with TLR signaling inducing antigen presentation that is prevented during efferocytosis.

Methods: We are working towards developing an in vitro model antigen tracking system consisting of E alpha peptide-ovalbumin fusion protein (EαOVA). Following phagocytosis or efferocytosis of bacteria or apoptotic mammalian cells that express EαOVA, murine antigen presenting cells will be co-cultured with T cells. Antigen presentation will be assessed as T cell activation and proliferation using flow cytometry. Additionally, efferocytosis of cells that simultaneously express EαOVA and FliC, a bacteria-derived danger signal recognized by TLR5, will allow us to study whether TLR signaling influences antigen presentation following efferocytosis.

Results: This is an on-going experiment and much of the described methods are in the process of being optimized. However, preliminary experiments show EαOVA expression in bacteria and mammalian cells. Phagocytosis and efferocytosis assays using primary bone marrow-derived dendritic cells (BMDCs) show these cells are capable of bacterial and mammalian cell internalization. Pilot experiments using the B3Z T cell hybridoma cell line and a colourimetric assay to detect activation suggest that BMDCs are capable of cross presenting exogenous antigen. Furthermore, we have also demonstrated FliC expression in mammalian cells.

Conclusions: Preliminary evidence shows the Eα-OVA model's potential to study and compare specific antigen presentation between phagocytosis and efferocytosis. Using this model, we hope to elucidate the antigen processing mechanisms of signaling tolerance following efferocytosis within dendritic cells.

Session Topic: Chronic Diseases

Presenter: Abankwa Abigail Akua[1]
Institution: Kwame Nkrumah University of Science And Technology, Kumasi Ghana
Co-Authors: B. Adrienne Caldwell[1], Alvin Shrier[1], Gil Bub[1]

[1] Department of Biochemistry and Biotechnology, Kwame Nkrumah University of Science and Technology, Kumasi, Ghana

Membrane channel diseases

Membranes are known to be selectively permeable, as they discriminate among substances that traverse them. Membranes also have channels that give its functions. The fluid mosaic model describes the basics of a membrane. In order for substances to traverse the membrane, the must pass through channels. These transmembrane channels are narrow and only allow specific substances to traverse it. Aquaporin and ion channel are the two main categories of membrane channels. Transmembrane channels present their associated diseases. Majority of the membrane channel diseases are based on mutations in the genes that encode these channels. The diseases include; familial neurological, cardiac, muscle and transport organ defects referred to as channelopathies. Usually, the mutations leading to these disorders are missense and affect channel kinetics. From literature, drugs administered against channelopathies are aimed at either blocking or opening the respective ion channels, which cannot respond to stimuli produced so that balance is set when membrane potential is generated. Most of these disorders have no individualized treatments, hence management of the disease progresses with progressing study of the condition.

Session Topic: Chronic Diseases

Presenter: Carolini Valadeo[1,2]
Institution: Universidade de Franca Unifran, Franca, Brasil

Co-Authors: Apollo Rodrigo Alves Senne[1,2], Carolini Bolonha Valadão[1]; Marina Morais Pimenta[1]

[1] Universidade de Franca, Unifran, Franca – SP, Brasil.
[2] Rua Evaldo Olímpio da Cunha, 3189 – Jardim Luiza II, Franca – SP 14407-650, Brasil, (16) 99259-0739, apollosenne@yahoo.com.

Physiotherapeutic interventions in the prevention of stress and burnout syndrome: a bibliographic review

Background: Occupational stress is the set of factors triggered during a long working day favoring the appearance of some diseases affecting their psychosocial health, thus leading to burnout syndrome. SB is recognized as chronic occupational risk characterized by lack of energy, psychosocial depletion, depersonalization and low professional achievement, common in education and health services with direct contact. Considered a global epidemiology. Prevention must involve a work of changes in the organizational culture, reduction of the workload, competitiveness, seeking goals that include the individual well-being. It is worth mentioning that the multi professional team is essential for prevention. Job, ergonomic and dynamic activities between boss and team are essential for professional performance, providing improvement of the state of depression, psychological, motivation, anxiety and stress.

Objective: To present symptoms related to occupational stress, highlighting SB triggers and prevention measures to improve professional performance and quality of life.

Methodology: Researches in Scielo, Medline, Lilacs and Google Scholar, using descriptors (DeCS) - professional exhaustion; Worker's health; Prevention; Occupational hazards, including articles in the Portuguese language published from 2006 to 2016, that address prevention, occupational stress, burnout syndrome and excluded articles with exclusive access to the abstract and that did not meet the objective of the research.

Final considerations: With the present review, it was possible to observe many studies in the Brazilian literature related to the occupational risks generating SB, especially in the health area.

Session Topic: Global Health

Presenter: Roger Chamaa
Institution: National and Kapodistrian University of Athens, Athens, Greece

The importance of e-health system in sustainable health development

Background: In order to identify the importance of e-health system in sustainable health development we have to focus on specific cases such as the case of Greece. Greece, has medical staff of great qualification and was evaluated by the UN with a percentage of 76% in 2016, surpassing technologically advanced, Japan. This distinction exists due to the fact that Greek Doctors are inclined to serve their science successfully and impartially.

Facts: However, during the following year Greece's rating fell by 68 points, 15 levels down in the world ranking (41st) due to the fact that it was not able to successfully deal with the multiple issues that arose. Therefore, talent is not considered enough but there is a need for a sense of organization and planning.

Result: More specifically, organization means reducing corruption and reducing bureaucracy but mainly means stability. Thereupon, the use of technology and advanced technological systems can solve numerous medical problems whereas at the same time it can bring stability inside the health sector that will lay the foundations for upper-efficiency in the e-health system. Alongside, this can decongest hospitals by helping doctors to respond properly to their tasks. On the other hand, decongestion will favor the treatment of serious incidents.
As a final statement, a pivotal foundation of the e-health system is considered the e-prescription which will be justified on the basis of the patient's record when each drug is administered, ending speculative phenomena.

Conclusion: It is therefore a Golden section between differentiated rational logics having as a logical axis the expertise arising from universities and empirical observation as well as technology, which rapidly tends to reduce red-tape (bureaucracy) at all levels of lifetime.

Session Topic: Global Health

Presenter: Helen Rich
Institution: University of Pittsburgh, Pittsburgh, United States

Co-Author: Collin McCourt[1], Wen Quan Zheng[1], Kevin J. McHugh[1], and John F Alcorn[1]

[1]UPMC Children's Hospital of Pittsburgh, Department of Pulmonology

Interferon lambda inhibits bacterial clearance during influenza super-infection

Rationale: While pandemic influenza A H1N1 infection causes significant morbidity and mortality on its own, it also renders an individual more susceptible to super-infection with myriad bacterial pathogens, notably Streptococcus pneumoniae and Staphylococcus aureus. We have previously shown that type I interferons produced by influenza impair bacterial defense six to seven days post-influenza infection. Similarly, mice that lack the receptor for type III interferon (IFNL, IL-28A/B) exhibit better clearance of S. aureus bacterial pneumonia, with or without preceding influenza. As IFNL therapy has been proposed as a treatment for patients with influenza, we investigated the effect of overexpressing IFNL during influenza infection on bacterial super-infection.

Methods: 6-8 week old male C57BL/6 mice were infected with 25 PFU of influenza H1N1 A/PR/8/34. Five days later, mice were treated with an adenoviral vector to overexpress mIL-28B or eGFP as control, one day later challenged with 5□107 CFU USA300 methicillin-resistant S. aureus or 1000 CFU S. pneumoniae serotype 3, and sacrificed 24 hours (S. aureus) or 48 hours (S. pneumoniae) following bacterial challenge. Mouse lungs were lavaged with 1 mL sterile PBS, and infiltrating cells were counted on a hemocytometer. Lungs were homogenized and plated for bacterial CFU counting, frozen in liquid nitrogen for protein analysis, or processed to a single cell suspension and stained for flow cytometry.

Results: IFNL overexpression increased bacterial burden upon both S. aureus and S. pneumoniae super-infection during influenza. Neutrophil numbers in bronchoalveolar lavage were decreased, while chemotactic cytokines were increased in the lung. When bacteria were labeled with FITC prior to infection, neutrophil binding and uptake of bacteria was significantly decreased.

Conclusions: IFNL overexpression increased bacterial burden in the lungs of super-infected mice, concurrent with fewer neutrophils measured in bronchoalveolar lavage. It is likely that the lungs of these mice over-produce chemotactic cytokines in response to the lack of neutrophils. Bacterial clearance was impaired by IFNL as shown by higher bacterial burden in the lungs, as well as lower FITC-labeled MRSA binding and uptake in vivo by lung neutrophils. These data suggest that IFNL treatment for influenza poses significant risks for patients, as bacterial super-infection is not an uncommon complication.

Session Topic: Global Health

Presenter: Elaine Liu
Institution: University of Western Ontario, London, Canada

Co-Authors: Sara Ndombele[1], Charles Yin[1], Bryan Heit[1]

[1]Department of Microbiology and Immunology, Schulich School of Medicine & Dentistry, University of Western Ontario, London, Canada

Differential antigen presentation following efferocytosis

Background: Efferocytosis is the engulfment and removal of dying cells by phagocytes. Although this process shares a common degradative pathway with pathogen phagocytosis, efferocytosis is immunosuppressive, suggesting that these processes differentially sort antigens. Dysregulated efferocytosis has been implicated in autoimmune disease, potentially via inappropriate presentation of apoptotic cell-derived antigens. Despite its importance in initiating appropriate immune responses, whether apoptotic cell-derived antigens are ultimately presented following efferocytosis and the effects of toll-like receptor (TLR) signaling on antigen presentation remains unclear. We hypothesize that phagocytosis and efferocytosis drive differential antigen presentation, with TLR signaling inducing antigen presentation that is prevented during efferocytosis.

Methods: We are working towards developing an in vitro model antigen tracking system consisting of E alpha peptide-ovalbumin fusion protein (EαOVA). Following phagocytosis or efferocytosis of bacteria or apoptotic mammalian cells that express EαOVA, murine antigen presenting cells will be co-cultured with T cells. Antigen presentation will be assessed as T cell activation and proliferation using flow cytometry. Additionally, efferocytosis of cells that simultaneously express EαOVA and FliC, a bacteria-derived danger signal recognized by TLR5, will allow us to study whether TLR signaling influences antigen presentation following efferocytosis.

Results: This is an on-going experiment and much of the described methods are in the process of being optimized. However, preliminary experiments show EαOVA expression in bacteria and mammalian cells. Phagocytosis and efferocytosis assays using primary bone marrow-derived dendritic cells (BMDCs) show these cells are capable of bacterial and mammalian cell internalization. Pilot experiments using the B3Z T cell hybridoma cell line and a colourimetric assay to detect activation suggest that BMDCs are capable of cross presenting exogenous antigen. Furthermore, we have also demonstrated FliC expression in mammalian cells.

Conclusions: Preliminary evidence shows the Eα-OVA model's potential to study and compare specific antigen presentation between phagocytosis and efferocytosis. Using this model, we hope to elucidate the antigen processing mechanisms of signaling tolerance following efferocytosis within dendritic cells.

Session Topic: Global Health

Presenter: Dr. Zeineb Zian
Institution: Biomedical Genomics and Oncogenetics Research Laboratory, Faculty of Sciences and Techniques of Tangier. University Abdelmalek Essaâdi, Tangier, Morocco
Co-Authors: Khaoula Hamdouch[1,2], Mouna Maamar[3], Amina Barakat[1], Naima Ghailani Nourouti[1], Manuel Valdivia[2], Naima Arji[4], Mohcine Bennani Mechita1

[1] Biomedical Genomics and Oncogenetics Research Laboratory. Faculty of Sciences and Techniques of Tangier, University of Abdelmalek Essaâdi, Morocco. E-mail: z.zian@uae.ac.ma
[2] Faculty of Sciences, University of Cadix, Spain.
[3] Internal Medicine Department, Hospital Ibn Sina, Rabat-Morocco.
[4] Auto-immunity Laboratory, National Institute of Hygiene, Rabat-Morocco.

Anti-CENP-B auto-antibodies in Moroccan patients with scleroderma

Background: Scleroderma, or Systemic sclerosis (SSc), is a rare autoimmune disease of the connective tissue which affects many organs including the skin, arterioles and microvessels leading to the development of fibrosis and vascular obliteration. SSc is characterized by an unknown etiology and the production of antinuclear (ANA) and anti-centromere auto-antibodies (ACA). Centromeric Protein B (CENP-B) is considered the major centromeric auto-antigen in SSc since one of the main ACA is produced against this protein. Thus, we studied the immune response against the CENP-B antigen by analyzing the reactivity of Scleroderma sera against the amino-terminal and carboxy-terminal expressed domains of the CENP-B protein (Nt-CENPB and Ct-CENPB).

Methods: Thirty Moroccan patients were diagnosed with SSc in the Internal Medicine Department at the University Hospital Center (Rabat-Morocco) between December 2011 and December 2013. Sera from all patients were screened for ANA and ACA by Indirect immunofluorescence on Hep-2 cells, followed by identification of anti-extractable nuclear antigen (ENA) antibodies by ELISA. Characterization of specific Nt-CENPB and Ct-CENPB epitopes in sera was realized by Western blot technique.

Results: 29 out of 30 (96, 66%) patients had positive ANA. 13 patients had positive anti-ENA antibodies whose identification showed: 11 patients had anti-Scl70 antibodies, whose one has reacted with anti-SSA and anti-SSB antibodies, and another with anti-SSB antibodies. 2 patients had anti-Sm/RNP antibodies whose one reacted with anti-SSA antibodies. 11 out of 30 (36, 67%) patients were ACA positive and 6 of them produced anti-Nt-CENPB auto-antibodies. None of all sera tested reacted against Ct-CENPB.

Conclusions: Our results demonstrate for the first time that the N-terminal region of CENP-B auto-antigen represents the dominant auto-epitope in Moroccan patients with scleroderma. Further studies are needed to confirm these findings and to study other auto-antigens that could be a potential marker in scleroderma patients.

Session Topic: Global Health

Presenter: Anthony Chen-En Huang
Institution: Department of Human Biology, University of Toronto, ON, Canada
Co-Authors: Anthony Cheng-En Huang[1,2,4], Karen Kai-Lin Fang[3,4], Brad Bass[5]

[1]Department of Molecular Genetics, University of Toronto, Toronto, Canada
[2]Department of Human Biology, University of Toronto, Toronto, Canada
[3]Department of Laboratory Medicine and Pathobiology, University of Toronto, Toronto, Canada
[4]Department of Immunology, University of Toronto, Toronto, Canada
[5]School of the Environment, University of Toronto, Toronto, Canada

In silico modelling of cancer cell response to NTR/MTZ Suicide Gene Therapy

Background: Suicide gene therapy, also known as Gene Directed Enzyme Prodrug Therapy (GDEPT), is an experimental treatment option for cancer. GDEPT allows for targeted expression of an enzyme-encoding gene construct into tumour cells, where prodrug administration will lead to the generation of apoptosis-inducing metabolites in the target cell population. Despite not yet approved for clinical use, pre-clinical studies of this therapeutic strategy reveal great potential. NTR/MTZ is one of the several "enzyme/prodrug" systems that have been under investigation, known for its ability to kill both proliferating and quiescent cells. However, few preliminary studies have been conducted regarding its anti-tumour activity.

Methods: We examine NTR/MTZ's anti-tumour efficiency by modelling normal and cancer cell response to this enzyme/product treatment. Complexity and Organized Behaviour Within Environmental Bounds (COBWEB) is an agent-based simulation software, which allows for operationalizing different variables at once and visualizing real-time data and documentation. For these reasons, different hallmarks of cancer can be successfully simulated by our group. Moreover, the reproducible in silico results can be generated in a matter of minutes per execution and at minimal costs.

Results: The in silico data indicate that compared to normal cells, cancer cells exhibit greater resistance to the NTR/MTZ treatment under both normoxic and hypoxic conditions. The greater difficulty of cell ablation against cancer cell lines can be attributable to their ability to establish tumour microenvironments, which induce selective-pressure mediated clonal evolution. Therefore, NTR/MTZ suicide gene system does not present strong efficacy against solid tumours; and may not demonstrate clinical significance such as tumour clearance or shrinkage in biological settings.

Conclusion: The limitations of the software include deviation of cellular behaviour and cell-drug interactions from the actual biological context due to the constraints such as modelling tumour morphology, heterogeneity, and other factors involved in cancer pathophysiology. Yet, our in silico model powered by COBWEB may serve as a cost-effective tool capable of predicting cell responses to enzyme/prodrug modalities prior to running wet-lab experimentation or clinical interventions; Notwithstanding, further software optimization, modelling efforts, and validations from web lab experimentation will be required.

Session Topic: Global Health

Presenter: Anthony Chen-En Huang
Institution: Department of Human Biology, University of Toronto, ON, Canada
Co-Authors: Anthony Cheng-En Huang[1,2,3], Chi-Chia Chang[4], Kuo-Chiang Hsia[4]

[1]Department of Molecular Genetics, University of Toronto, Toronto, Canada
[2]Department of Human Biology, University of Toronto, Toronto, Canada
[3]Department of Immunology, University of Toronto, Toronto, Canada
[4]Institute of Molecular Biology, Academia Sinica, Taipei, Taiwan

Structural Analysis of AKAP450 and its Participation of Microtubule Nucleation on the Cis-Golgi

Background: The spatial-temporal localization of microtubule (MT) nucleation is mediated by the γ-tubulin ring complex (γ-TuRC). γ-TuRC is composed of several proteins collectively recruited to a microtubule organizing centre (MTOC). In proliferating animal cells, the centrosome serves as the major MTOC responsible for the assembly of radial MT array, critical for faithful chromosome segregation and intracellular transport. However, previous studies revealed non-centrosomal MT arrays to be present on the cis-cisternae of the Golgi apparatus, acting as another MTOC in the cytoplasm. Further, recent experimental data and proposed molecular model suggested this process to be dependent of multiprotein complex recruitment. A-kinase anchoring protein of 450 kDa (AKAP450) is a scaffolding protein that interacts with γ-TuRC. Depletion of AKAP450 or Golgi Matrix Protein, GM130, leads to diminished non-centrosomal MT nucleation capacity. Although AKAP450 has been reported to be indispensable for γ-TuRC recruitment to the Golgi and participate in a GM130-dependent manner, the detailed protein-protein interactions at a molecular level remains elusive. We hypothesize AKAP450 to be a key binding partner with γ-TuRC subunits, integral to the molecular mechanism of MT nucleation.

Methods: AKAP450 was expressed via BL21 competent cell, and subjected to protein purification protocols (affinity, ionic-exchange, and size-exclusion chromatographies). SD200 gel filtration and the presence or absence of co-migration were used as a preliminary detection for protein binding.

Results: Co-migration in SD200 gel filtration reveals binding interaction between AKAP450 (AA150-800) and GCP2 (AA 1-169)/GCP8, while no binding interaction was observed between AKAP450 (AA150-630) and selected GCP2/GCP8 complexes. We propose that γ-tubulin complex protein 2 and 8 (GCP2 and GCP8) can form a complex, and there exists a binding site in AKAP450 that interacts with the N-terminal region of GCP2. Golgi-nucleated microtubules maintain structural integrity of the GA, they thus partake critical roles in cell migration, division, and homeostasis.

Conclusion: Taken together, we aim to enhance the resolution of AKAP450's binding interaction with other proteins to further elucidate its biomolecular properties as its 3D structure remains unsolved; meanwhile, we may explore relevant pathways and the implications thereof for metastasis in cancer through a structural perspective.

Session Topic: Global Health

Presenter: Dr. Fatima Abdelhakam
Institution: University of Khartoum, Faculty of Medicine, Institute of Endemic Diseases, Khartoum, Soudan
Co-Authors: Fatima A Elmugadam[1], Liena ELsayed[3], Haytham M Gorshi[2], Almigdad HMohammed[1], Murad Almak[1], IsraaH Hussain1 Mohammed A.Farag[1], Mohammed S.Tawar[1], Elhami A Ahmed[4], Almegdad S A[1], Wadah O Awad[1], Ahmed M Musa[2]

[1]Khartoum University, Faculty of Medicine, Sudan
[2]Institute of Endemic Diseases, Faculty of medicine, University of Khartoum, Sudan.
[3]Department of Biochemistry, Faculty of Medicine, University of Khartoum, Sudan.
[4]UNESCO chair in Bioethics, Faculty of Medicine, University of Khartoum, Sudan.

Knowledge, Attitude and practice towards Consanguineous marriage, in Sudan 2018

Aim: The study aimed to assess the knowledge, attitude and practice aspects on the relationship of consanguinity to negative health outcomes.

Background: Consanguinity (intra-familial marriage) is a global health problem with various adverse health outcomes. As this practice increases homozygosity of recessive alleles, it results in higher risk of early mortality and morbidity. Although, Sudan has one of the highest rates of consanguinity exceeding 40-50%.

Methodology: Data was collected from 1089 participants. Study was conducted in 13 different localities. using convenience sampling, on house based survey. Sudanese residents, 18 years and above, irrespective of their socio-economic status, were interviewed based on a locally generated and tested questionnaire. Analysis was done using descriptive and inferential statistics.

Results: 518 (48%) of participants were females, 571(52%) were males. about 800(73%) were among 18-40 years' age group. The majority of respondents 437(39%) were college graduates. 803(74%) agreed on the negative health consequences of consanguinity, while 150(14%) opposed and 136 (12%) said "I don't know". Among the respondents, 696(64%) showed non-preference for consanguineous marriage, Most frequently due to the possible transmission of respondents were willing to take pre marital genetic testing. genetic diseases. Of the 393 (36%) that showed preference the most frequent reason was that it contributes to stability of the marriage. 908(83%) were willing to undertake premarital genetic testing.

Conclusion: in our study, the overall awareness towards the issue was moderately high. But the practice still persists in high rates. We need to investigate the issue more in order to Integrate public health policies into the community, as they are the future consumers of this service.

Session Topic: Global Health

Presenter: Yanymee Nimesia Guillen Quispe
Institution: Hallym University, Chuncheon, South Korea

Co-Author: Seung Hwan Hwang[1], Zhiqiang Wang[1,2], Guanglei Zuo[1] and Soon Sung Lim[1,3,4]

[1]Department of Food Science and Nutrition, Hallym University, South Korea
[2]College of Public Health, Hebei University, Baoding, China
[3]Institute of Natural Medicine, Hallym University, Chuncheon, South Korea
[4]Institute of Korean Nutrition, Hallym University, Chuncheon, South Korea

Screening *in vitro* targets related to diabetes in herbal extracts from Peru: Identification of active compounds in *Hypericum laricifolium Juss.* by offline high-performance liquid chromatography

Background: According to the World Health Organization (WHO), the prevalence of diabetes continues to increase at an alarming rate. Globally, an estimated 346 million people are living with diabetes, figures that are predicted to have a severe impact on human health by 2025. Therapy for Diabetes mellitus (DM) relies on several approaches, many of which comprise drug targets for type 2 diabetes. Moreover, various efforts have been made to obtain other effective and safe enzyme inhibitors from plant extracts to control diabetes. There are different targets related to diabetes and its complications such as α-glucosidase, aldose reductase (AR), and free radicals.

Methods: This study investigates in vitro targets related to diabetes in 30 herbal extracts from Peru, for the first time, using α-glucosidase, aldose reductase (AR) inhibitory assays and 2,2-diphenyl-1-picrylhydrazyl (DPPH) and 2,2′-azino-bis(3-ethylbenzothiazoline-6-sulfonic acid) (ABTS) scavenging assays. Subsequently, an ultrafiltration method and offline DPPH- high-performance liquid chromatography (HPLC) and ABTS-HPLC assays to screen active compounds for Hypericum laricifolium Juss. (HL).

Results: Of the 30 herbal extracts assayed, only 23 crude extracts exhibited inhibition at 500 μg/mL in the α-glucosidase inhibition assay and AR inhibition assay. A total of 13 extracts presented relatively high antioxidant capacities (>50%). Among the 30 herbal extracts, Hypericum laricifolium Juss. (HL) was the herb which showed more than 50% inhibition in all assays, presenting 97.2 ± 2.0%, 56.9 ± 5.6%, 81.9 ± 2.5%, and 58.8 ± 4.6% inhibition for the α-glucosidase, AR, DPPH, and ABTS assays, respectively. Finally, six bioactive compounds, namely, protocatechuic acid, chlorogenic acid, caffeic acid, kaempferol 3-O-glucuronide, quercetin, and kaempferol were identified in HL by offline high-performance liquid chromatography (HPLC). Quercetin exhibited the strongest inhibition in all enzyme assays and the strongest antioxidant activity.

Conclusions: In this study, the results suggest that HL shows great potential for the complementary treatment of diabetes and its complications.

Session Topic: Global Health

Presenter: Abiola Adeosun[1,2]
Institution: Federal University of Agriculture, Abeokuta, Abeokuta, Nigeria
Co-Authors: Ighodaro O.M.[1], Akinloye O.A[2]

[1]Department of Biochemistry, Faculty of Basic Medical and Applied Sciences, Lead City University, Ibadan
[2]Department of Biochemistry, College of Biological Science, Federal University of Agriculture, Abeokuta.

New method for determining blood pressure in animals using noninvasive CONTEC 08a device with small cuff: a path to antihypertensive drug development study in developing countries

Invasive method of determining blood pressure has been the early method used in animal model of hypertension study. Current noninvasive blood pressure monitoring device are very costly and not affordable by researchers from developing or under developed countries. In our study, we designed a new method for determining blood pressure in animal model studies by using CONTEC 08A device with small cuff. Ten male wistar rats of 182-240 g were divided into two groups (n=5/group). The first group was the control group without treatment, the second group was administered dexamethasone 2mg/kg body weight supplemented with 4% table salt as drinking water to induce hypertension. Blood pressure readings were taken in each rat for five times at baseline (day 0) and after 7 days. CONTEC 08A yielded good reproducibility in both hypertensive and non-hypertensive rats. Better reproducibility was obtained in non-hypertensive rats.

Session Topic: Global Health

Presenter: Ivayla Gyurova[1,2]
Institution: Cincinnati Children's Hospital Medical Center, Cincinnati, USA
Co-Authors: Heinrich Schlums[3], David Bernstein[4,5], Yenan Bryceson[3], Stephen N. Waggoner[1,2,5]

[1]Center for Autoimmune Genomics and Etiology, Cincinnati Children's Hospital Medical Center, Cincinnati, OH
[2]Pathobiology and Molecular Medicine Graduate Program, University of Cincinnati, Cincinnati, USA
[3]Center for Hematology and Regenerative Medicine, Department of Medicine, Karolinska Institutet, Karolinska University Hospital Huddinge, Stockholm, Sweden
[4]Division of Infectious Diseases, Cincinnati Children's Hospital Medical Center, Cincinnati, USA
[5]Department of Pediatrics, University of Cincinnati College of Medicine, Cincinnati, USA

Dynamics of adaptive natural killer cells in longitudinal analysis of CMV vaccine recipients

Background: Classical vaccine efforts focusing on the induction of B- and T-cell memory have proven ineffective in the protection against pathogens such as cytomegalovirus (CMV). Thus, CMV remains a significant public health threat. There is clear evidence that patients lacking natural killer (NK) cells suffer recurrent, severe infections with multiple herpesviruses, including CMV, highlighting the importance of NK cells in controlling this pathogen. In addition, several studies describe the expansion and persistence of phenotypically and functionally distinct murine (Ly49H+) and human (NKG2C+, FcRγneg, EAT-2neg, SYKneg) NK-cell subsets with putatively enhanced antiviral effector function upon CMV infection. Therefore, one potentially pioneering approach to creating an efficacious CMV vaccine would include the induction of such NK cell adaptations.

Methods: To test whether current experimental CMV vaccine formulations can induce these cells, we used longitudinal peripheral blood mononuclear cells (PBMC) samples collected during a vaccine trial with CMV gB in MF59 adjuvant administered to CMV negative adolescent females. PBMCs of vaccinees (n=20) and placebo-treated (n=20) subjects from various time points (baseline and post treatment) were evaluated for the expression of NKG2C+, FcRγneg, EAT-2neg, and SYKneg subsets in CD3-CD56dim NK cells.

Results: We observed several patterns of transient and sustained elevations in the frequency of FcRγneg, EAT-2neg, and SYKneg subsets at various time points despite absence of detectable CMV infection in any trial participants. Surprisingly, these patterns were apparent in participants regardless of administration of vaccine or placebo.

Conclusions: In contrast to previous cross-sectional studies, we present evidence that these CMV-reactive adaptive NK cells exhibit continuous oscillations in the blood of CMV negative individuals, suggesting that they may react to unknown environmental or inflammatory cues.

Session Topic: Global Health

Presenter: Yevheniya Sharhorodska
Institution: Institute of Hereditary Pathology of National Academy of Medical Sciences of Ukraine, Lviv, Ukraine
Co-Authors: O.Shkolnyk[1], N.Prokopchuk[1], H.Makukh[1]

[1]Institute of Hereditary Pathology of the National Academy of Medical Sciences of Ukraine, Lviv, Ukraine

The occurrence and structure of congenital heart defects in newborns according to the data of Lviv Regional Clinical Hospital, Ukraine (2011-2015)

Background: Annually, more than 5,500 children with congenital heart defects are born in Ukraine. 14% of children with cardiac anomalies die during the first week of life and 25% of them during the first month, while about 40% do not survive up to 1 year. An important factor is the time of diagnosis of the congenital heart defects (CHD) (prenatal or postnatal), and the actions to be taken.

Methods: The collection for the analysis of clinical, epidemiological, and medical-statistical data of primary medical documentation was carried out by analyzing the following data: 170 cards of pregnant women who gave birth to children with CHD and 170 cards of women who gave birth to healthy children.

Results: Over the course of 5 years, 172 of 15429 newborns were born with heart defects. The frequency of congenital heart disease was 1.1%. It is established that in the spectrum of this disease, the most frequent condition is heart disease with the arteriovenous discharge of blood (""pale"") – 102 (59.6%); the second most frequent is heart disease with reduced or normal blood flow: 49 (28.5%); the third – heart diseases without discharge of blood, but with the presence of obstacles at the level of the valves or major blood vessels – 14 (8.1%). The fourth most frequent involves the heart diseases that are rare – 7 (4.1%). 28 (16.3%) children identified concomitant congenital pathology: multiple congenital malformations – 12 (7.0%), chromosomal disorders 7 (4.1%), and congenital malformations of the nervous system – 6 (3.5%). We have set that 40.1% of the heart defects were diagnosed prenatally. For one female patient (1.5%), a heart defect was detected during the first trimester. For 24 female patients (35.8%), it was detected during the II trimester. For 42 female patients (62.7 %), it was detected during the third trimester of pregnancy.

Conclusion: Perinatal pathology due to congenital heart defects accounts for 1.0% -1.3% of the total number of newborns. In the structure of congenital heart defects among newborns, the most common are faults with arteriovenous discharge of blood, - 102 (59.6 %). 28 (16.3%) children were born with concomitant congenital pathology, with 7 (4.1%) having chromosomal pathology. According to the ultrasound prenatal diagnosis, it was diagnosed 40.1% of the time with congenital heart defects, and 59.9% of the time with a timely diagnosis, constituting a reserved reduction of perinatal morbidity and mortality.

Session Topic: Global Health

Presenter: Bright Oppong Afranie
Institution: Kwame Nkrumah University of Science and Technology, Kumasi, Ghana

Co-Authors: Enoch Odame Anto[1,2], Christian Obirikorang[1], Emmanuel Acheampong[1], Bright Amankwaa[1], Bright Oppong Afranie[1], Sampson Donkor[1], Isaac Hope[3,4], Juliana Jommo[3] and Esther Osaah[3]

[1]Department of Molecular Medicine, School of Medical Sciences, Kwame Nkrumah University of Science and Technology, Kumasi, Ghana
[2]School of Medical and Health Sciences, Edith Cowan University, Perth, WA, Australia
[3]Laboratory Unit, Saint Francis Xavier Hospital, Assin Fosu, Ghana
[4]Department of Medical Laboratory Science, Royal Ann College of Health, Kumasi, Ghana

Evaluation of individual and combined markers of urine dipstick parameters and total lymphocyte count as a substitute for CD4 count in low-resource communities in Ghana

Introduction: We evaluated the individual and combined levels of urine dipstick and total lymphocyte count (TLC) as surrogate markers for CD4 count in a low-resource community in Ghana.

Methods: This cross-sectional study recruited 200 HIV-infected patients from the Saint Francis Xavier Hospital, Assin Fosu, Ghana. Complete blood count, CD4 count, and urine dipstick analysis were measured for participants. The threshold values were determined as <350 cells/µl for CD4, <1200 cells/µl for TLC, and ≥+on urine dipstick analysis.

Results: The mean age of participants was 43.09 years. Proteinuria≥+[aOR=4.30 (3.0–18.5)], leukocyturia≥+[aOR=2.91 (1.33–12.5)], hematuria ≥+[aOR=2.30 (1.08–9.64)], and TLC<1200 cells/µl [aOR=3.26 (3.94–15.29)] were significantly associated with increased risk of CD4 count<350 cells/µl. Using the individual markers, the best substitute marker for predicting CD4 count<350 cells/µl was proteinuria at a cutoff point≥2++, AUC of 0.973, sensitivity of 97.6%, specificity of 100.0%, PPV of 100.0%, and NPV of 89.1%. A combination of≤1200 TLC+≥2++ (leukocyturia+proteinuria+hematuria) yielded an AUC of 0.980, sensitivity (72.8%), specificity (100.0%), PPV (100.0%), and NPV (97.9%).

Conclusion: Proteinuria could serve as a noninvasive screening tool, but the combination of proteinuria, leukocyturia, hematuria, and TLC serves as a better substitute marker for CD4 count in monitoring the disease progression among HIV patients in low-resource communities.

Session Topic: Global Health

Presenter: Silvio Almeida Junior[1,2]
Institution: University of Franca, Franca, São Paulo, Brazil

Co-Authors: Nhaypi Iasmin Taveira Moreira[1], Fernanda Carolina da Silva,[1] Isabela de Castro Capoia[1], Inglity Lorrane da Silva Cruz[1], Danilo Cândido Bulgo[3] Rafaela Simei Pompolim[1]

[1]Research Group on Toxicology and Health Promotion (G.E.T.o.S) - Euro Anglo Franca, Franca, São Paulo, Brazil.
[2]Laboratory of Animal Science - Postgraduate Program in Animal Science, University of Franca, Franca, São Paulo, Brazil. [3] Postgraduate Program in Health Promotion, University of Franca, Franca, São Paulo, Brazil.

Use of plants by popular medicine in a medium-sized city in southeastern Brazil

Background: Brazil is a country with a rich diversity of flora, and despite the large number of plant species, there are few phytochemical studies and biological activities. The expression of this is the scientific research focused on university centers of great public and private institutions of the country. The use of popular medicine is already something millenarian and it brings great advances, being the plants of great interest in the pharmaceutical area because the discoveries of new drugs are promising. Faced with this, it is necessary ethnobotanical survey, as well as phytochemical studies, biological tests and their toxicological activities for safety analysis. The objective of this work is to evaluate the profile of plants used by people over 60 years of age, in a medium - sized city in southeastern Brazil.

Methods: Application of form to the local population and research in scientific bases.

Results: Among the surveys, the most cited ones due to their wide use were the “Capim cidreira” (Cymbopogon citratus), Camomila (Matricaria chamomilla), and Boldo (Peumus boldus). The lemon grass in its popular preparation, presents calming, hypnotic, analgesic, anti-inflammatory, antispasmodic, antihypertensive activities and through the essential oil, the plant has antibacterial, antifungal and antiparasitic activity. Chamomile has activity against flatulence, colic, hysteria, intermittent fever and strong anti-inflammatory, antiseptic and antioxidative activity. Boldo, a plant widely used in Latin America, presents great use related to gastric and hepatic problems. Plants are prepared through infusions or decoctions and are generally used fresh or dried aerial parts, filtered waters are used and are not sweetened and when they are, honey is used, in which it is widely used in folk medicine due to its already known biological activity.

Conclusion: Works such as this, of an exploratory nature, bring information about plants used in folk medicine beyond its already proven biological effect. It is of utmost importance to transmit scientific information to the community in an attempt to promote health and well-being for all. The work is in progress and shows promise within the region applied.

Session Topic: Global Health

Presenter: Avinash Kumar Singh
Institution: National Institute of Immunology, Delhi, India

Co-Authors: Vijaykumar S. Pawale[1], Sreetama Das[2], Venkatareddy Dadireddy[2], Suryanarayanarao Ramakumar[2], and Rajendra P. Roy[1]

[1]National Institute of Immunology, Delhi, India
[2]Department of Physics, Indian Institute of Science, Bangalore, India

A tale of substrate recognition in two housekeeping sortases.

Background: Cell wall anchoring of surface proteins in gram-positive bacteria is mediated by transpeptidase Sortase. In pathogenic bacteria sortases are potential drug targets, as many of the proteins that they display on the microbial surface play key roles in the infection process. Sortase enzymes are generally grouped into six classes (A-F) of which Class A sortase is considered as a housekeeping enzyme. The prototype Sortase A (SrtA) of Staphylococcus aureus recognizes a LPXTG pentapeptide motif in the C-terminal of sortase substrates, cleaves the T-G peptide bond and ligates Protein-LPXT to terminal aminoglycine branch of lipid II. The peptide ligation propensity of SrtA is very useful in protein engineering and semi-synthesis.

Methods: Here we describe the crystal structure and functional attributes of a new class of housekeeping sortase (SrtE) from Streptomyces avermitilis. SrtE prefers a LAXTG peptide substrate in contrast to LPXTG of SaSrtA. The crystal structure of SrtE, mutagenesis and biochemical experiments provide clues to the altered substrate specificity of SrtE.

Results: The results point to the role of a conserved Tyr residue (Tyr 112). Tyr 112 is conserved in all class E sortases despite the lack of high sequence identity between them. The mutation of Y112 to F112 resulted in 50-fold decrease in Ala specificity with no change in its specificity for the Pro-substrate. Interestingly mutation of the equivalent residue in SrtA (A104F) did not affect the specificity of SrtA.

Conclusions: In summary, cumulative results highlight Y112 residue of SavSrtE as a critical determinant of specificity. The significance of Y112 in substrate recognition is also borne out by the fact that evolved mutants of SaSrtA generated in the past with improved activity toward LAETG motif contained mutation of Y112 equivalent Ala104 residue. The retention of native-like Pro-specificity concomitant with several fold loss of Ala-specificity in a single Y112F mutant indicate some degree of natural divergence of LPXTG to LAXTG specificity in class E sortase. Furthermore, perturbation of activity by proximal mutations in the substrate binding cleft suggest that these residues may be contributing to the overall substrate recognition process in concert with the lead role of Y112. The studies pave the way for further selection of improved enzyme by directed evolution.

Session Topic: Global Health

Presenter: Faith Kamau[1,2]
Institution: Pan African University of Science, Technology and Innovation, Juja, Kenya

Co-Authors: Andrew Nyerere[3], Victor Riitho[4], James Njung'e[2], Moses Ngari[2], James A Berkley[2], Prendergast AJ[4]
[1]Department of molecular Biology and Biotechnology, Pan African University Institute for Basic sciences, Technology and Innovation, Juja, Kenya.
[2]Clinical trials facility, KEMRI-Wellcome Trust Research Program, Kilifi, Kenya.
[3]Department of medical microbiology, Jomo Kenyatta University of Agriculture and Technology, Juja, Kenya.
[4]Blizard Institute, Queen Mary University of London, London, United Kingdom.

Discriminatory value of plasma calprotectin for mortality in individuals with untreated HIV/AIDS

Background: Continued infection with human immunodeficiency virus (HIV) without treatment leads to acquired immunodeficiency syndrome (AIDS). AIDS is characterized by co-infections and immune system dysfunction, leading to mortality and morbidity. The death rate is particularly high after Anti-Retroviral Therapy (ART) administration and the risk increases sharply with decrease in pre-ART CD4+ T cells count. Measurements of soluble biomarkers has highlighted inflammation is an independent predictor of all-cause mortality in chronic HIV. Soluble markers of inflammation, not T cell activation, have been shown to independently predict clinical events. Plasma calprotectin is an antimicrobial peptide present in the cytosol of neutrophils and is secreted during inflammation. It has been found to be a biomarker of subsequent post-discharge mortality among children with severe malnutrition, however, the heterodimer has not been examined in the context of chronic HIV, particularly patients that have not started ARV. These observations prompted us to determine the discriminatory value of plasma calprotectin levels for early and all mortality in individuals with advanced untreated HIV/AIDS.

Methods: This work analyzed longitudinal archived REALITY trial samples from baseline and 4 weeks post-ART initiation among advanced HIV/AIDS individuals from Kilifi and Eldoret in Kenya. Plasma calprotectin was investigated as a mortality predictor by enzyme linked immune-sorbent assay (ELISA). Mortality was categorized in to early (cases between baseline and week 4 after treatment) and all (All cases regardless of when they occurred during the trial) mortality.

Results: Baseline calprotectin levels were shown to predict both early and later mortality after initiation of ART treatment with the area under ROC curves being 0.8272 and 0.7029 respectively. Plasma calprotectin before treatment among HIV/AIDS patients in this work is strongly associated with early mortality.

Conclusion: Baseline calprotectin predicted early and all mortality among HIV/AIDS patients naïve to ART treatment in Kenya. More studies among different populations infected with HIV would be needed to validate this, before incorporation in to clinical practice.
Discriminatory value of plasma calprotectin for mortality in individuals with untreated HIV/AIDS.

Session Topic: Global Health

Presenter: Mohameedkhalar Adan
Institution: University of Nairobi, Nairobi, Kenya

Co-Authors: Samantha Mukonjia[2], Nickson K. Lang'at[3], Philip J. Oboyie[4], Ruth K. Onderi[4], Susan Mutuku[3] and Gilbert Kirui[5]

[1]School of Nursing, University of Nairobi, Kenyatta National Hospital, Nairobi, Kenya
[2]Faculty of Medicine, University of Nairobi, Kenyatta National Hospital, Nairobi, Kenya
[3]Faculty of Veterinary Medicine, University of Nairobi, Nairobi, Kenya
[4]School of Public Health, Moi University, Eldoret, Kenya
[5]Department of Clinical Studies, Faculty of Veterinary Medicine, University of Nairobi, Nairobi, Kenya

Amboseli ecosystem

Introduction: Universal health coverage (UHC) is a healthcare system that ensures all communities have access to quality and affordable health care services including preventive, curative and palliative care. Ensuring UHC is challenging especially for communities living in sparsely populated areas where conservation efforts are in place such as those living in Amboseli Ecosystem due to among other reasons land use systems and the close human, animal and environmental interaction. There is limited information on appropriate interventions and approaches for improving access to sustainable UHC for communities living in Biosphere using One Health (OH) approach.

Objective: To develop and implement simple, sustainable interventions for improving access to Universal health Care using the One Health approach for Tukuta Manyatta community, Loitokitok, Kenya.

Methodology: A multidisciplinary group of students and faculty were engaged in a field based intervention in Amboseli Ecosystem for a period of two weeks in August in 2018. To assess the community OH needs, we used direct observation, structured questionnaires, KII, SII, structure groups, community groups and FGDs. Linear ranking tools using meta-cards, matrix scoring and fishbone diagram were used to prioritize the OH needs in Tukuta Manyatta. A skit and demonstrations on general health education was used, explaining the root causes of inadequate access to health care facilities for both animals and humans. A monitoring and evaluation framework for the OH problem in Tukuta Manyatta was established through a logical framework.The priority One Health needs at the humans, animals and the environment interface that were identified included human diseases like malaria, eye infections (trachoma) and complications of childbirth; animal diseases like Malignant Catarrhal Fever (MCF), Cysticercosis, and Contagious Caprine Pleuropneumonia(CCPP); human-wildlife conflict, water scarcity and limited access to health care facilities. The topmost prioritized need after doing matrix piling was limited access to health care services. Various interventions were agreed upon to help reduce the problem. These included preventive care (deworming dogs to prevent Coenurosis, hand washing before eating and after visiting the toilet, and building pit latrines) and fencing to reduce HWC.

Conclusion: The interventions identified priority OH challenges in Tukuta Manyatta, that were contributory to the impediment towards UHC.

Session Topic: Global Health

Presenter: Swatantra Kumar
Institution: Center for Advanced Research, King George's Medical University, India

Co-Author: Vimal K Maurya[1], Madan LB Bhatt[1], Shailendra K Saxena[1, 2]
[1]Center for Advanced Research (CFAR)-Stem Cell/Cell Culture Unit, King George's Medical University, Lucknow, India
[2]CSIR-Centre for Cellular and Molecular Biology, Uppal Road, Hyderabad, India

Global perspective of novel therapeutic strategies for the management of neuroAIDS

Among Human immunodeficiency virus (HIV) infected individuals, around two-thirds of patients present with neuroAIDS, where HIV-associated neurocognitive disorders (HAND), and HIV-associated dementia (HAD) are the most prevailing neurological complications. The neuropathology of neuroAIDS can be characterized by the presence of HIV infected macrophages and microglia in the brain, with the formation of multinucleated giant cells. Global predominant subtypes of HIV-1 clade B and C infections influence the differential effect of immune and neuronal dysfunctions, leading to cladespecific clinical variation in neuroAIDS patient cohorts. Highly active antiretroviral therapy (HAART) enhances the survival rate among AIDS patients, but due to the inability to cross the Blood-Brain-Barrier (BBB), incidence of neuroAIDS during disease progression may be envisaged. The complex structure of blood-brainbarrier, and poor pharmacokinetic profile coupled with weak bio-distribution of antiretroviral drugs, are the principle barriers for the treatment of neuroAIDS. In the combined antiretroviral therapy (cART) era, the frequency of HAD has decreased; however, the incidence of asymptomatic neurocognitive impairment (ANI) and minor neurocognitive disorder (MND) remains consistent. Therefore, several effective novel nanotechnology based.

# Both the authors contributed equally.
Therapeutic approaches have been developed to improve the availability of antiretroviral drugs in the brain for the management of neuroAIDS.

Session Topic: Global Health

Presenter: Albert Doughan
Institution: Kwame Nkrumah University of Science and Technology, Kumasi, Ghana

Co-Authors: Albert Afful[1], Rawdat Baba-Adam[1] and Alexander Kwarteng[1]

[1]Department of Biochemistry and Biotechnology, Kwame Nkrumah University of Science and Technology, Kumasi, Ghana.

Monitoring the cold chain: temperature variations & practices at vaccine units of health facilities in Accra, Ghana.

Background: The introduction of vaccines has contributed to the sharp reduction in morbidity and mortality rates across the globe, particularly among children in developing countries. The criteria for quality vaccine is measured by a functional cold chain system, well-trained personnel, reliable transport and storage facilities and efficient management practices. Although Ghana has been involved in immunization programs since 1974, there are little documentation to show for the compliance of health facilities to vaccine storage guidelines.

Methods: Towards this goal, we conveniently sampled 25 public health facilities with functional vaccine units within Accra (Ghana) metropolitan area, from June to August of 2017.

Results: Out of this number, 36% (9 facilities) could not provide records of daily temperature readings. For the 64% (16 facilities) that provided data records, it was found that 31.3% (5 facilities) failed to record actual temperature readings, instead recorded time. Moreover, of the remaining 68.7% (11 facilities), only 63.6% (7 facilities) provided daily temperature records of up to 3 years (2014-2016). Interestingly, all 7 facilities (100%), had at least 2% to 43% of the 3-year data missing.

Conclusion: We observed that proper record keeping was a general problem among the participating health facilities. Our findings suggest the need for effective training and supervision of health personnel involved in vaccine storage and handling in the Accra Metro Area.

Session Topic: Global Health

Presenter: Avinash Kumar Singh
Institution: National Institute of Immunology, New Delhi, India

Co-Authors: Vijaykumar S. Pawale[1], Sreetama Das[2], Suryanarayanarao Ramakumar[2], Rajendra P. Roy[1]

[1]National Institute of Immunology, Delhi, India
[2]Department of Physics, Indian Institute of Science, Bangalore, India

A tale of substrate recognition in two housekeeping sortases.

Background: Cell wall anchoring of surface proteins in gram-positive bacteria is mediated by transpeptidase Sortase. In pathogenic bacteria sortases are potential drug targets, as many of the proteins that they display on the microbial surface play key roles in the infection process. Sortase enzymes are generally grouped into six classes(A-F) of which Class A sortase is considered as a housekeeping enzyme. The prototype Sortase A (SrtA) of Staphylococcus aureus recognizes a LPXTG pentapeptide motif in the C-terminal of sortase substrates, cleaves the T-G peptide bond and ligates Protein-LPXT to terminal aminoglycine branch of lipid II. The peptide ligation propensity of SrtA is very useful in protein engineering and semi-synthesis.

Methods: Here we describe the crystal structure and functional attributes of a new class of housekeeping sortase (SrtE) from Streptomyces avermitilis. SrtE prefers a LAXTG peptide substrate in contrast to LPXTG of SaSrtA. The crystal structure of SrtE, mutagenesis and biochemical experiments provide clues to the altered substrate specificity of SrtE.

Results: The results point to the role of a conserved Tyr residue (Tyr 112). Tyr 112 is conserved in all class E sortases despite the lack of high sequence identity between them. The mutation of Y112 to F112 resulted in 50-fold decrease in Ala specificity with no change in its specificity for the Pro-substrate. Interestingly mutation of the equivalent residue in SrtA (A104F) did not affect the specificity of SrtA.

Conclusions: In summary, cumulative results highlight Y112 residue of SavSrtE as a critical determinant of specificity. The significance of Y112 in substrate recognition is also borne out by the fact that evolved mutants of SaSrtA generated in the past with improved activity toward LAETG motif contained mutation of Y112 equivalent Ala104 residue. The retention of native-like Pro-specificity concomitant with several fold loss of Ala-specificity in a single Y112F mutant indicate some degree of natural divergence of LPXTG to LAXTG specificity in class E sortase. Furthermore, perturbation of activity by proximal mutations in the substrate binding cleft suggest that these residues may be contributing to the overall substrate recognition process in concert with the lead role of Y112. The studies pave the way for further selection of improved enzyme by directed evolution.

Session Topic: Global Health

Presenter: Anees Bahji[1,2]
Institution: Queen's University, Kingston, Canada

[1]Department of Psychiatry, Queen's University, Kingston, ON, Canada
[2]Department of Public Health Sciences, Queen's University, Kingston, ON, Canada

Hospital-based interventions for individuals with opioid use disorder: a scoping systematic review

Background: Various strategies, such as methadone-maintenance and buprenorphine therapies, have been proposed for the community-based treatment of individuals with severe opioid use disorder (OUD). However, research on the effectiveness of hospital-based interventions for individuals with OUD has been more limited.
Objectives: to systematically evaluate outcomes of hospital-based interventions in individuals with OUD.

Methods: Searches were conducted (up to October 2018) in the MEDLINE, CINAHL, Embase, PsycINFO, and Cochrane Central Register of Controlled Trials databases. Furthermore, relevant journals were searched by hand. References from identified studies were examined. Randomized and non-randomized intervention trials were considered. Trial quality was assessed according to the Cochrane Risk of Bias Tool.

Results: 22 of 354 retrieved papers met inclusion criteria. A total of 3604 individuals were included in the review, and 2 papers involved only children <5 years old. Papers were of average quality and all but eight had been published during the previous 10 years, 9 of which were from the United States. Study interventions were organized into three broad categories: detoxification programs (n = 7), prevention programs (n = 11), neonatal programs (n = 2), and combination programs (n = 2). Both interventions and outcome measures varied widely between studies. Overall findings demonstrate the effectiveness of the interventions considered.

Conclusions: There is evidence for the positive effects of hospital-based interventions for individuals for opioid use disorder. The effectiveness of these interventions aligns with community-based interventions for individuals with OUD, strengthening the importance of continuity of care across multiple settings of care. Moreover, it is important that knowledge translation, research, and debate extend to the medical community in order to ensure clinically effective care provision for these individuals.

Session Topic: Global Health

Presenter: Christos Tsagkaris
Institution: University of Crete, Faculty of Medicine, Greece

Co-Authors: Valeria Danilchenko[1], Lolita Matiashova[2], Christos Tsagkaris[3]

[1]Department of pediatrics #1 with propaedeutics and neonatology Ukrainian Medical Stomatological Academy, Poltava, Ukraine
[2]Kharkiv medical academy of postgraduate education
[3]Medical Museum, Faculty of Medicine, University of Crete, Heraklion, Greece

History and development of Umbilical Cord Blood Banking (UCBB)

Background: Umbilical Cord Blood Banking (UCBB) consists of collecting and storing Umbilical Cord Blood (UCB) for allogeneic or autologous transplantation. Currently there are several approved therapeutic applications of UCB and a considerable amount of ongoing research projects and clinical trials in several fields. Revisiting the history of UCBB appears as a source of inspiration for the future. In the frame of medical humanities such reminiscence is beneficial for clinicians and researchers in multiple ways. The purpose of our study is to summarize the history of UCBB as well as the mythological and historical concepts that paved the way to its development.

Methods: A review of the literature was conducted. We searched PubMed and Scopus databases with keywords (Umbilical cord blood banking, umbilical cord blood, history, mythology). Inclusion criteria included English language, focus on mythology or history, accuracy and lack of conflict of interests. Conflicts of interest or irrelevance to the topic were the main exclusion criteria.

Results: UCBB is linked to mythology in the frame of regenerative medicine. Such concepts appear in Greek and Hindu mythology as well as Romantic literature. Historically the works of Christian H. Pander and Rudolf Wirchov on tissue's regeneration have been associated with the formulation of UCBB concept. UCBB was initiated in 1983 when Dr. Hal Broxmayer and his colleagues suggested the use of umbilical cord as a viable alternative to bone marrow as a source for Hematopoietic Stem Cells. In 1992, the New York Blood Center established the first public bank for umbilical cord blood and in 1996 an FDA approval was obtained for further research on therapeutic applications of UCB.

Conclusions: It is believed that in 2022 every country will have an Umbilical Cord Blood Bank. Educating physicians and counseling patients are considered as the major challenges that UCBB faces nowadays. Moreover, there is a considerable debate as far as public and private UCBB is concerned. In the future attention will be paid to educating a voluntary spirit of donation, similar to the one of blood or BM donation as well as mapping potential donors, and applying the principles of precision medicine to UCBB.

BEYOND SCIENCES INITIATIVE

4TH INTERNATIONAL REMOTE CONFERENCE: SCIENCE & SOCIETY

DIGITAL POSTER ABSTRACTS

To Access: http://www.beyondsciences.org/posters/

Password: science&society

Session Topic: Bioinformatics/Biotechnology

Presenter: Ashwinder Bhamra
Institution: Moi University, Eldoret, Kenya
Co-Author: Dr. Kirtika Patel[1]

[1]Moi University, Eldoret, Kenya

A descriptive study on the role of immunohistochemistry in cancer diagnosis at the MOI teaching and referral hospital (MTRH), Eldoret, Kenya

Background: Immunohistochemistry (IHC) is a specialised novel diagnostic technique that aids in clinical management on the basis of the characteristics of intracellular or cell surface proteins. Unfortunately, these services are available in Kenya mostly at private healthcare facilities, which are not primary options for a majority. The establishment of IHC at MTRH, the only public hospital in Western Kenya with such services, was envisioned to help enforce cancer care in the region. However, limited clinician uptake alongside with erratic resource availability limit the overall impact that IHC can have. This study therefore aimed to highlight the impact IHC has had in service delivery thus far, and by extension be an avenue to justify its better uptake.

Methods: The study was a retrospective descriptive study that involved retrieval, collection and analysis of data related to all immunohistochemistry tests performed at the laboratory from January 2012 to November 2017. The data was collected using the data management software Microsoft Excel. A spreadsheet with blank templates containing key fields was designed and populated along the process until all records to the date of completion of data collection were recorded. The complete reported tests were then further clustered into categories based on the diagnoses reached and thereafter frequencies for each cluster were derived.

Results: A total of 948 immunohistochemistry tests have been performed as per the logs and reports maintained at the laboratory. Out of this number, 677 results have been reported to patients, 200 tests were controls used and 71 were repeats. Breast cancer leads with 39.9% (n=270) of the total reported tests; Anti-LANA tests for Kaposi Sarcoma closely follow at 15.1% (102), followed by Non-Hodgkin's lymphoma at 13.4% (n=91). Various carcinomas, rhabdomyosarcomas, Hodgkin's disease, neuroendocrine tumors, and melanomas represent but just a few of the various conditions that have been able to be diagnosed using IHC.

Conclusion: It is appreciable that the introduction of immunohistochemistry services at the MTRH has had a tremendous impact on the provision of healthcare, especially aiding in diagnosis of clinically difficult conditions. This goes far in influencing patient management all the way from the treatment modalities to the overall prognosis of the patient. More resource allocation however remains central to truly appreciating the impact IHC can have as a diagnostic tool.

Session Topic: Bioinformatics/Biotechnology

Presenter: Rodrigue Kamga Wouambo[1,2]
Institution: University of Buea, Buea, Cameroon
Co-Authors: Dagang Bibian Junior[1], Bodji Rowline[1], Mafang Panebeng Annella[1], Nwatsock Mougnol[1], Djoda Bello[1,2], Tchatchouang Serges [1, 2,3]

[1]EFPSA: Health Personnel Training Center of Douala
[2]IUES/INSAM/ISSAS: Estuary Academic and Strategic Institute, High Institute of Health Applied Sciences, University of Buea
[3]Department of Biochemistry, University of Yaounde

Evaluation of performances of a rapid diagnostic test for detection of Hepatitis B surface antigen in Douala, Cameroon

Background: Cameroon is a high endemic country of hepatitis B. To ensure safe blood transfusion implies a meticulous screening of Hepatitis B surface antigen (HBsAg) among donors. In resource-limited countries especially in community area, rapids diagnostics test are commonly used for that purpose. The objective of this study was to evaluate performances of diaspot-HBsAg, a rapid diagnostic test usually used for hepatitis antigen detection.

Methods: A cross-sectional and prospective study was undertaken at the blood bank of Laquintinie during six months from November 2017 to April, 2018. Hepatitis B antigen detection was performed on blood of each donor by 2 techniques: immunonographic- Diaspot® and ELISA-Fortress (Gold standard). Comparison of categorical variables were performed by Epi info 7.0 using a X2 test and for p<0,05, the difference was considered as statistically significant.

Results: Out of 376 blood donors ignoring their AgHBs status, men were predominant compared to women (89% vs 11%) and the mean age was 49.5□1.9 years (min:18 ; max : 68). The Frequency of HBsAg was 7.98% (30/376) by Diaspot®-AgHBs and 8.78% (33/376) by FORTRESS-ELISA. Diaspot®-AgHBs performances were: sensibility 75.75%, specificity 98,54%, positive predictive value.33%, negative predictive value 97,68%, accuracy 96,5 %.

Conclusion: This study revealed that the test Diaspot®-AgHBs used for the screening of HBsAg in our context has lower sensibility than what is recommended by WHO for rapids diagnostic test (Se>95%). A local technical evaluation most always be done before and after use as far as rapid diagnostic test concerns.

Session Topic: Bioinformatics/Biotechnology

Presenter: Samuel Sowole Oladimeji
Institution: African Institute for Mathematical Sciences, Mbour, Senegal
Co-Authors: Dosumu Olanrewaju[1], Daouda Sangare[2]

[1]Department of Mathematics, Lagos State University, Lagos, Nigeria
[2]Gaston Berger University, Senegal

Background: Infectious diseases like measles have of all time been a burning part of a human history. From the advent of literacy when history has started been recorded till date; there have been epidemics that have invaded human populations which usually causes many deaths before disappearing, and potentially re-occurring years later, possibly reducing in severity as populations developed some immunity against the diseases. Each year significant number of people are recorded dying of infectious diseases like measles in Africa.

Methods: In the study, we model a measles disease using Susceptible-Exposed-Infectives-Recovered (SEIR) epidemiological model to study the prevalence and control of the measles disease in Senegal. By using measles data pertinent to Senegal, we carried out the stability of the model, established the existence and uniqueness of the solution to the model. Runge-Kutta fourth order method is used to solve the model numerically. This is used to do a simulation of the model by using MatLab programming language to determine the best strategies to adopt in controlling the measles disease.

Results: The model realised that the exposed individuals at latent period play a significant role in controlling the disease. It is established that if more people at latent period goes for treatment and therapy during this state, before they become infectives, the disease will be eradicated more speedily with time.

Conclusions: Our SEIR model shown a significant success in attempting to predict the causes of measles disease transmission within a given population. This model strongly indicated that the spread of a disease largely depend on the contact rates of susceptible individuals with infected individuals within a population.

From the model we established that early detection of measles disease has a positive impact on the reduction of measles transmission; that is there is a need to detect new cases as early as possible so as to provide early treatment for the disease especially from the exposed individuals at latent period. More people should be educated in order to create awareness of the disease transmission so that society will be aware of this deadly disease.

Session Topic: Bioinformatics/Biotechnology

Presenter: Sonali Raut
Institution: Indian Agricultural Research Institute, New Delhi, India
Co-Authors: Sonali Raut[2], Roshan Kumar[1], Anjali Shailani[2], Manas Ranjan Sahu[2], Nupur Gupta[2], Abhishek Singh

[1]Department of Human Genetics & Molecular Medicine, Central University of Punjab, Bathinda, Punjab, India
[2]Division of Microbiology, Indian Agricultural Research Institute, New Delhi, India.

Assessment of phenolics compound from cyanobacteria isolated from different region of India

Background: Cyanobacteria are also considered as rich source of natural phenolic compounds due to their potent antioxidant properties and their marked effects in the prevention of various oxidative stress associated diseases such as cancer.

Methods: In order to identify new sources of safe and inexpensive natural compounds. 20 cyanobacterial strains isolated from different parts of India, were evaluated with respect to phenolics. (Singleton and Rossi, 1965)

Results: Out of the 20 strains 5 best strain were showed maximum phenolics production namely Microcoleus, Oscillatoria, Lyngbya, Anabaena and Nostoc.

Conclusions: The influence of environmental variables and nutrient supplementation on phenolics production on cyanobacteria was found to be variable in selected genera. Production of phenolics under optimized conditions in selected cyanobacterial genera may be used in biotechnological applications.

Session Topic: Bioinformatics/Biotechnology

Presenter: Miluska Vanessa Baylon Cuba
Institution: National University of Tumbes, Tumbes, Perú
Co-Authors: Mialhe Matonnier, Eric Louis[2], Fabián Domínguez, Fredy[1, 3], Vásquez Roja, Lourdes[1, 3], Masías Ramírez, Pedro Miguel[2]

[1]Universidad Nacional de Tumbes
[2]Inca´Biotec S.A.C
[3]BIOTECOOP

Molecular characterization of lactic acid bacteria and protozoar eimeria sp. of the gastrointestinal microbiote of *gallus gallus domesticus*

The knowledge of the chicken microbiota Gallus *gallus domesticus*, is essential in the poultry production, in physiological, zootechnical and veterinary terms. At a global level, studies are presented as a priority of the poultry sector with research focused on probiotic and / or pathogenic microorganisms. In the framework of the present work, bacterial strains isolated from the different gastrointestinal compartments of the chicken were characterized molecularly using the PCR technique (Polymerase Chain Reaction), with which in vitro tests were carried out as resistance to acid pH, resistance to bile and antagonism tests against Salmonella typhimurium. Likewise, bacterial strains and parasites Eimeria sp., using the double mass spectrometry technique MALDI-TOF-TOF of the shotgun proteomics type. 32 bacterial strains were isolated, partial sequencing of the 16S rRNA gene allowed the molecular identification of eight bacterial lactic acid strains from the ventricle (Weissella sp.), The small intestine (Lactobacillus brevis, Lactobacillus farciminis, Lactobacillus plantarum, Lactobacillus pentosus) and large intestine (Pediococcus pentosaceos, Enterococcus hirae and Enterococcus faecium). The bacterial strains withstood acidic pH (2.5, 3.5 and 5.0) and bile (0.10, 0.15 and 0.30), showed halos of inhibition against Salmonella typhimurium. Originally, it was possible to identify lactic acid bacteria by means of their proteins, as well as the identification of seven species of Eimeria sp., based on the peptide footprint of oocysts previously purified in Percoll density gradient. A total of 41 proteins were identified for bacterial strains and 42 proteins belonging to protozoa of the genus Eimeria. These results will contribute to the availability of new probiotic strains for the poultry production sector and to the modernization of technologies for the characterization and molecular identification of the microorganisms of the chicken microbiota.

Session Topic: Bioinformatics/Biotechnology

Presenter: Anji Zhang
Institution: University of Toronto, Toronto, Canada

Solid-state "green" synthesis of admanatane-cyclodextrin inclusion complexes

The field of solid-state synthesis has taken on an increasingly prevalent role in pharmaceutical research. Its many benefits recognize solid-state reactions as superior to those in liquid-state with regards to efficiency, cost, and sustainability. A significant application of this is exemplified by combinatorial chemistry, in which large quantities of commercial drugs are produced in the solid phase. Before this method was discovered, synthesis of these compounds occurred in solution, which required expensive solvents and wasteful purification steps. While effective when possible, solid-state synthesis is limited to the production of a finite range of compounds; many reactions are known to occur exclusively in liquid state. As a result, chemists in this field are discovering methods that allow more reactions to be accomplished in the solid phase, saving money, resources, and time.

With similar pharmaceutical potential, b-cyclodextrin proves to be an effective agent for drug delivery. Its hydrophobic interior allows it to carry lipophillic drugs into the body, and its hydrophillic exterior allows it to effectively deliver these drugs into the bloodstream by increasing their solubility. Many anticancer drugs classified as weakly soluble have been improved by the formation of cyclodextrin inclusion complexes around them. Similarly, adamantane presents itself as a promising pharmaceutical agent due to its incredible stability and hydrophobic properties. These two compounds are known to interact with ease in solution. However, finding a mechanism that will successfully initiate this interaction in the solid state would make the formation of this complex greener by reducing cost and waste.

Using mortar and pestle techniques, heat, liquid-assisted solid-state synthesis procedures, and P-XRD (powder X-Ray diffraction) analysis, initiation of the mechanochemical interaction between b-cyclodextrin and adamantane was attempted. Although no successful inclusion complex was made, the data obtained from these trials allowed for better understanding of the mechanochemical properties of these compounds. Moreover, the appearance of each sample's increasing amorphousness gave way to the hypothesis that a more efficient grinding method (i.e., a ball mill) was required, as the mortar and pestle was sufficient to decrease particle size, but insufficient for reacting the particles. To further this work, using a ball mill would provide opportunity for continued development.

Session Topic: Bioinformatics/Biotechnology

Presenter: Elukunbi Awoyelu
Institution: Ladoke Akintola University of Technology, Ogbomoso, Nigeria
Co-Authors: Oladipo E.K.[2], Oloke J.K.[1]

[1]Department of Pure and Applied Biology (Microbiology / Virology Unit), Ladoke Akintola University of Technology, Ogbomoso, Oyo State, Nigeria.
[2]Department of Microbiology, Molecular Biology, Immunology and Bioinformatics Laboratory, Adeleke University, Ede, Osun State, Nigeria.

Molecular tracing of hepatitis C virus genotype 1 isolates in Nigeria: 2000-2018

Background: Hepatitis C virus (HCV) has been classified into 7 genotypes and different subtypes. This classification is distributed through various risk groups and origins in geographical regions. Hence, a well-established phylogenetic relationship can simplify the tracing of HCV hierarchical strata into geographic regions. This study aimed at investigating the genetic relationship among all HCV-1 sequences derived from Nigeria and some selected countries by applying phylogenetic analysis based on NS5B nucleotide sequences with an understanding of the source of spread of HCV-1 in Nigeria.

Methods: Phylogenetic analysis was performed based on nucleotide sequences of NS5B gene of HCV-1 which were registered in GenBank within the years 2000 and 2018.

Results: In this study, 25 sequences comprising of 5 sequences from Nigeria, 5 from Ghana, 5 HCV-1 sequences from Iran, 5 HCV-1 sequences from USA, 5 HCV-1 sequences from United Kingdom underwent phylogenetic analysis. Phylogenetic analysis of NS5B gene from all the sequences revealed two lineages with different clusters in the phylogenetic tree. It also showed the likelihood of HCV-1 isolates from Nigerian patients having similarities with Ghanaian patients.

Conclusions: The obtained phylogenetic tree of the analyzed HCV-1 sequences from this study has provided the ancestral relationship of the HCV-1 isolates from Nigerian patients with Ghanaian patients, and also showed the likelihood of domestic origin as the source of the spread.

Correspondence: Awoyelu E.H., Department of Pure & Applied Biology (Microbiology/Virology Unit), Ladoke Akintola University of Technology, P.M.B. 4000, Ogbomoso, Nigeria, elukunbi@yahoo.com

Session Topic: Bioinformatics/Biotechnology

Presenter: Erivelto Araújo-Junior[1]
Institution: São Paulo State University (Unesp), Araçatuba, Brazil
Co-Authors: Leandro Encarnação Garcia[1], Matheus Janeck Araújo[1], Itamar Souza Oliveira-Junior[2], Daniel Robert Arnold[1], Flavia Lombardi Lopes[1], Márcia Marinho[1]

[1]Department of Support, Production and Animal Health, São Paulo State University (Unesp), School of Veterinary Medicine, Araçatuba, SP, Brazil.
[2]Department of Surgery, Discipline of Anesthesia, Pain and Intensive Medicine, Federal University of São Paulo, São Paulo, SP, Brazil.

Transcriptome of murine macrophages infected with different strains of *Leptospira spp* reveals that infection is independent of the degree of virulence

Background: Leptospirosis is a re-emerging neglected zoonosis, causes by pathogenic spirochete bacteria from the genus Leptospira and estimated to infect more than a million people with approximately 60.000 deaths annually. Leptospira genus contains species that affect human health with varying degrees of pathogenicity. In this context, we aimed to evaluate the differences in modulation of host gene expression by strains of Leptospira with varied virulence degrees.

Methods: Total RNA was extracted from murine macrophage cell lineJ774A.1 infected with virulent, attenuated or saprophyte strains of Leptospira, as well as control non-infected cells, 6h post in vitro infection. Affymetrix microarray was performed to obtain transcriptomic profiles ofthe infected and control groups. Raw data was deposited at NCBI GEO Data Sets (GSE105141).

Results: . Our data showed a high number of differentially transcripts expressed in murine macrophages following 6h of infection with both virulent and culture-attenuated L. interrogans and in a lower rate with the saprophyte strain L. biflexa. That suggests mRNAs are modulated by Leptospira infection in macrophages independent of their degree of virulence. A plethora of genes and pathways are identified as part of the mechanisms involved in immune response. Ingenuity pathway analysis indicated that inflammation, immune response, cytokine signaling, DNA replication, recombination, repair, cellular movement, cell death and survival were significantly activated by following infection with the virulent strain.

Conclusions: 1) Inflammation and immune response, cytokine signaling, DNA repair, cell movement, death and cell survival were significantly activated following 6 hours of infection, suggesting that apoptosis may occur through DNA degradation.

2) The results demonstrated that the microorganisms were responsive to the three inocula and that a certain group of genes were regulated by antigens present in the genus Leptospira, regardless of virulence.

Session Topic: Bioinformatics/Biotechnology

Presenter: Jason Naude[1]
Institution: University of Cape Town, South Africa
Co-Authors: Jason Naude[1], Ann Meyers[1] and Edward Rybicki[1]

[1]Biopharming Research Unit, Department of Molecular and Cell Biology, University of Cape Town, Cape Town, South Africa

Expression of chikungunya virus proteins in tobacco plants for the development of a Ddiagnostic reagent and a candidate vaccine

Background: Chikungunya virus (CHIKV) is a non-fatal but highly debilitating zoonotic arbovirus transmitted by mosquitos of the Aedes genus. CHIKV is distributed in Africa, Asia and America. There is no cheap, rapid diagnostic test to distinguish CHIKV from similarly-symptomatic viruses which is problematic as prognosis, patient care, and persistent symptoms of these viruses are different. Additionally, no licensed vaccine is available. Virus-like particle (VLP) candidate vaccines using CHIKV proteins such as E2 have been the only approach to make it to clinical trials. However, these VLPs were developed in costly and poorly-scalable mammalian and insect cells. As such, a cheap and rapid diagnostic reagent and a licensed vaccine is desperately needed. We hypothesise that optimising a plant-expression platform to transiently express CHIKV proteins will be a cost-effective and scalable strategy for biopharmaceutical development.
Methods: Two variants of a recombinant CHIKV E2 envelope gene were synthesised and cloned into a plant expression vector and electroporated into Agrobacterium tumefaciens. Following this, the constructs were transformed into Nicotiana benthamiana leaves via Agrobacterium-mediated small-scale syringe-infiltration. Both constructs were co-infiltrated and co-expressed with constructs encoding either human chaperones CRT and CNX, the plant silencing-suppressor NSs or a combination thereof. Leaves were sampled on 3, 5 and 7 days post-infiltration (dpi), ground up in buffer and levels of recombinant proteins in the crude extracts then assessed by western blotting.

Results: Both E2 variants were expressed transiently in the leaves with one higher than the other. When co-infiltrated with chaperones, expression levels increased significantly, however co-infiltration with the silencing suppressor made no detectable difference. The E2 protein lacking its transmembrane domain showed the highest levels of expression when co-infiltrated with CRT compared to the full-length protein when expressed with its co-infiltrates.

Conclusions: Our findings demonstrate that co-expression of the CHIKV E2 gene lacking its transmembrane domain with CRT results in the highest levels of recombinant E2 expression in plants. This is potentially an alternative, cheaper strategy of biopharmaceutical development and this combination of constructs will be taken further to scale up production of the protein, purify it and characterise it.

Session Topic: Cancer

Presenter: Jecinta Wanjiru Ndung'u[1,2]
Institution: Rongo University, Rongo, Kenya
Co-Authors: Edward Anino[1], Douglas Kahura Njuguna[3], Reginah Mwangangi[4] , Mercy Jepkorir[5] , Regina Wachuka Mbugua[2,4], Jean Chepng'etich[6], Chrispus Mutuku Ngule[2,6] and Peter Mwitari[2]

[1]Department of Biochemistry, Rongo University, Rongo, Kenya.
[2]Centre for Traditional Medicine and Drug Research, Kenya Medical Research Institute, Nairobi, Kenya.
[3]Department of Biochemistry and Molecular Biology, Egerton University, Egerton, Kenya.
[4]Department of Biochemistry and Biotechnology, Kenyatta University, Nairobi, Kenya.
[5]Department of Chemistry and Biochemistry, Laikipia University, Nyahururu, Kenya.
[6]Department of Biochemistry, Jomo Kenyatta University of Agriculture and Technology, Nairobi, Kenya.

Phytochemical screening and synergistic antiproliferative activity against selected cancer cell lines of *Moringa oleifera* and *Indigofera arrecta* leaf extracts

Background: Medicinal plants present a plausible source for anticancer agents. Combination of plant extracts and plant-derived compounds with the currently used cancer drugs has shown a marked improvement of the conventional drugs' efficacy and reduced toxicity. This study evaluated; phytochemical screening, antiproliferative activity and drug interaction potentials of Moringa oleifera and Indigofera arrecta leaf extracts with 5-fluoro uracil against selected cancer cell lines.

Methods: Phytochemical screening was done using standard procedures. The common 3– (4, 5-dimethylthiazol-2-yr) -2, 5- diphenyltetrazolium (MTT) assay was used to determine the growth inhibitory potential of the extracts towards cancer cells. Drug interaction assays were done using constant ratio combination method.

Results: Alkaloids, terpenoids, tannins, flavonoids, glycosides, phenols and saponins were found to be present in the plant's extracts. M. oleifera and I. arrecta methanol-dichloromethane extracts had the highest activity compared to water extracts. All the extracts showed antiproliferative activities towards; HCC 1395 (breast), DU145 (prostate) and Hela (cervical) cancer cell lines. The extracts were not cytotoxic towards Vero cells (IC50>1000 µg/ml). I. arrecta and M. oleifera inhibited DU145 the most with IC50 values of 111.110 µg/ml and 66.290 µg/ml respectively.

Conclusions: The plant extracts synergistically inhibited the growth of cancer cells (CI1). Further studies to isolate the bioactive compounds and deduce the probable mechanisms of action are recommended.

Session Topic: Cancer

Presenter: Abu Talha Bin Fokhrul
Institution: Sylhet MAG Osmani Medical College, Sylhet, Bangladesh
Co-Author: Sirajum Munira[1]

[1]Sylhet MAG Osmani Medical College, Sylhet, Bangladesh

Reconstruction options of cancer of head and neck region

Background: Incidences of head and neck cancer includes cancers of the lip, oral cavity, tongue, larynx, pharynx, nose with paranasal sinuses, salivary glands and neck. Appearance, mastication, chewing are the main functions of head and neck. Surgery is the best option but most ablative surgery needs reconstruction. In this paper, we will discuss about the reconstruction options of cancer of head and neck region in Sylhet MAG Osmani Medical College and Hospital and give a glimpse of work going on in this department.

Materials and Methods: It was an observational study from July 2012 to June 2016 with convenient sampling. We took 30 patients of various regions of head and neck cancer in Sylhet MAG Osmani Medical College. Data collection was questionnaire and data collection procedure was face to face.

Results: The results reported that among 30 patients, 10 were female and the rest were male. The age groups were 11-20, 21-30, 31-40, 41-50, 51-60, 61-70, 71-80. Youngest patient was 7 years old and the oldest patient was 87 years old. Longest follow up period was 3 years. All local flaps survived. One free flap undergone total necrosis while another one undergone partial necrosis. One patient died in post-operative period owing to the lack of reliable monitoring.

Conclusion: Reconstruction has become an integral part of the multidisciplinary care of head and neck cancers in Bangladesh. Precise surgical techniques, avoidance of mechanical obstruction and better monitoring of buried flaps may further improve the success rate of free tissue transfer in complex head and neck reconstruction.

Session Topic: Cancer

Presenter: Abu Talha Bin Fokhrul
Institution: Sylhet MAG Osmani Medical College, Sylhet, Bangladesh
Co-Authors: Sirajum Munira[1]

[1]Sylhet MAG Osmani Medical College, Sylhet, Bangladesh

Oral cancer: presentation and treatment in Bangladesh

Background: Presentation and treatment of oral cancer is of utmost important because a good oral health enables a person to eat, speak as well as to socialize without active discomfort or embarrassment. Oral cancer, the eleventh most dominant cancer in the world, mostly affects the area of lips, tongue, mouth, salivary glands and oropharynx. The aim of the study is to discuss about the effective changes in presentation and treatment of oral cancer in Bangladesh.

Materials and Methods: The research design was longitudinal and we took convenient type samples. We apparently viewed 150 patients diagnosed for oral cancer for various causes in Sylhet MAG Osmani Medical College in the period between july 2015 and June 2016. It was random sampling, the data collection was questionnaire where data collection procedure was face to face.

Results: The results reported that 35% were males and 65% were females. The age groups were 11-20, 21-30, 31-40, 41-50, 51-60, 61-70, 71-80. Furthermore, oral cancer was greatly notified in 40-50 ages' people. The affected sites were floor of the mouth, hard palate, soft palate, lips, oral cavity, parotid gland, vestibule of mouth, uvula, submandibular gland, tonsil, tonsillar fossa, anterior surface of epiglottis, bronchial cleft, oropharynx. Among all sites, tongue, oral cavity and parotid gland were the greatest affected sites. Successful outcome was gained.

Conclusion: For maintaining oral cancer, the greatest challenge is the lower socio-economic people of Bangladesh. It is the burning question that how we can treat the patients of oral cancer. The aim of this presentation is to convey the importance of presentation and treatment of oral cancer in Bangladesh.

Session Topic: Cancer

Presenter: Abhishek Moturu and Alex Chang
Institution: University of Toronto, Toronto, Canada
Co-Authors: Abhishek Moturu[1], Alex Chang[1], Dr. Joseph Barfett[2], Dr. Kenneth R. Jackson[1]

[1]Department of Computer Science, University of Toronto, Toronto, Canada
[2]Department of Medical Imaging, St. Michael's Hospital, Toronto, Canada

Creation of synthetic X-rays to train a neural network to detect lung cancer

Mutated cells that proliferate uncontrollably, known as tumors (or nodules when less than 3cm in diameter), are often detected at very late stages when occurring in the lungs. With one of the lowest 5-year net survival rates amongst cancers, lung cancer is one of the deadliest cancers, making early and accurate diagnosis especially important.

In recent studies, neural networks, trained with real X-rays, which are a relatively inexpensive and accessible diagnostic test that measure the intensity loss of X-rays passing through the body, have shown reasonably accurate disease detection rates, with up to 74-91% sensitivity and 75-91% specificity, depending on the lung abnormality. However, due to confidentiality regulations, real-patient datasets are scarce, which suggests the need for artificially generated X-rays.

The purpose of this research is to create effective training data for a neural network to detect lung cancer. Using several chest X-ray Computed Tomography (CT) scans as 3D models of a body, nodules of various shapes, sizes, and radiodensities can be inserted into a CT scan at various positions within the lungs to generate a large set of diverse synthetic frontal chest X-rays using ray tracing and Beer's Law.

This research project involves lung segmentation to separate lungs within CT scans and randomize nodule placement, nodule generation to grow nodules of random size and radiodensity, bone removal to obtain soft-tissue dual-energy X-rays, ray tracing to create X-rays from CT scans from several point sources using Beer's Law, image processing to produce realistic X-rays with uniform orientation, dimensions, and contrast, and analyzing these various methods along the results of the neural network to improve accuracy when compared to real X-rays, while reducing space complexity and time complexity. Different aspects of the project have been programmed in the most suitable languages, such as Python's NumPy for handling large matrices, C++ for its flexible memory allocation, and MatLab for its Image Processing Toolbox.

This research may be helpful in producing a classifier that is able to assist radiologists with diagnosing lung cancer in patients at an early stage using X-rays.

This project is currently ongoing. Alex Chang and I have produced two batches of X-rays and are preparing to test the new and improved second batch of X-rays using the AlexNet convolutional neural network by the end of November.

Session Topic: Cancer

Presenter: Ashwinder Bhamra
Institution: Moi University, Eldoret, Kenya
Co-Author: Dr. Kirtika Patel[1]
[1]Moi University, Eldoret, Kenya

A descriptive study on the role of immunohistochemistry in cancer diagnosis at the MOI Teaching and Referral Hospital (MTRH), Eldoret, Kenya

Introduction: Immunohistochemistry (IHC) is a specialised novel diagnostic technique that aids in clinical management on the basis of the characteristics of intracellular or cell surface proteins. Unfortunately, these services are available in Kenya mostly at private healthcare facilities, which are not primary options for a majority. The establishment of IHC at MTRH, the only public hospital in Western Kenya with such services, was envisioned to help enforce cancer care in the region. However, limited clinician uptake alongside with erratic resource availability limit the overall impact that IHC can have. This study therefore aimed to highlight the impact IHC has had in service delivery thus far, and by extension be an avenue to justify its better uptake.

Methods: The study was a retrospective descriptive study that involved retrieval, collection and analysis of data related to all immunohistochemistry tests performed at the laboratory from January 2012 to November 2017. The data was collected using the data management software Microsoft Excel. A spreadsheet with blank templates containing key fields was designed and populated along the process until all records to the date of completion of data collection were recorded. The complete reported tests were then further clustered into categories based on the diagnoses reached and thereafter frequencies for each cluster were derived.

Results: A total of 948 immunohistochemistry tests have been performed as per the logs and reports maintained at the laboratory. Out of this number, 677 results have been reported to patients, 200 tests were controls used and 71 were repeats. Breast cancer leads with 39.9% (n=270) of the total reported tests; Anti-LANA tests for Kaposi Sarcoma closely follow at 15.1% (102), followed by Non-Hodgkin's lymphoma at 13.4% (n=91). Various carcinomas, rhabdomyosarcomas, Hodgkin's disease, neuroendocrine tumors, and melanomas represent but just a few of the various conditions that have been able to be diagnosed using IHC.

Conclusion: It is appreciable that the introduction of immunohistochemistry services at the MTRH has had a tremendous impact on the provision of healthcare, especially aiding in diagnosis of clinically difficult conditions. This goes far in influencing patient management all the way from the treatment modalities to the overall prognosis of the patient. More resource allocation however remains central to truly appreciating the impact IHC can have as a diagnostic tool

Session Topic: Cancer

Presenter: Derrick Bary Abila
Institution: Makerere University, Kampala, Uganda
Co-Authors: Abila Derrick Bary[1], Bwogi Fred[2], Henry Wabinga[1], Andrew Okwi[1]

[1]Makerere University College of Health Sciences, Pathology Department
[2]UCI-Fred Hutch Cancer Center, Kampala, Uganda

Use of a population based cancer registry to track incidence of childhood and adolescent cancers in Uganda

Background: Cancer is relatively rare in childhood compared to later in life. Worldwide, the common malignant diseases of childhood are leukaemia, lymphomas, central nervous system tumors and embryonic solid tumors whereas among the adolescents, sarcomas of bone and soft tissue, and tumors of the male and female genital tracts. In Africa, the distribution of childhood cancers is quite similar, commonest being Kaposi sarcoma, Burkitt's lymphoma, retinoblastoma, leukaemia and Hodgkin lymphomas.

Objectives: To describe the incidence of cancer among children and adolescents in Kampala and Wakiso Districts, Uganda from 2009 to 2014.

Methodology: This was a retrospective cross-sectional study which involved review of cancer patient's information from Kampala cancer registry which collects information on cancers diagnosed within Kampala and part of Wakiso districts and included children (0-14 years) and adolescents (15-19 years). The data was analysed using SPSS,

Key Results: A total of 752 patients, 71.7% (n=539) were children (0-14 years) and 29.3% (n=213) were adolescents (15-19 years) diagnosed with cancer between January, 2009 and December, 2014. Among the children, Hodgkin lymphoma was 21%, 12% Kaposi Sarcoma, 9% nephroblastoma, 7% retinoblastoma, 11% unspecified malignancies and 40% others. Among the adolescents, 20% were Kaposi Sarcoma, 18% Non-Hodgkin lymphoma, 8% Hodgkin lymphoma, 7% Hodgkin Lymphoma, 6% Chronic Myeloid leukaemia and 41% other malignancies..

Conclusion: Cancer common among children compared to adolescents. Nephroblastoma and retinoblastoma cases were found in only the children.

Recommendations: National cancer registries should be put in place to provide timely information on the changing incidences of childhood and adolescent cancers. New prospective studies should be done on children and adolescent cancers.

Session Topic: Cancer

Presenter: Nicholas Kisilu[1]
Institution: AMPATH Oncology in Moi Teaching and Referral Hospital, Eldoret, Kenya
Co-Authors: Chite Asirwa F.[1,2] ,Busakhala N. [1,3], Njiru E.[3], Job Kisuya[1], Seth Kirui[1], Joyce Musimbi[1]

[1]AMPATH Oncology Institute (Moi Teaching and Referral Hospital)
[2]Indiana School of Medicine
[3]Moi University School of Medicine

Recurrent kaposi's sarcoma; experience from patients enrolled in pd-1 study at MOI Teaching and Referral Hospital (MTRH)

Background: Kaposi's sarcoma is the commonest HIV/AIDS associated malignancy and most of the disease burden is found in Sub Sahara Africa. However it has also been reported in HIV negative patients. In seronegative patients it has been shown to be typically limited to the lower extremities while in seropositive patients it is a multifocal systemic disease. Advanced cases of KS especially those with involvement of the lower extremities, are often associated with lymphedema. Treatment of advanced KS in HIV/AIDS patients involves HAART with combination of chemotherapy. Pegylated liposomal doxorubicin has been proven to be efficacious in patients with advanced KS even in those who failed prior chemotherapy.

Objective: To describe the characteristics of the patients with recurrent Kaposi's Sarcoma and their treatment outcomes.

Method: This is a descriptive retrospective study involving patients with recurrent Kaposi's sarcoma in Moi Teaching and Referral Hospital from March to August 2018. We included only adults patients, previously confirmed cases of KS by histology, have failed atleast 1 chemotherapy regimen and have received atleast 6 cycles of pegylated liposomal doxorubicin. Their demographic data, presenting manifestations, viral load, CD4 counts and ECOG performance were collected and analyzed.

Results: Between March and August 2018, there were a total of 26 adult patients with recurrent Kaposi's sarcoma. 62% (16) were male, 15% (4) were sero-negative and the median age was 35 (28-73). 88% (23) patients presented with both cutaneous manifestations and lymphedema while 12% (3) had cutaneous manifestations only. 88% (23) patients had a baseline performance status of ECOG 0 and 1 and 3 (4%) had ECOG 2, after chemotherapy all patients had a performance status of ECOG 0 and 1. After 6 cycles of chemotherapy, CD4 counts and performance status of the patients improved significantly (p value=0.020 and p value=0.001) respectively while there was no improvements in viral load (p value=0.62)

Conclusion: The most common presentations were cutaneous manifestation with lymphedema and majority of the patients had both clinical and CD4 count improvement after treatment.

Session Topic: Cancer

Presenter: Hassan Filali[1]
Institution: Université Hassan II de Casablanca, Mohammedia, Maroc
Co-Authors: Ayoub Lahmadi[1], Asmaa Quessar[2], Souad Aboudkhil[1]

[1]Laboratory of Biochemistry, Environment and Agrifood (URAC 36)
Faculty of Science and Technology Mohammedia-University Hassan II of Casablanca - Morocco.
[2]Hematology and Pediatric Oncology Service-Hospital August 20 University Hospital Center IBN ROCHD Casablanca- Morocco.

Differences in proteasome activity in plasma of patients with hematologic malignancy

Background : The proteasome, proteolytic heart of ""ubiquitin-proteasome pathway"" has a very broad substrate spectrum, most play a role in: the cell cycle, DNA repair, apoptosis (p53 and Caspase) angiogenesis (VEGF), inflammation (NF-kB, IL6 ....) immune response (antigen presentation) (Adams, 2002).

Present both in the cytoplasm and nucleus of all eukaryotic cells, the 20S proteasome can be detected in peripheral blood (serum or plasma) (Stoebner and al, 2005).

Objectives: This study focused on a study in a large cohort of patients with Moroccan Hematologic malignancies in order to follow the evolution of the 20S proteasome in serum and intracellular according to clinical status.

Differences in Proteasome Activity in Plasma of Patients with Hematologic Malignancy : Quantitative and functional analysis of the proteasome was conducted at the subcellular level and serum during a pathological phenomenon (hematologic malignancy) in 145 Moroccan patients (sex ratio: 1.10 / average age: 47.9 ± 15.3 years) with ELISA assay, and by following the fluorescence emitted after enzymatic digestion of specific peptides by the chymotrypsin-like activity.

Result & Conclusion: The evolutionary trend of subcellular proteasome is significantly linked to the rate of chymotrypsin-like activity, the entire population of 60 patients called back for a second blood test after three months of treatment reported a significant drop in the rate and the activity of the proteasome in serum and intracellular level.

The use of proteasome circulating assay as a biomarker of tumor and a tool that could be very satisfying to follow patients after remission to prevent a possible fall. So Intracellular dosage proteasome reveals important because it allows estimating the predictive score of the risk of toxicity.

Session Topic: Cancer

Presenter: Hassan Filali[1]
Institution: Université Hassan II de Casablanca, Mohammedia, Maroc
Co-Authors: Ayoub Lahmadi[1], Asmaa Quessar[2], Souad Aboudkhil[1]

[1]Laboratory of Biochemistry, Environment and Agrifood (URAC 36)
Faculty of Science and Technology Mohammedia-University Hassan II of Casablanca - Morocco.
[2]Hematology and Pediatric Oncology Service-Hospital August 20 University Hospital Center IBN ROCHD Casablanca- Morocco.

Proteasome as a key element of the tumoral process in a Moroccan population suffering from different forms of malignant hemopathies between the year 2012-2015.

Background: The relationship between clinical condition and concentration of the proteasome has been reported in various diseases, especially in patients with blood cancer, in eukaryotic cells, the ubiquitin-proteasome pathway is the central non-lysosomal pathway for protein degradation and regulation of many processes in the cell which are important for tumour cell growth and survival. Inhibition of proteasome function has emerged as a powerful strategy for anti-cancer therapy.

Objective: This study focused on a study in a large cohort of patients with Moroccan Hematologic malignancies in order to follow the evolution of the 20S proteasome in serum and intracellular according to clinical status.

Materials and Methods: Quantitative and functional analysis of the proteasome was conducted at the subcellular level and serum during a pathological phenomenon (hematologic malignancy) in Moroccan patients (n=145; sex ratio: 1.10 / average age: 47.9 ± 15.3 years) with ELISA assay, and by following the fluorescence emitted after enzymatic digestion of specific peptides by the chymotrypsin-like activity.

Results: The evolutionary trend of subcellular proteasome is significantly linked to the rate of chymotrypsin-like activity. All patients (n= 145) with Hematologic malignancies express proteolysis rate more pronounced in serum compared to the control. The entire population of 60 patients called back for a second blood test after three months of treatment reported a significant drop in the rate and the activity of the proteasome in serum and intracellular level.

Conclusion: The intense proteasome activity observed in tumor cells appears, in particular, to participate in the resistance to apoptosis. The use of proteasome circulating assay as a biomarker of tumor and a tool that could be very satisfying to follow patients after remission to prevent a possible fall. So Intracellular dosage proteasome reveals important because it allows estimating the predictive score of the risk of toxicity.

Session Topic: Cancer

Presenter: Naseer Ue Din Shah[1]
Institution: University of Kashmir, Srinagar, India
Co-Authors: Md Niamat Ali[1], Syed Mudassar[2], Mosin Saleem Khan[2], Jasbir Kour[1] and Bashir A Ganai[1]

[1]Cytogenetic and Molecular Biology Research Laboratory, Centre of Research for Development, University of Kashmir, Srinagar, India
[2]Department of Clinical Biochemistry, Sheri-I-Kashmir Institute of Medical Sciences, Soura, Srinagar, India.

Elucidation of KRAS gene mutation and RASSF1A promoter methylation in non-small cell lung cancer in Indian Kashmiri population.

Background: Epigenetic inactivation of tumor suppressor gene RASSF1A recognized as a major contributor to the development of cancer. RASSF1A contains a Ras association domain and is potentially an effector of the KRAS oncoprotein. This study evaluated the role of KRAS gene mutation and RASSF1A gene promoter hypermethylation in non-small cell lung cancer (NSCLC) in Indian Kashmiri population and correlation with clinicopathological variables.

Methods: We investigated 60 primary NSCLC patients, including 30 adenocarcinomas(ADC), 12 large cell carcinomas, and 18 squamous cell carcinomas(SCC). DNA was extracted using Geneaid DNA extraction Kit protocol. DNA was amplified for KRAS gene mutation analysis using set of Primers. DNA was modified using Bisulphite treatment Kit provided by epigenetix. DNA was Amplified foe both unmethylation and methylation using two different sets of primers

Results: Mutational analysis of KRAS showed: 30% (9 of 30) of adenocarcinomas, 25% (3 of 12) of large cell carcinomas, and only 5.5% (1 of 18) of squamous cell carcinomas contained activated KRAS mutation at codon 12 or 13. RASSF1A promoter hypermethylation was detected in ADC (60%), large cell carcinomas (25%), and SCC (27.77%). Interestingly, combined RASSF1A hypermethylation and KRAS mutation was found in approximately 9% ADC/SCC patients, whereas 26.66% ADC, 50% large cell carcinomas, and 77.77% SCC showed neither KRAS mutation nor RASSF1A promoter methylation. These results showed inverse relationship between KRAS activation and RASSF1A promoter methylation in the majority of the primary NSCLC patients, and both RASSF1A inactivation and KRAS mutation events occur frequently in ADC and SCC.

Conclusion: KRAS (exon 2) mutation is a common molecular alteration in NSCLC and occurs most predominantly on codon 12, 13, characterizing 30%. These mutations are significantly associated with clinicopathological characteristics histological type, smoking status, TNM staging and metastasis. RASSF1A methylation and KRAS mutation is associated with lung adenocarcinoma and squamous cell carcinoma.

Session Topic: Cancer

Presenter: Jecinta Ndungú[1,2]
Institution: Rongo University, Rongo, Kenya
Co-Authors: Edward Anino[1], Douglas Kahura Njuguna[3], Reginah Mwangangi[4] , Mercy Jepkorir[5], Regina Wachuka Mbugua[2,4], Jean Chepng'etich[6], Chrispus Mutuku Ngule[2,6], Peter Mwitari[2]

[1]Department of Biochemistry, Rongo University, Rongo, Kenya.
[2]Centre for Traditional Medicine and Drug Research, Kenya Medical Research Institute, Nairobi, Kenya.
[3]Department of Biochemistry and Molecular Biology, Egerton University, Egerton, Kenya.
[4]Department of Biochemistry and Biotechnology, Kenyatta University, Nairobi, Kenya.
[5]Department of Chemistry and Biochemistry, Laikipia University, Nyahururu, Kenya.
[6]Department of Biochemistry, Jomo Kenyatta University of Agriculture and Technology, Nairobi, Kenya.

Phytochemical screening and synergistic antiproliferative activity against selected cancer cell lines of *moringa oleifera* and *indigofera arrecta* leaf extracts

Background: Medicinal plants present a plausible source for anticancer agents. Combination of plant extracts and plant-derived compounds with the currently used cancer drugs has shown a marked improvement of the conventional drugs' efficacy and reduced toxicity. This study evaluated; phytochemical screening, antiproliferative activity and drug interaction potentials of Moringa oleifera and Indigofera arrecta leaf extracts with 5-fluoro uracil against selected cancer cell lines.

Methods: Phytochemical screening was done using standard procedures. The common 3– (4, 5-dimethylthiazol-2-yr) -2, 5- diphenyltetrazolium (MTT) assay was used to determine the growth inhibitory potential of the extracts towards cancer cells. Drug interaction assays were done using constant ratio combination method.

Results: Alkaloids, terpenoids, tannins, flavonoids, glycosides, phenols and saponins were found to be present in the plant's extracts. M. oleifera and I. arrecta methanol-dichloromethane extracts had the highest activity compared to water extracts. All the extracts showed antiproliferative activities towards; HCC 1395 (breast), DU145 (prostate) and Hela (cervical) cancer cell lines. The extracts were not cytotoxic towards Vero cells (IC50>1000 µg/ml). I. arrecta and M. oleifera inhibited DU145 the most with IC50 values of 111.110 µg/ml and 66.290 µg/ml respectively.

Conclusions: The plant extracts synergistically inhibited the growth of cancer cells (CI1). Further studies to isolate the bioactive compounds and deduce the probable mechanisms of action are recommended.

Session Topic: Cancer

Presenter: Emerson Melo
Institution: University of Franca, Franca, São Paulo, Brazil
Co-Authors: Larissa Cristina Batista[1], André Luiz Gonçalves de Oliveira[1], Noemi Marchini de Souza Couto[1]

1 University of France (UNIFRAN). Franca (SP), Brazil.

Palliative care in pediatrics: a physiotherapy approach in the hospital framework

Introduction: According to the World Health Organization (WHO), in a concept defined in 1990 and updated in 2002, palliative care consists of the assistance promoted by a multidisciplinary team, which aims to improve the quality of life of patients and their relatives, that threatens life, through the prevention and relief of suffering, early identification, impeccable assessment and treatment of pain and other physical, social, psychological and spiritual symptoms.

Objective: Based on this the present study aimed to verify the performance of the physiotherapist and the influence of spirituality in the process of palliative care in pediatrics in the hospital setting.

Methods: We used scientific documents found in the databases SCIELO, MEDLINE, PUBMED.

Results: We found 239 scientific papers where 14 of them met the criteria for inclusion. This study presents evidences that can subsidize or guide palliative care initiatives by physiotherapy professionals, as well as other health areas.

Conclusion: In the midst of the insecurity and uncertainty of the patients in the hospital, all confidence and security is deposited in the multidisciplinary team, portato palliative care is a public health and humanitarian need, and that it is necessary to train professionals with humanist profiles, so that then it is possible to offer worthy and effective care.

Session Topic: Cancer

Presenter: Emerson Melo
Institution: University of Franca, Franca, São Paulo, Brazil.
Co-Authors: Borges, Jessica Carvalho[1]; Polati, Daniela Santana da Silveira[1].

[1]University of Franca, São Paulo.

Quality of death in the pediatric intensive therapy unit: literature review

Introduction: Neoplastic diseases are considered to be the second largest cause of pediatric death in the world, surpassed only by injuries resulting from accidents, being one of the main public health problems in the world4. The present study aimed to highlight the importance of palliative care in patients with childhood and juvenile neoplasia and psycho-social-spiritual assistance to their families.

Materials and Methods: This is a literature review, found in the Scielo and Medline databases, with the help of the ""AND"" and ""NOT"" Boolean operators, crossed with the scientific descriptors. Selected articles in Portuguese and English published from 2013 to 2018, which had the theme as the main subject and excluded those that did not approach the theme with main focus of the study.

Results and Discussion: Initially, 29 scientific papers were found in the Scielo and Medline databases, among the 29 documents selected 07, for addressing the quality of death in infanto-juvenile patients, then excluded 22 because they did not address the desired content. Monteiro MC et al2 emphasizes the importance of the relationship between the health team and the family of the patients, considering the appropriate communication, emphasizing respect and compassion for the patient and his family, and Turolla KR9 and Duarte et al12 complete saying that in situations of teminality becomes complex due to the factors involved, because when the child enters the hospital he is faced with an environment totally different from the usual, being that the presence of strange people and continuous procedures, can inflict pain and suffering.

Conclusion: It is necessary to train and discuss the theme among health professionals and undergraduate students, highlighting the need for the humanist profile, allowing it to offer a better quality of death for this patient and an amparo to their relatives.

Session Topic: Cancer

Presenter: Fernanda Silva Vieira
Institution: University of Franca, Franca, Brasil
Co-Authors: Oliveira, Naiara Borges[1], Andrade, Ana Paula[1]

[1]Department of Physiotherapy, University of Franca, Franca, Brasil

Humanized approach to spirituality in the process of coping with death in oncology: literature review

Background: Estimates from the World Health Organization (WHO) indicate that by 2030, cancer will reach approximately 27 million cases, 17 million deaths and 75 million people diagnosed annually worldwide. Cancer, threatening the continuity of life, often brings a series of losses, one of them being autonomy, self-image and physical capacity, not only the patient, but the family is also forced get along and often without being prepared for this. The novelty is the possibility of the approach from the point of view of spirituality, it is an area still little discussed by health professionals and becomes essential in the care of those who are dying.

Methods: This study proposed to accomplish a systematic literature review in order to verify the importance of the approach of spirituality in palliative care by the multi-professional team. The identified scientific descriptors will be used in isolation and / or interleaved by the term Boolean AND on the VHL data platform. Were selected articles that Cited cancer, Spirituality and Palliative Care between 2010 and 2018. As an exclusion criterion, pathologies that are not oncology and articles before the year 2010. Identified 894,437 articles from the descriptor Cancer, added Spirituality and were located 660 and lastly added the descriptor Palliative Care that 120 articles were found and selected 23.

Results: Of the 23 articles selected, only 15 were used. There was variation regarding the year of publication, with a greater presence of the year 2013. In relation to periodic that present the analyzed publications there was a predominance of those that the topics covered presented a multidisciplinary perspective, not being predominant by specific areas. Therefore, the conceptions about spirituality in palliative care in oncology found in the 23 articles were humanized approach and valuing of life, dying as a natural process, communication and support in mourning. It has been pointed out in the articles that these conceptions are deeply related.

Conclusions: The spirituality practiced by professionals with patients provides more sense to the work in palliative care, making it necessary to understand that this intervention affects not only quality of life and acceptance of the due conditions, but also shows itself as a facilitator in the formation of bonds between team, patient and his family.

Session Topic: Cancer

Presenter: Samanta Marcelino[1]
Institution: University of Franca, Franca, Brasil
Co-Authors: Débora de Jesus Santos Fernandes[1], Sheila Cristina Santos1, Daniel Gottardo de Souza[2]

[1]Departamento de fisioterapia. Universidade de Franca, UNIFRAN
[2]Doutor em Promoção da saúde. Universidade de Franca, UNIFRAN

Physiotherapy in women with mammary neoplasia.

Background: Breast cancer is the rapid and disorderly growth of breast cells that cause a tumor that can be characterized as benign tumor or malignant tumor. The late discovery of breast cancer can lead to total withdrawal of the breast, and may in some cases have the onset of metastasis.

Objective: To show the effectiveness of physiotherapy in the rehabilitation of women diagnosed and submitted to breast cancer surgeries, and their early action is indispensable both for the prevention and treatment of common complications after surgery.

Methodology: The literature review was carried out from the online VHL (Virtual Health Library), SciELO (Scientific Electronic Library Online) and LILACS (Latin American and Caribbean Literature in Health Sciences) between 2007 and 2017. Through this search, the total number of articles obtained was 13, in which 9 articles were identified that met the inclusion criteria for this study.

Final Considerations: The efficacy of early physiotherapy to women diagnosed for breast cancer prevents complications that may occur, and is capable of improving the quality of life of women who underwent mastectomy surgeries, as well as preserving, maintaining, developing, and restoring the kinetic-functional integrity of organs and systems. Therefore, the participation of professionals in this area is of great importance in the pre- and postoperative period of breast cancer, in addition to a multidisciplinary team for an effective result.

Session Topic: Cancer

Presenter: Silvio Almeida Junior
Institution: University of Franca, Franca, São Paulo
Co-Authors: Nhaypi Iasmin Taveira Moreira[1], Fernanda Carolina da Silva[1], Isabela de Castro Capoia[1], Inglity Lorrane da Silva Cruz[1], Danilo Candido Bulgo[2], Silvio de Almeida Junior[1,3]

[1]Research Group on Toxicology and Health Promotion - Euro Anglo Franca.
[2]Master in the Postgraduate Program in Health Promotion
[3]Laboratory of Animal Science - Post-Graduate Program in Animal Science, University of Franca, Franca, São Paulo, Brazil.

A review on cancer and cell therapy

Background: Generic name given to a group of diseases, in which they are classified into several types, and all occur due to uncontrolled and abnormal growth and multiplication of cells, thus characterizing a neoplasm. Instead of dying, the cancer cells grow continuously, thus causing the formation of new anomalous cells. Cancer cells usually multiply rapidly, which explains the growth of tumors. Many drugs are used in the treatment of cancer precisely because they selectively attack cells that multiply rapidly and thus kill tumor cells.

Methods: Bibliographical survey in scientific articles with up to five years counting of this date.

Results: What makes a cancer cell is its out-of-control growth and invasion among other tissues. A major reason for cells to become cancerous is a damage in the DNA in which they have and some of these instructions is to control the growth and division of cells, the genes that provide this cell division is called oncogenes. Genes that delay cell division or lead to death are called tumor suppressor genes. One treatment currently performed is gene therapy, in which it involves the genetic modification of cells as a form of treatment. Although gene therapy is still an experimental procedure, there are studies on development, safety and efficiency. Most gene therapy clinical trials have been done on cancer patients, usually in advanced stages.

Conclusions: Greater disclosure about gene therapies and their potential for cure and future possible improvements to treatments would also be a form of awareness.

Session Topic: Chronic Diseases

Presenter: Ana Paula Andrade
Institution: University of Franca, Franca, Brasil
Co-Authors: Fernanda Silva Vieira[1], Naiara Borges Oliveira[1]
[1]Department of Physiotherapy, University of Franca, Franca, Brasil

The use of virtual reality as an additional rehabilitation therapy of the elderly: literature review

Background: Statistics from the UN (World Health Organization) indicate that in 2025, Brazil is occupying the sixth position among the countries with the highest incidence of the elderly, reaching 32 million inhabitants, with a life expectancy of 74 years. In concomitance, the prevalence of chronic-degenerative diseases that tend to increase with age, evidencing a population with increasing limitations, functional dependencies and consequently incapacities. The objective of this present study is to emphasize the importance of a therapeutic rehabilitation approach that is different from the traditional one, and which promotes the combination of conventional physiotherapeutic resources, and can be used as a valuable complement to the therapeutic process, thus improving the patient's adherence to treatment through technology. Virtual Reality (VR) emerged in Brazil in the 1990s, being driven by technological advances and the exposure of researchers to new technologies.

Methods: The scientific descriptors identified will be used in isolation and or intercalated by the term Boolean AND, in the following PubMed, Scielo and VHL data platforms. Regarding the inclusion criteria, articles were selected that addressed the Elderly descriptors; Virtual reality; Physiotherapy and Treatment. Dated between the years 2012 to 2018 in the VHL Regional Portal database. As an exclusion criterion,articles inferior to 2012 that did not speak about Elderly People and Virtual Reality.

Results: 621,628 articles were identified from the descriptor Elderly; Virtual Reality was added and 108 articles were located; Physiotherapy was added and 18; and was lastly included the descriptor Treatment and it was found and selected 10 articles.

Conclusions: The use of VR in physiotherapeutic practice has several benefits in the treatment of dysfunctions: improvement of ROM, cognition, fine motor, posture and balance, therefore, it is necessary to complement proprioceptive techniques. It should be very cautious with the behavior to be performed, in addition to following the objectives of the evaluation. The therapist in charge of the treatment must know the benefits and adapting to each patient, respecting their individualities.

Session Topic: Chronic Diseases

Presenter: Diego Mauricio Bados-Enriquez[1,5]
Institution: University of Tolima, Florencia, Colombia
Co-Authors: Bilbao Acosta[1], Basante-Gomez[1], Benavides Castellanos[1], Santofimio-Bernal, OA[2], Martinez, Andres[3], Mejía- Gonzales[4].

[1]Faculty of Health Sciences. Tolima University. Ibague-Colombia.
[2]Internal medic. Tolima University.
[3]Faculty of Health Sciences. Northern University. Barranquilla, Colombia.
[4]Faculty of Health Sciences. CES University. Medellin Colombia.
[5]Red Colombiana de Investigacion Diabetes Mellitus- RECI-DM.

Obesity, Cardiovascular risk and physical activity in medical students: 3 Colombian universities multicenter study.

Background: A major change in public health that had the 21 century was the specter of increased body weight as a pandemic. In Colombia young and adulos one in three is overweight (37.7%), while one in five is obese (18.7%).

Methods: A multicenter cross-sectional descriptive study was performed. 3 Colombian universities participated. Data analysis Descriptive analysis for the variables of interest was performed. Classification and characterization were carried out using the values provided by the instruments.

Results: 233 medical students were selected. When analyzing BMI as many people were in a normal range with 75% followed by a 19, 9% classifies overweight. With respect to physical activity found that 46.7% of individuals carried a high level of physical activity, the 34, 2% perform moderate level of physical activity. Our study is consistent with the global reality, as the 19.9% are overweight. Physical activity where 58, 7% are sedentary evidenced by the time they remain sitting where 110 people remains between 6 and 10 hours.

Conclusions: Research on cardiovascular risk factors, obesity and metabolism increasingly focuses on start analyzing these variables since its inception, it is clearly necessary to continue being resolved on this issue and chart the future that leads to remission of this global pandemic.

Session Topic: Chronic Diseases

Presenter: Oduah Mary-Tiffany
Institution: Poznan University of Medical Sciences Center for Medical Education in English, Poznan, Poland
Co-Authors: Wojciech Telec[1], Piotr Kalmucki[1], Mary-Tiffany Oduah[2], Patrick Biskupski[2], Adam Turalinski[2], Karol Kochman[1], Tomasz Siminiak[1], Artur Baszko[1]

[1]2nd Department of Cardiology, Poznan University of Medical Sciences
[2]English Students' Research Association, Cardiology Group, Poznan University of Medical Sciences

Differences between European Society of Cardiology and European Resuscitation Council criteria for diagnosis of ST-segment elevation myocardial infarction

Background: ESC and ERC provide different criteria for electrocardiographic diagnosis of anterior STEMI. We prospectively analysed patients that have had anterior STEMI confirmed by ESC criteria and looked into the subgroup that would have not met the criteria if ERC guidelines were applied.

Methods: We performed a single-centre, prospective study in patients referred for primary PCI as a routine STEMI management. In all patients the time from symptoms to admission and PCI was assessed. All patients had ECG performed on admission, 90 minutes after PCI and at discharge. Several clinical (age, sex, risk factors), echocardiographic (LV EF), ECG (sum of ST elevations, > 50% ST segment resolution, QRS score) and angiographic (TIMI flow, GPIIb/IIIa) parameters were analyzed. From cohort of consecutive patients with STEMI, all with anterior STEMI accordingly to ESC ECG criteria were selected. Subsequently the ECG tracings were analysed based on ERC criteria. Patients with anterior STEMI accordingly to ESC criteria who failed to meet ERC criteria were categorized into „non-ERC" group, whereas the rest of the patients fell into „ERC" group.

Results: From 172 STEMI patients admitted to our centre between February 2015 and July 2017, 60 patients had anterior wall STEMI (ESC criteria). All patients had angiographically confirmed coronary artery disease with LAD involvement. From the group of 60 anterior STEMI patients (ESC criteria) there were 26 patients (43,3%) who did not meet ERC Council criteria ("non-ERC").

Conclusions: As many as 43% of firmly diagnosed anterior STEMI patients do not meet European Resuscitation Council criteria in first ECG. Differences between ESC and ERC guidelines for diagnosis of anterior STEMI affect significant number of patients (43% in our study). Patients with anterior STEMI (ESC) who do not fulfill ERC criteria experience significant delays in optimal management, have smaller resolution of ST-segment at 90 minutes which may affect acute and long term outcome. There is a need to analyze how differences in ESC and ERC criteria affect management and long term results as our study group was relatively small.

Session Topic: Chronic Diseases

Presenter: Rodrigue Kamga Wouambo
Institution: University of buea, LOUM
Co-Authors: Tchatchouang Serges[1,2], Enni Barbara Munya[1], Panka Tchinda Gaelle[1], Sandeu Maurice Marcel[3]

[1]IUES/INSAM/ISSAS: Estuary Academic and Strategic Institute, Higher Institute of Applied Health Sciences, University of Buea.
[2]Department of Biochemistry, University of Yaounde

Prevalence and risk factors of malaria among symptomatic children under 5 years at Obala, Cameroon

Background: Malaria remains the most prevalent parasitic disease worldwide. In Cameroon, despite different control efforts, this disease is still of primary health concern among children under five, and motivates up to 47.7% of hospitalizations and 38 % of mortality. Here, we proposed to evaluate the prevalence and risk factors of malaria transmission among children at Obala, a semi-communal area in center region of Cameroon.

Methods: Parasite densities were determined microscopically from thick blood smears prepared from blood of symptomatic children attending Obala District Hospital from February 21st to April 21st, 2018 after getting the authorization of the director. Besides, the risk factors were determined by a questionnaire giving to each mother of the children included in the study. The X2-test was used to establish the relationship between prevalence of infection and risk factors and $p<0,05$ was considered as statistically significant.

Results: A total of fifty one children aged 0-5 years with clinical symptoms of malaria were enrolled in this study. Among them, 70.5% (n=36) were females while 29.5% (n=15) were males. The prevalence of malaria in our study population was 98.03% (50/51). Gender was not associated to malaria infection (women vs men; p=0.21(. Most of parents who didn't understand what the disease was and means of transmission, those who practiced self-prescription, lived in swampy area and around stagnant water premises were more likely to be malaria positive. But no statistically significant association has been found. Surprisingly, the parents of quasi-totality of children who were malaria positive declared the systematically use of mosquito nets (98.03% (50/51).

Conclusions: Prevalence of malaria remains high at Obala but no factor was associated to it. So, a large study on a year is important in order to appreciate its distribution. However, it would be vital to improve hygienic conditions around environment and sensitization.

Session Topic: Chronic Diseases

Presenter: Rodrigue Kamga Wouambo
Institution: University of buea, Buea, Cameroon
Co-Authors: Mafang Panebeng Ornella, Bodji Rowline, Tchatchouang serges[1,2]

[1]IUES/INSAM/ISSAS: Estuary Academic and Strategic Institute, Higher Institute of Applied Health Sciences, University of Buea.
[2]Department of Biochemistry, University of Yaounde

Seroprevalence of the coinfection HIV, HBV, HCV among clinic attender at Laquintinie Hospital, Douala, Cameroon

Background: In Cameroon, the new national AIDS control strategy test and treat regardless from lymphocytes TCD4 rate to achieve 90-90-90 target impose a systematical screening and the early management of HIV. However, HIV, HBV, and HBC share the same routes of transmissions increasing the risk of co-infection and of severe damage. This study was undertaken to evaluate the prevalence of the co-infection HIV/HBV/HCV among subjects aged from 15-75 years at Laquintinie Hospital, Douala, Cameroon.

Methods: A cross-sectional, prospective study was held from October, 2017 to March 2018 at Laquintinie Hospital. HIV, HBV and HCV immunochromatograhic test were performed to each ignorant participants and HIV positives cases were confirmed by oral Quick as recommended by the National AIDS control Committee in 2016. Datas analysis were performed using Epi info 7.0. P value <0.05 was considered as statistically significant.

Results: Out of 247 patients enrolled, there were 51.52% of women and the mean age among participants was 42,3(1.98 years [min : 15; max : 75]. The seroprevalence of HIV was 10,12% (25/247), HBV 7,69 % (13/247), and HCV 4,04 % (10/247). The co-infection HIV/HBV was 1.21% (3/247), HIV/HCV (2.02%) and HBV/HCV (1.61%). Women seemed to be most affected by HIV infection (12,5% vs.7,5% men, p=0.28) and co-infection HIV/HBV (1,5%vs.0,8%, p=0,9), HIV/HCV (2,3%vs.1,6%, p=0,9) whereas male subjects by HCV (5,0% vs. 3,1% women, p=0,65), HBV (10,0%vs. 5,4%, p=0,89) and the co-infection HBV/HVC (2,5% Vs. 0,8%, p=0,56). Subjects aged (45; 60(were more likely to be positives either by HIV 23,6%(9/38), HBV 12,1%(5/38), HCV 7,8% (3/38) or by co-infection HIV/HBV 7,8% (3/38), HIV/HCV 7,8% (3/38).

Conclusions: We should keep intensifying sensitization on prevention measures against HIV, HBV, HCV in the town of Douala-Cameroon.

Session Topic: Chronic Diseases

Presenter: Rodrigue Kamga Wouambo[1,2,3]
Institution: University of buea, Buea, Cameroon
Co-Authors: Dopmo N. B. Michel[1], Bakam K. Babeth[1], Panka T. gaelle[1], Nguwoh P. Salomon[1,2,3,4]

[1]IUES/INSAM/ISSAS: Estuary Academy and Strategic Institute, Institut des Sciences Appliquées à la Santé, University of Buea
[2]The Higher Institute of Health Sciences (ISPS-UNG'Déré/Douala)
[3]Faculty of medicine and pharmaceutical sciences of Douala
[4]National Public Health Laboratory-Ministry of Public Health

Renal and hepatitis function of illicit drugs users in Yaounde-Cameroon

Background: The consumption rate of illicit drugs in low and middle income Countries is permanently increasing. In Cameroon for example this worrying phenomenon touches more and more the young generation, with consequences such as early damages of body's function. While liver is considered as the excellent metabolic center, the kidney seems to be the perfect filter clearing away the blood from toxic waste. This study was to evaluate the impact of illicit drugs use on renal and hepatic function.

Methods: A cross sectional, prospective and descriptive study took place at LAMA laboratory-Yaounde-Cameroon from March to June 2017. The Rapid detection of Illicit drugs (Immunochrommatography), HBsAg, HCVAc, high blood sugar (one touch glucometer), the kinetic titration of ALAT/ASAT, Uree/creatinine and an estimation of Glomerular filtration rate eGFR (MDRD study equation) were simultaneously done to each participant. Significant threshold 5%.

Results: Out of Sixty positives illicit drugs users were enrolled, Mean age: 27.47 ± 0,99 years [min :15 ; max :65], Men 80% (48/60) and young aged [15 ; 25] were predominant. Cannabis 23.33% (14/60), Benzodiazépine, and mixture of 2 and more than 2 illicit drugs were the most consumed. The number of consumers and drugs consumption's rate decreased with the age of participants. The frequency of hepatic failure (concomitant ALAT and ASAT abnormal) was 20% with more consuming illicit drugs mixtures. Hepatic failure seemed increasing with the age (p=0.66). Moreover, 18.33 %(11/60) showed kidneys failure (eGFR< 90) with 10patients of mild renal impairment (60<eGFR<90) and one of severe renal failure (eGFR< 15). Males subjects were the most affected by renal dysfunction (p= 0.02).

Conclusions: Drugs consumption rate has a negative impact on hepatic and renal function. We therefore recommend to avoid illicit drugs consumption especially drugs mixtures. Renal and hepatic function of drugs addicted should be frequently controlled.

Session Topic: Chronic Diseases

Presenter: Maha Ibrahim Abdelfattah
Institution: Suez Canal University, Ismailia, Egypt
Co-Author: Mona Abdel Aziz[1]

[1]Department of Physical Medicine, Rheumatology and Rehabilitation, Suez Canal University.

Influence of urban design on pain and disability in women with chronic low back pain in urban Cairo

Background: Chronic low back pain (CLBP) is a challenging healthcare condition. Failure of the traditional biomedical model to explain the poor correlation between pain and disability on one hand, and physical factors has led to the adoption of the biopsychosocial model to recognize the influence of physical, social and psychological factors implicated in CLBP. Urban design of the built community has been shown to exert a significant influence on physical and psychological health. Little research has investigated the relationship between elements of the built environment, and pain and disability of women with CLBP. As Egypt embarks on building a new capital city, better understanding of this relationship could greatly reduce the economic and human costs of this widespread medical problem for women.

Methods: This study was designed as an exploratory mixed design study. Twenty-Six women with CLBP living in two neighborhoods in Cairo, different in their urban structure, but adjacent in their locations (Old Maadi and New Maadi) were subjected to semi-structured interviews (8 from Old Maadi and 18 from New Maadi). New Maadi is a neighborhood with the characteristic modern urban style (narrow streets and tall buildings), while Old Maadi is known for being greener, quieter and more relaxed than the usual urban districts of Cairo. The interviews examined their perceptions of the built environment (building shapes and colors, street light), as well as their sense of safety and comfort, and how it affects their physical and psychological health and their CLBP. They were asked to fill questionnaires to measure their pain, disability and psychological health.

Results: Women in both districts had moderate pain and disability with no significant differences between the two districts. However, those living in New Maadi had significantly worse scores on the psychological health than those living in Old Maadi. Most women did not feel that specific elements of the built environment affected their CLBP, however, they expressed distress of the elements that were ugly, distorted or damaged, especially where they could not avoid or fix them.

Conclusions: Elements of the built environment do not exert a direct effect on CLBP. However, the perception of women regarding these elements affects their mood states, and their levels of stress, making them a possible indirect cause of increased suffering in these women.

Session Topic: Chronic Diseases

Presenter: Renan Nunesaha Aguiar
Institution: University of Franca, Franca, Brazil
Co-Authors: Bruno Henrique Barbosa De Souza[2], Maylen Beatriz Rezende Oliveira[2], Cristian Ribeiro Gonçalves[3], Danilo Cândido Bulgo[4]

[1]Department of physiotherapy and pedagogy, University of Franca, Franca, Brazil.
[2]Department of physiotherapy, University of Franca, Franca, Brazil.
[3]Department physical education and of the master's Degree in Health Promotion, University of Franca, Franca, Brazil.
[4]Department of physiotherapy and of the master's Degree in Health Promotion, University of Franca, Franca, Brazil.

Recognition of goldenhar syndrome: literature review

Background: Goldenhar's Syndrome (GS) is a rare and congenital syndrome with unknown etiology, affecting the first and second gill arches, with possible diagnosis during gestation through fetal ultrasound or genetic study. To present a review of the literature on the GS, with the intention of collaborating for an adequate recognition of its aspects, assisting the multidisciplinary health team.

Methods: A literature review was performed from the LILACS database with the key word ""Goldenhar Syndrome"". As inclusion criteria were selected scientific articles that addressed the GS, which were between the years of 2012 to 2018 and in the languages in english, spanish and portuguese. As criteria of non-inclusion articles that associated other syndromes and that did not address the pathophysiology of the syndrome in question.

Results: In the first stage of the research 64 scientific articles were found. With the application of the inclusion and non-inclusion criteria, we selected 06 articles that composed this review.

Conclusions: It was possible to observe that the GS presents peculiarities in its etiology, being necessary a qualification of the multidisciplinary health team in front of this syndrome, being able to corroborate for the increase in the quality of life in individuals affected by the GS.

Session Topic: Chronic Diseases

Presenter: Silvio Almeida Junior
Institution: University of Franca, Franca, São Paulo, Brazil
Co-Authors: Mariane Lança Garcia[1], Gabriel Vinicius Morais[1], Silvio de Almeida Junior[1,2]

[1]Research Group on Toxicology and Health Promotion - Euro Anglo Franca.
[2]Laboratory of Animal Science - Post-Graduate Program in Animal Science, University of Franca, Franca, São Paulo, Brazil.

Characterization and treatments in Parkinson's disease

Background: Parkinson's disease (PD) is characterized by progressive loss of neurons in the compact part of the black substance of the midbrain and functional changes in other brainstem nuclei, accompanied by the formation of intracellular inclusions called Lewy bodies. This results in depletion of dopamine, the neurotransmitter used by degenerating neurons, in the target neuron extensions of the black substance, which is called the striatum. With the evolution of the disease, there is additionally the involvement of other neurotransmitter systems. Typical motor disorders of the disease, such as rest tremor, slow movements and muscular rigidity, are often accompanied by postural instability, visceral dysfunction and cognitive disorders. The mechanisms that lead to the death of neurons of the black substance are still controversial. Faced with this problem, this study aims to build knowledge about the characterization and treatments of PD.

Methods: Bibliographical survey in scientific articles with up to five years counting of this date.

Results: Some drugs can replace L-dopa like amantadine and the dopamine agonist (drugs that act as dopamine, stimulating the same receptors in brain cells). Stimulation of the brain, a surgical process, is taken into account if the person has advanced disease but no dementia or psychiatric symptoms, and the medications are not effective and do not present serious side effects. Cellular therapies to restore dopaminergic neurons in the black substance may possibly benefit patients with PD, but clinical trials with fetal nerve transplants have so far shown discrete effects and have suggested the possibility of transmission of the disease to the patient. Gene therapy strategies for PD include the induction of local production of dopamine in the striatum, the provision of neurotrophic factors to reduce the progressive loss of dopaminergic neurons or the compensation of functional imbalance in the cellular communication network of the base nuclei. The production of dopamine depends essentially on the activity of three enzymes. Techniques for producing dopamine in the depleted striatum generally involve the induction of one or more of these enzymes by viral vectors.

Conclusions: Within the field of science, PD has advances in diagnostics and treatment, but no drug has the ability to cure the disease, with possible future alternative gene therapy.

Session Topic: Chronic Diseases

Presenter: Danilo Bulgo
Institution: University of Franca, Franca, Brazil
Co-Authors: Silvio de Almeida Junior[1], Letícia Natália de Oliveira[1], Cristian Ribeiro Gonçalves[1], Joao Filipe Alfenas Da Silva[1], Priscila dos Reis Oliveira[1], Renan Nunes de Aguiar[1]

[1]University of Franca – UNIFRAN

Family facing the terminality of a loved one with cancer in palliative care

Background: The family has a fundamental role with the patient in facing the cancer or some disease that threatens his life. The objective was to understand the perception of family members regarding the terminality of a loved one in the approach to palliative care. This is a study with descriptive-exploratory bibliographic review approach. In this context, palliative care aims at respecting the patient's autonomy and dignity, treating it in a holistic and humanized way, preserving the importance of communication established between care staff, patients and family members. The studies show that palliative care represents an important tool for coping with the disease until the time of termination of the patients, resulting in a differentiated, palliative and humanized care.

Session Topic: Chronic Diseases

Presenter: João Filipe Alfenas Silva
Institution: University of Franca, Franca, São Paulo, Brazil
Co-Authors: Daniel dos Santos[1], Danilo Cândido Bulgo[1]

[1]Universidade de Franca/SP

Which are the chronic diseases most interpreting in the quality of life of two military police groups of the fifth region of the military police (5th RPM) of Minas Gerais.

Background: The military police of the municipality of Uberaba / MG are constantly exposed to several dangers, however, aware of the mission entrusted to them, daily seek to maintain public order. In view of this, we intend to analyze which are the chronic diseases that most interfere in the quality of life of those brave heroes, dividing them according to the tasks they perform, being they in the administrative and operational environment.

Methods: The search will feature searches in the databases of Scholar sites Google, Scielo and Periódicos Capes, using the keywords, ""Chronic Diseases"" and ""military police"". Only papers with a maximum of five years of publication that contain the search terms in the title, abstract or in the keywords will be considered.

Results: We found 163 papers, 128 of which were excluded because they did not contain the search terms in the research, or in the pre-defined text locations. Thus, only 35 papers will be included in the research.

Conclusions: Some studies refer to the chronic diseases that most affect the military police, however the selected research was only observational and did not perform interventions to promote an improvement in the quality of life of this population. Thus, the need for new research to trace intervention strategies that promote actions to improve the quality of life of Uberaba / MG military police officers is highlighted.

Session Topic: Chronic Diseases

Presenter: Jasbir Kour
Institution: University of Kashmir, Srinagar, India
Co-Authors: Md Niamat Ali[1], Naseer ue din Shah[1]

[1]Cytogenetics & Molecular Biology Research Laboratory, Centre of Research for Development, University of Kashmir, Srinagar 190 006, JK, India

Antimutagenic/anticarcinogenic studies of medicinal plants: a potential source for drug formulations

Background: Medicinal plants have always been the important sources of bioactive compounds and over the decades have been prized for their therapeutic potentials. The secondary metabolites or the bioactive compounds from the plants have been evaluated for various biological activities like antimutagenic, antimicrobial, antioxidant, antidiabetic, anti-inflammatory, antiaging, anticancer and many more activities. In the past decade, an increasing interest towards the natural bioactive compounds from medicinal plants for scientific research, pharmaceutical and food industries has been seen.

The genomes of all living organisms are constantly subjected to damage by many mutagenic and carcinogenic agents present in the environment. Plants and their products have served as the main sources for the important bioactive compounds with antimutagenic/anticarcinogenic potential against a variety of genotoxic agents. Plants serve as the potential source for the drug formulation in the pharmaceutical industry. In the past few decades, the limited success of clinical therapies like radiation, chemotherapy, immunomodulation and surgery in the treatment of cancer has indicated that there is an indispensable need of alternative strategies in the management of diseases like cancer. The indiscriminate use of antimicrobial drugs on commercial basis has led to drug resistance. Therefore, scientists have been trying to discover new alternates for conventional treatment systems from various plant sources.

Medicinal plants have thus become a focal point to improve the present and future health need. This is because their use can have less or no harmful effects at all. Today approximately 80 % of antimicrobial, cardiovascular, immunosuppressive and anticancer drugs are of plant origin, derived from plants directly or synthetic analogues. In India there are approximately 2000 medicinal plants species and only limited species have been investigated so far. There is still much work needed to search for novel and effective bioactive compounds from more medicinal and dietary plants against a number of diseases including cancer. More work in this field has to be carried out so that the several mechanistic processes can be revealed and confirmatory human clinical trials of these plants can be performed.

Session Topic: Chronic Diseases

Presenter: Naiara Oliveira
Institution: UNIFRAN Universidade de Franca, Franca, Brazil
Co-Authors: Ana Paula de Andrade[2], Fernanda Silva Vieira[3], Danilo Cândido Bulgo[4], Larissa Cristina Batista[5]

[1]Discente do curso de fisioterapia da Universidade de Franca - UNIFRAN, Franca, São Paulo - SP, Brasil.
[2]Discente do curso de fisioterapia da Universidade de Franca - UNIFRAN, Franca, São Paulo - SP, Brasil.
[3]Discente do curso de fisioterapia da Universidade de Franca - UNIFRAN, Franca, São Paulo - SP, Brasil.
[4]Mestrando em Promoção de Saúde pela Universidade de Franca. Graduação em Fisioterapia, Letras bacharelado: Tradutor e Intérprete, Licenciatura em letras com habilitação em Língua Inglesa, Portuguesa e suas respectivas literaturas e licenciatura em Pedagogia pela Universidade de Franca.Pós-graduado em Saúde coletiva com ênfase no gerenciamento de serviços, Psicopedagogia, Educação especial com ênfase em deficiência intelectual, física e psicomotora, Tutoria e ambientes virtuais em educação a distância, Gestão Escolar e Gestão Empresarial. Docente do setor de Educação a Distância da Universidade de Franca – UNIFRAN, Franca, São Paulo – SP, Brasil.
[5]Discente do curso de fisioterapia da Universidade de Franca - UNIFRAN, Franca, São Paulo - SP, Brasil

The performance of physiotherapy in patients with cardiac insufficiency in a cardiovascular rehabilitation program: Literature review

Background:
INTRODUCTION: Defined as the final pathway of heart disease, heart failure is a chronic and progressive condition that generates metabolic, vascular, myocardial and hemodynamic changes due to inefficiency of oxygen to the body, resulting in physical and functional limitations.

OBJECTIVE: To present a review of the literature on the performance of physical therapy in patients with heart failure in a cardiovascular rehabilitation program.

Methods: For the construction of this bibliographic review article, were used articles related to cardiovascular rehabilitation, heart failure and physiotherapy in databases of Scientific Electronic Library Online (Scielo), virtual library in health (VHL), digital library of Pindamonhangaba and book, were included articles and books between the years of 1997 to 2017 in Portuguese language. Using the descriptors: Guideline AND Rehabilitation, Guidelines AND South American Prevention, Cardiopulmonary AND Directive and Physiotherapeutic Performance AND Heart Failure.

Results: 54 scientific articles were found. With the application of the inclusion and exclusion criteria, were selected 06 articles that composed this literature review.

Conclusions: Physiotherapy in a cardiovascular rehabilitation program in the patient with cardiac insufficiency, followed by an aerobic anaerobic and respiratory exercise protocol, provides an improvement in the clinical condition, such as an increase in functional capacity, reducing signs and symptoms of dyspnea and fatigue, increased oxygen consumption, with an improvement in the quality of life for these patients.

Session Topic: Chronic Diseases

Presenter: Larissa Batista
Institution: UNIFRAN Universidade de Franca, Franca, Brazil
Co-Authors: Emerson Souza Melo[1], Naiara Borges de Olivera[1], Cynthia Kallas Bachur[2]

[1]Graduandos do curso de fisioterapia pela Universidade de Franca/SP-UNIFRAN, Brasil.
[2]Docente do curso de fisioterapia na Universidade de Franca/SP- UNIFRAN, Brasil.

Prevention of cardiovascular diseases in the health of workers

Background:
Introduction: Cardiovascular diseases are currently considered the leading cause of death in the world, and one of the main risk factors is arterial hypertension (AH), which also affects a large part of the world population, being a current public health problem.

Objective: To promote education action focused on the health of the worker, with a focus on the prevention of cardiovascular diseases.

Methods: The study is an experience report, which in June 2018, the Physiotherapy course of a private institution, promoted action in favor of human health, aimed at employees of the same institution. The students of the 4th year were subdivided into groups, constituting 9 stations, with different themes. At the blood pressure station, hypertension was addressed as a focus, with distribution of educational booklets, explaining the risks and severity of the problem, emphasizing eating habits as a direct factor to develop them.

Results: It was observed that most participants were not aware of the risks and severity of hypertension, such as acute myocardial infarction and stroke. They reported that the action was of great value, because they did not know that simple changes in life habits could prevent and / or control hypertension.

Conclusions: There is a need for more actions aimed at the health of men, since they do not seek medical assistance frequently and this is due to a certain fear regarding consultations and tests, hindering the process of diagnosis and prognosis of these individuals.

Session Topic: Chronic Diseases

Presenter: Edna Manda
Institution: University of KwaZulu-Natal, Pietermaritzburg, South Africa
Co-Author: Faraimunashe Chirove[1]

[1]University of KwaZulu-Natal, School of Mathematics, Statistics and Computer Science, Pietermaritzburg, South Africa

A theoretical model of chronic hepatitis b virus with sub-optimal adherence and drug resistance

Background: Hepatocellular Carcinoma (HCC), liver cancer is a major health problem worldwide and the third common cause of cancer related deaths.Hepatitis B infection has been identified as a potential life-threating liver infection caused by HB virus. It is the leading cause of primary hepatitis, chronic hepatitis,cirrhosis and HCC.We will focus on the chronic phase of HCC. The aim of this study is to design a mathematical model to investigate the benefits of incorporating treatment with interferon alpha and lamivudine as intervention strategies in the chronic phase of hepatitis B virus infection with realistic pharmacokinetics treatment dynamics captured using time varying efficacy functions. We seek to answer the question:Can sub-optimal adherence to drugs increase HBV burden more than natural drug resistance from combined treatment of Interferon alpha and lamivudine in the chronic phase?

Methods: In this paper, we formulate and analyze within-host hepatitis B viral theoretical mathematical model for hepatitis B virus infection in the chronic phase of liver cancer with sub-optimal adherence and drug resistance. The model incorporates hepatocytes, hepatitis B virus, immune cells and cytokine dynamics using a system of ordinary differential equations. Treatment was captured using efficacy functions replicating the realistic pharmacokinetics properties of two drugs, one of which is administered intravenously and the other orally.

Results: Our results showed that predictions with both immune cells and cytokine effects give a more realistic picture as they capture some of the important ingredients of immune responses in the chronic phase of hepatitis B virus infection. Using realistic pharmacokinetics, combination therapy of both lamivudine and interferon alpha proved to be more efficient in delaying infection than taking each of the two drugs separately in the treatment of chronic hepatitis B virus infection even though using lamivudine drugs only has more significant effects in reducing HBV infection than taking interferon alpha injection only.

Conclusions: Our results suggest that natural drug resistance increases the hepatitis B virus burden more than sub-optimal adherence to drugs from both monotherapies and combined therapies. The results also suggest that the inclusion of both immune cells and cytokine responses is essential and that combination therapies are more significant in reducing hepatitis B virus infection than mono-therapies.

Session Topic: Global Health

Presenter: Idowu Adeosun
Institution: Adeleke University, Ede, Nigeria
Co-Authors: Ajayeoba Titilayo Adenike[1], Oluwatosin Akinola Ajibade[1], Elijah Kolawole Oladipo[1]

[1]Department of Microbiology, Adeleke University, Ede, Nigeria

Resistance pattern of *Staphylococcus aureus* isolated from State Specialist Hospital, Osogbo, Osun State, Nigeria

Background: Staphylococcus aureus is one of the most highly resistant bacterial pathogens that have been increasingly reported around the world. This study focused on the isolation and antibiotic sensitivity patterns of Staphylococcus aureus isolated from Osun state specialist hospital, Asubiaro environment, Osogbo, Osun state, Nigeria.

Methods: A total of 36 swab samples were collected from different spots within various units/wards of the hospital and susceptibility test was carried out on the identified S.aureus using disc diffusion method. The susceptibility results were interpreted using CLSI, 2011 criteria.

Results: Out of a total of 269 S. aureus isolates, 32 strains exhibited beta hemolysis, 15 strains exhibited alpha hemolysis while 222 strains exhibited gamma hemolysis. The percentage distribution of antibiotics sensitivity test showed that the hemolytic strains were mostly resistant to Ampicillin (100.00%), followed by Tetracycline (78.12%), Chloramphenicol (56.25%), Ciprofloxacin (34.38%) and the least was Gentamicin (15.62%).

Conclusions: There is need for consistent on-going antimicrobial resistance surveillance for important and commonly isolated clinically significant pathogens of Staphylococcal species to form the basis for developing and implementing measures that can reduce the burden of antimicrobial resistance and prevent a possible impending public health problem. The study therefore evaluated the incidence of the hemolytic strain and antibiotic sensitivity pattern of Staphylococcus aureus isolated from the hospital environment.

Session Topic: Global Health/ Biotechnology

Presenter: Johanna Valenzuela
Institution: National University of San Marcos, Lima, Peru
Co-Authors: Alvaro Jimenez-Kairuz, Mónica García

Bioadhesive films based on Acyclovir – Chitosan/hyaluronic acid interpolyelectrolyte for topical application

Background: Herpes is a disease caused by a type of virus belonging to the family Herpesviridae that represents an important public health problem worldwide. Polymeric films based on drug-interpolyelectrolyte complexes (DIPEC) represent an interesting therapeutic strategy that allows controlled drug release, providing a prolonged effect.

Methods: DIPEC dispersions were prepared by coacervation method. First, chitosan (Ch) was partially neutralized with HCl 1N, followed the addition of acyclovir (ACI) to neutralize 50% of ionizable amine groups of Ch. Then, sodium hyaluronate (HA) 0.005 M was added to neutralize 10% of ionizable amine groups of Ch. Solids of DIPEC were obtained by lyophilization. DIPEC dispersions were characterized by DLS, pH measurements and ionic displacement were also evaluated. Solid DIPEC, pure ACI, Ch, HA and the physical mixture (PM) were characterized by DSC and TGA, XRPD and optical microscopy. Films were obtained using solvent casting method. Glycerin (2% w/v) was added to the DIPEC dispersions as plasticizer. Polymeric films were characterized through uniformity weight and content test, swelling, in vitro bioadhesion and release studies.

Results: DIPEC dispersions showed pH=4.19±0.01, Dh=834.3±59.0 nm and ZP=59.6±0.8 mV. Addition of NaCl produced changes in the dispersion pH, which indicated ionic displacement, which revealed ionic interaction between ACI and Ch. DSC showed endothermic peak in the curve of ACI and PM, while this was not present in the solid DIPEC. TGA curves showed drug decomposition at 275 C. XRPD of DIPEC showed a characteristic pattern of an amorphous solid. The films obtained had excellent ACI content uniformity with very low percentage of coefficient of variation (lower than 5%). A higher sorption capacity was observed in both unloaded and loaded films. In presence of the films the zeta potential of mucin switched from negative to positive, which indicated that electrostatic interactions occur between the films and mucin, thus revealing their bioadhesive properties of the films. In vitro release studies showed a controlled release of ACI from the films.

Conclusions: Polymeric films showed promising properties for the treatment of skin wound produced by herpes virus. Further studies regarding effectiveness of them are required to confirm the usefulness for these purposes.

Session Topic: Global Health/Bioinformatics

Presenter: Bojana Radan
Institution: Western University, London, Canada
Co-Authors: Dr. Michael Shkrum[1, 2], and Japheth Ogendi[3]

[1]Schulich School of Medicine and Dentistry, Western University
[2]Department of Pathology and Laboratory Medicine, London Health Sciences Centre
[3]Department of Public Health, School of Public Health and Community Development, Maseno University

Creation of a coding and documentation hospital trauma registry system for fatal and non-fatal road traffic accident-collisions in Kisumu County, Kenya

Background: The World Health Organization (WHO) estimates that about 1.25 million people die each year as a result of Road Traffic Accidents (RTA) and that 90% of these fatalities occur in low and middle-income countries. Road traffic accidents are a major public health concern in Kenya with about 3,000 deaths occurring each year from roadside accidents alone, of which 40% are pedestrians. A significant public health issue in Kenya is the poor documentation and capturing of information at the accident scene, hospital and mortuary, of patient injuries and deaths due to RTAs. This documentation blind spot in hospital networks creates a gap in the systemic response to tackle motor vehicle-related trauma rapidly and effectively, leading to higher rates of more severe disability.

Methods: Through an interventional pilot study, a trauma registry (coding system) will be created and launched in the major provincial hospital in Kisumu City, Kenya; to document common patient injuries, fatalities and patient outcomes from those involved in road traffic accidents. This coding system will also include patients brought to the hospital dead on the accident scene. In parallel, semi-structured interviewers will be conducted with patients and/or family members (or primary care givers) to understand the multi-dimensional impact of road traffic injuries.

Results: In Jaramogi Oginga Odinga Teaching and Referral Hospital (JOOTRH), in Kisumu City, Western Kenya; three main coding gaps were identified. 1) Outpatient Casualty Ward Coding; there is no hospital documentation quantifying the impact of RTI-related patient visits in the casualty ward that are not admitted. 2) Absence of a Hospital-Wide Trauma Registry; patient medical files are coded through the ICD-10 system, but there is no additional coding for trauma patients. 3) Police / Hospital RTA Connection; there is no exchange of communication/ information between the two, hindering patient compensation.

Conclusions: The next phase of the project will be the creation of a trauma registry to systemically implement in the Casualty Ward of JOOTRH to quantify the burden of RTIs in this region. The goal of this data collection will be to provide an evidence-based dataset on the health impact and burden of motor vehicle collision-trauma and fatalities on the Kenyan healthcare system, and to provide patterns of MVC injury and death so as to better respond and invest in this growing epidemic.

Session Topic: Global Health

Presenter: Diana Tuekpe
Institution: Kwame Nkrumah University of Science and Technology (KNUST), Kumasi, Ghana
Co-Authors: Godwin Opoku Agyemang[1], Reginald Adjetey Annan[1]

[1]Department of Biochemistry and Biotechnology, KNUST, Kumasi, Ghana

Effectiveness of nutrition education on knowledge and nutritional status of school-aged children in the Kumasi metropolis

Background: Adequate nutrition is required for growth and cognitive development in children, thus poor nutrition presents a huge health, social and economic burden. However, data on nutritional status of school children are limited and the effect of nutritional education on knowledge, dietary intake and nutritional status in school-aged children is unknown in Ghana. This longitudinal school-based intervention study aimed at testing the effectiveness of nutrition education on knowledge and status of school-aged children in the Kumasi Metropolis.

Methods: Ten primary schools were randomly selected from all government primary schools and randomly allocated into 3 different interventions groups: nutrition education (3 schools), physical activity education (3 schools), and both interventions (2 schools), control (2 schools). After assessing the baseline nutrition and physical activity knowledge and status in 433 class 5 children, the interventions were carried out for 6 months and followed by post intervention assessment.

Results: Mean age of the children was 11.1 years, 51.5% of the children were females and 302 (appox. 70%) children completed the study. The results showed that the overall BMI-for-age z score (BFA) improved after the intervention (from mean=-0.263 to 0.101, p=0.000). Within the intervention groups, the strongest improvement was observed in the nutrition group (mean difference between baseline and post BFA z score 0.658, p=0.000), compared to the controls (0.18, p=0.001), PA group (0.224, p=0.000) and both intervention group (0.268, p=0.000). Between the intervention groups, mean BFA mean z score were not significantly different at baseline (p=1), but significantly differed between nutrition and controls (+0.512, p=0.025) and between nutrition and PA group (+0.53, p=0.009) after the intervention. Similar observations were found in terms of nutrition knowledge. Moreover, significant positive correlations were observed between baseline and post intervention BFA and nutrition knowledge, indicating that children who knew more or had better status at baseline remained better off after the intervention (r=0.683, p value =0.000).

Conclusions: Nutrition education was effective in improving knowledge and BMI-for-age in school-aged children.

Session Topic: Global Health

Presenter: Rodrigue Kamga Wouambo
Institution: University of Buea, Buea, Cameroon
Co-Authors: Dagang Bibian Junior[1], Bodji Rowline[1], Mafang Panebeng Annella[1], Nwatsock Mougnol[1], Djoda Bello[1,2], Tchatchouang Serges[1,2,3]

[1]EFPSA: Health Personnel Training Center of Douala
[2]IUES/INSAM/ISSAS: Estuary Academic and Strategic Institute, High Institute of Health Applied Sciences, University of Buea
[3]Department of Biochemistry, University of Yaounde 1

Evaluation of performances of a rapid diagnostic test for detection of Hepatitis B surface antigen in Douala, Cameroon

Background: Cameroon is a high endemic country of hepatitis B. To ensure safe blood transfusion implies a meticulous screening of Hepatitis B surface antigen (HBsAg) among donors. In resource-limited countries especially in community area, rapids diagnostics test are commonly used for that purpose. The objective of this study was to evaluate performances of diaspot-HBsAg, a rapid diagnostic test usually used for hepatitis antigen detection.

Methods: A cross-sectional and prospective study was undertaken at the blood bank of Laquintinie during six months from November 2017 to April, 2018. Hepatitis B antigen detection was performed on blood of each donor by 2 techniques: immunonographic- Diaspot® and ELISA-Fortress (Gold standard). Comparison of categorical variables were performed by Epi info 7.0 using a X2 test and for p<0,05, the difference was considered as statistically significant.

Results: Out of 376 blood donors ignoring their AgHBs status, men were predominant compared to women (89% vs 11%) and the mean age was 49.5 1.9 years (min:18 ; max : 68). The Frequency of HBsAg was 7.98% (30/376) by Diaspot®-AgHBs and 8.78% (33/376) by FORTRESS-ELISA. Diaspot®-AgHBs performances were: sensibility 75.75%, specificity 98,54%, positive predictive value.33%, negative predictive value 97,68%, accuracy 96,5 %.

Conclusions: This study revealed that the test Diaspot®-AgHBs used for the screening of HBsAg in our context has lower sensibility than what is recommended by WHO for rapids diagnostic test (Se>95%). A local technical evaluation most always be done before and after use as far as rapid diagnostic test concerns.

Session Topic: Global Health/ Bioinformatics

Presenter: Romaisa Pervez[1]
Institution: University of Western Ontario, London, Canada
Co-Authors: Victoria Mutiso[2], David Ndetei[2], Regina Casey[3], Terry Krupa[4], Rosemary Lysaght[4], Marlene Janzen Le Ber[5], Sean Kidd[6], Arlene MacDougall[1,7,8]

[1]Department of Epidemiology and Biostatistics, Schulich School of Medicine & Dentistry, Western University
[2]Africa Mental Health Foundation
[3]Douglas College
[4]School of rehabilitation Therapy, Queen's University,
[5]Brescia University College
[6]Department of Psychiatry, University of Toronto.
[7]Department of Psychiatry, Schulich School of Medicine & Dentistry, Western University,
[8]Lawson Health Research Institute

Building a sustainable model and evaluation plan for psychosocial rehabilitation in Kenya: An implementation research study

Background: Training, expertise and uptake of psychosocial rehabilitation (PSR) approaches is limited in Kenya for people with serious mental illness (PWSMI). Through the development of the "PSR Toolkit", the CREATE Kenya initiative is striving to address this need for evidence-based and cost-effective community-based rehabilitation for PWSMI in Kenya and other low resource settings. Since 2015, the PSR Toolkit has been tested in various Kenyan settings (i.e., social enterprise, mental healthcare) with promising results. However, it is not clear how the PSR Toolkit can and will be sustained locally in Kenya after initial research is complete. This study aims to develop a robust and engaging implementation and evaluation strategy for the PSR Toolkit, and to improve the outcomes for PWSMI and their loved ones in Kenya.

Methods: This mixed methods study is guided by current literature in implementation science. Using focus groups, different stakeholders (e.g., primary beneficiaries of the PSR Toolkit, community members, local policy makers etc.) will be consulted regarding their needs, interest, readiness to engage with the Toolkit delivery and how it may be further adapted to the local setting. Stakeholder groups will also be involved in developing an implementation strategy that identifies their needs and ability to contribute to this step. Finally, we will consider how best to develop an ongoing evaluation process that could improve future applications. In keeping with community-based research, we will collaborate to identify and engage stakeholders and seek to better understand system complexities.

Results: The expected completion date of data collection is February 2019. We expect to report on the findings related to the PSR Toolkit training, delivery and evaluation. Using these findings, we will collaborate with the key local stakeholders to (i) refine how the PSR Toolkit is implemented to better fit with the local context needs and resources, (ii) develop a sustainable plan to evaluate the PSR Toolkit's ongoing use, adaptation and the ways in which it impacts the lives of PWSMI in Kenya.

Conclusion: The CREATE PSR Toolkit has been piloted in different Kenyan settings. This study focuses on conducting an evaluation of the implementation of the PSR Toolkit to understand the issues that impede and facilitate this intervention's effective implementation.

Session Topic: Global Health/Bioinformatics

Presenter: Woldegebriel Assefa Woldegerima[1,2]
Institution: Mekelle University, Mekelle, Ethiopia
Co-Authors: Miranda I. Teboh-Ewungkem[3], Gideon A. Ngwa[1]
[1]Department of Mathematics, University of Buea, P.O. Box 63, Buea, Cameroon
[2]African Institute for the Mathematical Sciences (AIMS) Cameroon, Limbe, Cameroon
[3]Department of Mathematics, Lehigh University, Bethlehem, PA 18015, USA

The impact of recruitment on the dynamics of within-human–host model of the Plasmodium falciparum parasite

A model is developed and used to study within-human malaria parasite dynamics. The model integrates actors involved in the development–progression of parasitemia, gametocytogenesis and mechanisms for immune response activation. Model analyses under immune suppression reveal different dynamical behaviours for different healthy red blood cell (HRBC) generation functions. Existence of a threshold parameter determines conditions for HRBCs depletion. Oscillatory dynamics reminiscent of malaria parasitemia are obtained. A dependence exists on the type of recruitment function used to generate HRBCs, with complexities observed for a more nonlinear function. An upper bound that delimits the size of feasible parasitized steady-state solution exists for a logistic function but not a constant function. The upper bound is completely characterized and is affected by parameters associated with HRBCs recruitment, parasitized red blood cells generation and the release and time-to-release of free merozoites. A stable density size for mature gametocytes, the bridge to invertebrate hosts, is derived.

Session Topic: Global Health/Bioinformatics

Presenter: Samuel Sowole Oladimeji
Institution: African Institute for Mathematical Sciences, Mbour, Senegal
Co-Authors: Dosumu Olanrewaju[1], Daouda Sangare[2]
[1]Department of Mathematics, Lagos State University, Lagos, Nigeria
[2]Gaston Berger University, Senegal

Mathematical epidemiological model for measles disease in Africa: using Senegal as a case study

Backgrounds: Infectious diseases like measles have of all time been a burning part of a human history. From the advent of literacy when history has started been recorded till date; there have been epidemics that have invaded human populations which usually causes many deaths before disappearing, and potentially re-occurring years later, possibly reducing in severity as populations developed some immunity against the diseases.Each year significant number of people are recorded dying of infectious diseases like measles in Africa.

Methods: In the study, we model a measles disease using Susceptible-Exposed-Infectives-Recovered (SEIR) epidemiological model to study the prevalence and control of the measles disease in Senegal. By using measles data pertinent to Senegal , we carried out the stability of the model, established the existence and uniqueness of the solution to the model. Runge-Kutta fourth order method is used to solve the model numerically. This is used to do a simulation of the model by using MatLab programming language to determine the best strategies to adopt in controlling the measles disease.

Results: The model realised that the exposed individuals at latent period play a significant role in controlling the disease. It is established that if more people at latent period goes for treatment and therapy during this state, before they become infectives, the disease will be eradicated more speedily with time.

Conclusions: Our SEIR model shown a significant success in attempting to predict the causes of measles disease transmission within a given population. This model strongly indicated that the spread of a disease largely depend on the contact rates of susceptible individuals with infected individuals within a population.
From the model we established that early detection of measles disease has a positive impact on the reduction of measles transmission; that is there is a need to detect new cases as early as possible so as to provide early treatment for the disease especially from the exposed individuals at latent period. More people should be educated in order to create awareness of the disease transmission so that society will be aware of this deadly disease.

Session Topic: Global Health

Presenters: Joseph Michael Ochieng Oduor[1,2]
Institution: KAVI- Institute of Clinical Research, University of Nairobi, Nairobi, Kenya
Co-Authors: Nyamongo Onkoba[3], Fredrick Maloba[4], Atunga Nyachieo[1]

[1]Institute of Primate Research, Karen-Nairobi, Kenya
[2]School of Medicine, Kenyatta University, Nairobi- Kenya
[3]Technical University of Kenya
[4]School of Applied Pure Science, Kenyatta University, Nairobi-Kenya,

Therapeutic potential of phage therapy against hematogenous *staphylococcus aureus* meningitis

Background: Staphylococcus aureus is a major nosocomial infection leading to meningitis with high mortality rate [1]. The infection is further aggravated by multi-drug resistant *S.aureus* (MDRSA). The scenario has been worsened by absence of new antibacterial molecules as pharmaceutical firms are no longer interested in antibiotic research and development since it is less profitable. Alternative antibacterial agents such as bacteriophages are at present being explored for therapeutic purpose. Recent experimental treatment case reports show that phage therapy is safe and effective against bacterial infections [2].
Objective: To establish an experimental animal model for hematogenous brain infections caused by *S.aureus* and to evaluate the efficacy of phage therapy against the disease.

Methods: Phages and MDRSA were isolated from sewage and waste water collected from Nairobi sewage treatment plant. Multi-drug resistant nature of the bacterium was established through antibiogram tests. Thirty BALB/c mice were randomly assigned into three groups; the MDRSA infection group (n=20), the phage-infection group (n=5) and non-infection group (n=5). Infected mice were either treated with a single dose of clindamycin (8mg/kg/bwt) or 10^8 PFU/ml of *S.aureus* phage or a combination (clindamycin and *S.aureus* phage) at 72 hours post-infection (p.i.). Thereafter, the animals' physical health and bacteremia levels were monitored for one week.

Results: Administration of phage rescued 100% of the MDRSA infected mice. Brain tissues from the mice in phage therapy group had normal morphology unlike those from other treatment groups.

Conclusion: This is a proof of concept that phage therapy is applicable against *S.aureus* meningitis as phages can cross the blood brain barrier.

References

1. Huang, W.-C., Lee, C.-H. & Liu, J.-W. Clinical characteristics and risk factors for mortality in patients with meningitis caused by Staphylococcus aureus and vancomycin minimal inhibitory concentrations against these isolates. J. Microbiol. Immunol. Infect. Wei Mian Yu Gan Ran Za Zhi 43, 470–477 (2010)
2. Schooley, R. T. et al. Development and Use of Personalized Bacteriophage-Based Therapeutic Cocktails To Treat a Patient with a Disseminated Resistant Acinetobacter baumannii Infection. Antimicrob. Agents Chemother. 61, (2017).

Session Topic: Global Health

Presenter: Fernanda de Castro Nakamura[1,2]
Institution: Universidade Estadual Paulista "Júlio Mesquita Filho" UNESP, Franca, Brazil
Co-Author: Silvio de Almeida Junior[3]

[1]São Paulo State University (Universidade Estadual Paulista ""Júlio Mesquita Filho"" - Faculdade de Ciências Humanas e Sociais) – Faculty of Humanities and Social Sciences, located in the city of Franca, State of São Paulo, Brazil.
[2]CAPES scholarship, PhD Student in Social Services and Master in Analysis and Planning of Public Policies by the São Paulo State University (Universidade Estadual Paulista ""Júlio Mesquita Filho"" - Faculdade de Ciências Humanas e Sociais) – Faculty of Humanities and Social Sciences.
[3]Postgraduate program in animal science in UNIFRAN (Universidade de Franca - Franca University)

Regional epidemiological study and social development: knowledge of the population profile for the planning of public policies in Brazil

The regional epidemiological study is part of medicine that studies different factors that intervene in the spread of diseases, as well as their frequency and distribution by sites. It also evaluates the evolution, prophylaxis and diagnostic methods. In practical application, when these activities are applied to public means, they must be conducted by qualified professionals, since from epidemiological studies it is possible to target public funds and create programs and policies with the intention of preventing or promoting health required area. In countries of continental dimensions such as Brazil, this study faithfully reports on regional peculiarities and serves as a subsidy for the planning of public policies and actions to confront health, prevention and treatment of diseases. In this respect, the analysis refers to the reading of documents such as international legislation and recommendations that place health as a universal right that must be guaranteed by the State to all citizens residing in a given territory.

Results and Conclusion
Taking into account the right to health in the Brazilian Constitution of 1988, it has to be universal and must be guaranteed through social and economic policies aimed at the prevention and treatment of diseases. Starting from this bias, it is known that the knowledge of the regional population health represents as effective means for the correct management of public resources and delineation of actions that aim at the social promotion of the Brazilian population. In addition, it allows to know the regional health of the population, in order to articulate political projects that aim at the socioeconomic development of the different regions of the country, and can be applied in other countries that take health as a social and universal right.

Session Topic: Global Health

Presenter: Vamsi Varahabhatla
Institution: Zaporizhzhya State Medical University, Zaporizhzhya, Ukraine
Co-Authors: Onischenko Tatiana, Sukrit Bajpai[3], Basavaprabhu Achappa, Padmanabh Kamath

[1,2]Zaporozhye State Medical University, Ukraine.
[3,4]Kasturba Medical College, Mangalore, Affiliated to Manipal Academy of Higher Education, Karnataka, India.

Non-invasive vascular profile and aortic stiffness in HIV patients.

Introduction: The effects of chronic infection on arterial stiffness(AS) and vascular age is controversial and debatable. Very less information on non-invasive vascular profile (NIVP) in these patient groups is available. HIV and its effects on immune system activation leading to silent systemic inflammation and atherogenesis is known from literature.

Aim: To study and describe the arterial stiffness and NIVP in HIV patients.

Methods and materials: A systematic literature review was performed using a standardised published methodology and analysis of literature from google search engine, Pubmed central and NCBI with keywords like HIV, arterial stiffness, central blood pressure, pulse wave analysis was made, of which 15 articles were identified with inclusion criteria.

Results: An increased cardiovascular morbidity (CVM) has been reported in patients with HIV infection in recent studies. The main causes for CVM in patients with HIV are chronic inflammation and dyslipidemia. HIV patients receiving (HAART) highly active anti-retroviral therapy are more prone to increased AS and subclinical cardiovascular damage. HIV Protease inhibitors in combination with other antiretroviral drugs show evidence of alterations in total cholesterol, low density lipoproteins and triglycerides.

Conclusions: From the evidence collected from recent studies, it can be concluded that HAART in HIV patients has an increased AS effect along with prolonged inflammation and alterations in lipid profile in these population group. Metabolic crisis and hypertension are commonly described with increased vascular senescence and calcification. NIVP analysis and frequent monitoring of central aortic systolic pressure can be carried out in the clinical setting to identify and modulate novel treatment strategies in these patients."

Session Topic: Global Health/Bioninformatics

Presenter: Rehab Rayan[1,2]
Institution: University of Alexandria, Alexandria, Egypt
Co-Authors: Hatem Hussain[3], Nawal M. Khalafallah[2]
[1]Department of Epidemiology, High Institute of Public Health, University of Alexandria, Alexandria, Egypt
[2]Department of Pharmaceutics, Faculty of Pharmacy, University of Alexandria, Alexandria, Egypt
[3]Faculty of Pharmacy, University of Cairo, Cairo, Egypt

Potential reach of mobile health for educating, empowering and engaging chronically diseased patients: evidence from a survey in Egypt

Background: Patient education includes multiple interventions teaching patients about their health to improve their outcomes. The term has evolved to the more active terms (patient engagement and empowerment). Patients, who are diagnosed with chronic diseases that cost patients a lifelong treatment and dangerous complications (e.g. Diabetes Mellitus) need to be responsible for their health by self-management. With more computers and mobile devices owners globally, telehealth offers promising healthcare technology interventions to improve patient's health literacy.

Methods: This study involves a structured questionnaire administered online to examine the level of acceptance to use mobile technology (a form of telehealth approaches) to deliver health-related education. We collected data through a survey targeting a sample of 56 Egyptian patients aged between 25 and 65 years old in 2014.

Results: The results showed a promising acceptance rate (54%) among respondents; mostly those aged between 25-35 years agreed to use mobile technology like Short Message Service (SMS) to deliver health-related educational information to improve their self-managing experience and health outcomes.

Conclusion: We conclude that accompanying the rise in mobile phones subscription and willingness to receive health-related SMS, mobile health presents an opportunity for health education programs, especially when targeting younger adults.

Implications: These findings emphasize the potential to introduce more individualized, innovative and engaging approaches to educate and leverage patients with their own health using technology in a developing country. We recommend further studies to evaluate the effect of mobile-based patient education on a sample of chronically diseased patients (e.g. diabetics patients) to measure the desired outcomes such as lifestyle and self-care behaviours (medication adherence, improved knowledge, satisfaction and quality of life).

Session Topic: Global Health

Presenter: Erasme Gbaguidi[1]
Institution: University of Abomey Calavi, Cotonou, Benin
Co-Authors: Emmanuel Elanga Ndille[2,3], Dominique Cerqueira[1] , Gilles Cottrell[1,4,5], Achille Massougbodji [1], André Garçia [1,4,5], Franck Remoue [2, 3], David Courtin [1,4,5]

[1]CERPAGE, Université d'Abomey-Calavi, Faculté des Sciences de la Santé, Cotonou, Benin.
[2]UMR MIVEGEC (IRD224–CNRS5290– Universités Montpellier 1 et 2), Institut de Recherche pour le Développement (IRD), Montpellier, France.
[3]IRD-UMR MIVEGEC (IRD224 – CNRS5290 – Universités Montpellier 1 et 2), Centre de Recherche Entomologique de Cotonou (CREC), Cotonou, Bénin.
[4]IRD UMR 216 Mère et enfant face aux infections tropicales, 75006 Paris, France.
[5]Faculté de Pharmacie, Université Paris Descartes, Sorbonne Paris Cité, 75006 Paris, France.

Use of IgG antibody response to *Anopheles* gSG6-P1 salivary peptide as potential biomarker of malaria infection risk in infants from endemic area in Tori Bossito, Benin

Background: The assessment of human exposure to mosquito bites faces several limitations. To overcome these issues, a new experimental tool, was established to estimate the human-vector contact, by the salivary peptide gSG6-P1. The utilization of the IgG specific response to this biomarker of exposure was already validated in adults, but have to be also tested in young children, the main victims of malaria. Our objectives were to evaluate the human-vector contact with children from birth to 18 months-old.

Methods: The study was conducted in the region Tori Bossito in Benin. A longitudinal survey with parasitological, clinical, immunological, entomological, environmental and behavioral data was performed on 71 children from birth to 18 months-old. Drops of blood samples on blotting quarterly performed were used to quantify the levels of IgG anti-gSG6-P1 by ELISA after elution blotters. Mixed linear model and mixed logistic regression were used to show the correlations between the levels of IgG anti-gSG6-P1, environmental factors, *Anopheles* density and the occurrence of malaria infection.

Results: The mean level of IgG increase with age. A significant association between the level of IgG anti-gSG6-P1 and malaria infection was observe. Individuals with high levels of IgG anti-gSG6-P1 are more likely to be infected (Odds Ratio 2,708; p=0,042). The variables such as placental infection, the use of mosquito nets and gravidity were not related to malaria infection in our study. The number of mosquitoes caught was also related to the level of IgG directed against the peptide gSG6-P1. The correlation was only significant in children with a mean expression of IgG anti-gSG6-P1. Though, no significant association was observed between the level of IgG anti-gSG6-P1 and the predictor variable environmental risk.

Conclusion: We have shown that the amount of IgG specific *Anopheles* salivary peptide gSG6-P1 has been associated with malaria infection and Anopheles density in very young children. However, this association with the *Anopheles* density is only significant among children with the mean level of IgG anti-gSG6-P1 (Class 3). No correlation was found with environmental factors. Our results confirm the interest of using this biomarker to assess the exposition to mosquito bites, but also to assess the risk of malaria infection in newborns.

Session Topic: BioInformatics

Presenter: Abdullah Hasan
Institution: University of Calgary, Calgary, Canada
Co-Authors: Jacky Chow[1]

[1]University of Calgary, Calgary, Canada

A data-based study of global motor vehicle mortality

Introduction: Motor vehicles can improve mobility of people and goods, generally leading to more economic benefit. While such increase in transportation efficiency can help the economy grow, it may come at the expense of reduced road safety. Traffic accidents are now the leading cause of death among young peoples aged 15-29 irrespective of geographic location. The United Nations' current Sustainable Development Goals for the year 2020 is to reduce the mortality due to car crashes by 50%. To achieve this goal, it is important to analyze driving data from different countries objectively to identify areas for government spending/legislation/advocacy that can have the most significant impact.

Methods: We applied various popular machine learning techniques to a publicly available dataset from the World Health Organization (WHO) in order to separate countries with the highest ratio of motor vehicle crash mortality from the lowest ones. The dataset has eight attributes from 190 countries, they are: 1) Training in medical emergency available for doctors 2) Training in medical emergency available for nurses 3) Existence of a national drink driving law 4) Existence of a national road safety strategy 5) Number of registered vehicles 6) Seat belt wearing rate 7) Maximum speed limit in rural areas 8) Maximum speed limit in urban areas.

Results: Using a bagged decision tree model with a 5-fold cross-validation we were able to achieve a classification accuracy of 90%. Furthermore, the top three factors considered by the classifier were 1) seatbelt wearing rate, 2) training in medical emergency available to nurses, and 3) maximum speed limits in rural areas.

Conclusion: Our data analysis provided us with some objective measures regarding the importance of different parameters as they correlate with car crash mortality. In agreement with the WHO report, increasing seatbelt wearing rate and reducing the maximum speed limits can greatly reduce mortality. Surprisingly, availability of specialized training in medical emergency for nurses differs greatly between countries with the highest and lowest car mortality rate. Therefore, it appears that more training for nurses is a worthwhile endeavour for governments.

Session Topic: Global Health

Presenter: Elukunbi Awoyelu[1]
Institution: Ladoke Akintola University of Technology, Ogbomoso, Nigeria
Co-Authors: Oladipo E.K.[2] and Oloke J.K.[1]
[1]Department of Pure and Applied Biology (Microbiology / Virology Unit), Ladoke Akintola University of Technology, Ogbomoso, Oyo State, Nigeria.
[2]Department of Microbiology, Molecular Biology, Immunology and Bioinformatics Laboratory, Adeleke University, Ede, Osun State, Nigeria.

Molecular tracing of hepatitis C virus genotype 1 isolates in Nigeria: 2000-2018

Background: Hepatitis C virus (HCV) has been classified into 7 genotypes and different subtypes. This classification is distributed through various risk groups and origins in geographical regions. Hence, a well-established phylogenetic relationship can simplify the tracing of HCV hierarchical strata into geographic regions. This present study aimed to investigate the genetic relationship among all HCV-1 sequences derived from Nigeria and some selected countries by applying phylogenetic analysis based on NS5B nucleotide sequences and understanding the source of spread of HCV-1 in Nigeria.

Methods: Phylogenetic analysis was performed based on nucleotide sequences of NS5B gene of HCV-1 which were registered in GenBank within the years 2000 and 2018.

Results: In this study, 25 sequences comprising of 5 sequence from Nigeria, 5 from Ghana, 5 HCV-1 (comprising both 3 HCV-1a and 2 HCV-1b) sequences from Iran, 5 HCV-1 (comprising 2 HCV-1a and 3 HCV-1b) sequences from USA, 5 HCV-1 (comprising 3 HCV-1a and 2 HCV-1b) sequences from United Kingdom underwent phylogenetic analysis. Phylogenetic analysis of NS5B gene from all the sequences revealed two lineages with different clusters in the phylogenetic tree. The results showed that the HCV-1 isolates from Nigerian patients may have similarities with Ghanaian ones.

Conclusions: The obtained phylogenetic tree of the analyzed HCV-1 sequences from this study has provided the ancestral relationship of the HCV-1 isolates from Nigerian patients with Ghanaian patients, and also showed the likelihood of domestic origin.

Session Topic: Global Health

Presenter: Erivelto Araújo-Junior[1]
Institution: São Paulo State University (Unesp), Araçatuba, Brazil
Co-Authors: Leandro Encarnação Garcia[1], Matheus Janeck Araújo[1], Itamar Souza Oliveira-Junior[2], Daniel Robert Arnold[1], Flavia Lombardi Lopes[1], Márcia Marinho[1]

[1]Department of Support, Production and Animal Health, São Paulo State University (Unesp), School of Veterinary Medicine, Araçatuba, SP, Brazil.
[2]Department of Surgery, Discipline of Anesthesia, Pain and Intensive Medicine, Federal University of São Paulo, São Paulo, SP, Brazil.

Transcriptome of murine macrophages infected with different strains of *Leptospira spp* reveals that infection is independent of the degree of virulence

Background: Leptospirosis is a re-emerging neglected zoonosis, causes by pathogenic spirochete bacteria from the genus *Leptospira* and estimated to infect more than a million people with approximately 60.000 deaths annually. Leptospira genus contains species that affect human health with varying degrees of pathogenicity. In this context, we aimed to evaluate the differences in modulation of host gene expression by strains of *Leptospira* with varied virulence degrees.

Methods: Total RNA was extracted from murine macrophage cell lineJ774A.1 infected with virulent, attenuated or saprophyte strains of *Leptospira*, as well as control non-infected cells, 6h post in vitro infection. Affymetrix microarray was performed to obtain transcriptomic profiles ofthe infected and control groups. Raw data was deposited at NCBI GEO Data Sets (GSE105141).

Results: . Our data showed a high number of differentially transcripts expressed in murine macrophages following 6h of infection with both virulent and culture-attenuated *L. interrogans* and in a lower rate with the saprophyte strain *L. biflexa*. That suggests mRNAs are modulated by *Leptospira* infection in macrophages independent of their degree of virulence. A plethora of genes and pathways are identified as part of the mechanisms involved in immune response. Ingenuity pathway analysis indicated that inflammation, immune response, cytokine signaling, DNA replication, recombination, repair, cellular movement, cell death and survival were significantly activated by following infection with the virulent strain.

Conclusions: 1) Inflammation and immune response, cytokine signaling, DNA repair, cell movement, death and cell survival were significantly activated following 6 hours of infection, suggesting that apoptosis may occur through DNA degradation.
2) The results demonstrated that the microorganisms were responsive to the three inocula and that a certain group of genes were regulated by antigens present in the genus *Leptospira*, regardless of virulence.

Session Topic: Global Health

Presenter: Tecla Chelagat
Institution: Strathmore University Business School, Nairobi, Kenya
Co-Authors: Gilbert Kokwaro[1], Joseph Onyango[1]

[1] Strathmore University Business School, Nairobi, Kenya

Strengthening health systems performance indicators through team coaching approach: evidence from healthcare leaders in Kenya.

Background: The study endeavored to investigate the impact of team coaching approach on health systems performance indicators in Kenya. Coaching is defined as a process of supporting coaches to step back, and take in the "big picture," and craft a future they desire through commitment to the goal. Team coaching is a process helping the team improve performance and the processes by which performance is achieved, through reflection and dialogue. The Challenge Model is a systematic approach to problem solving that program participants use to apply these practices to a real worksite problem. The challenge model team coaching approach enables managers to practice leadership, management and governance by identifying and addressing key health service delivery challenges.

Methods: The Strathmore Business School integrated Leadership development and team coaching framework applied in the healthcare leadership programs was designed to help teams achieve superior performance, through immediate application of knowledge. The program introduced leadership and management practices and a methodology for identifying and addressing key health systems performance challenges. 69 teams of health workers participated in the program between the years (2010-2016). The purpose of this study was scan the cross-sectorial health system leadership challenges and assess impact of the leadership development training. Coaches are therefore tasked with the responsibility to help leaders grow notably by demonstrating their own leadership skills through practice. The study adopted a retrospective quasi-experimental design without a random assignment to empirically estimate the impact of team-coaching on identified institutional priority project's indicators, by comparing baseline, endline and post-training.

Results: The results showed that teams achieved highly statistically significant increases anticipated desired measurable results indicators. Paired t-tests comparing baseline to endline and endline to postline revealed significant increases in priority project goal attainment P(0.034 and 0.235) respectively. The sustainability of the achieved results was 88% post-training.

Conclusion: Utilization of challenge model as a coaching and knowledge transfer tool was a significant predictor on achievement of desired measurable result. The results will inform human resources for health policies and guide future training activities in leadership towards improve health system performance.

Session Topic: Global Health

Presenter: Fernanda de Castro Nakamura[1,2*]
Institution: Universidade Estadual Paulista "Júlio Mesquita Filho", Franca, Brazil
Co-Author: Agnaldo de Sousa Barbosa [1,3]

[1]São Paulo State University (Universidade Estadual Paulista ""Júlio Mesquita Filho"" - Faculdade de Ciências Humanas e Sociais) – Faculty of Humanities and Social Sciences, located in the city of Franca, State of São Paulo, Brazil.
[2]CAPES scholarship, PhD Student in Social Services and Master in Analysis and Planning of Public Policies by the São Paulo State University (Universidade Estadual Paulista ""Júlio Mesquita Filho"" - Faculdade de Ciências Humanas e Sociais) – Faculty of Humanities and Social Sciences.
[3]Professor of Sociology in Law Course and Professor of Public Policies in the Postgraduate Program in Social Service at São Paulo State University (Universidade Estadual Paulista ""Júlio Mesquita Filho"". PhD in Sociology by São Paulo State University (Universidade Estadual Paulista ""Júlio Mesquita Filho"". Coordinator of the Master´s Degree Program in Analysis and Planning of Public Policies in São Paulo State University (Universidade Estadual Paulista ""Júlio Mesquita Filho"" - Faculdade de Ciências Humanas e Sociais) – Faculty of Humanities and Social Sciences.

[*]This study was financed in part by the Coordenação de Aperfeiçoamento de Pessoal de Nível Superior - Brasil (CAPES) - Finance Code 001."

The judicialization of health and regional diseases: parameters for effecting the public policy of free drugs supply

Background: This study aims to analyze the dynamics of the judicialization of health in the sphere of free drugs supply. In countries where the right to health appears as a social right and a universal guarantee, public policy planning must take into account social demands aimed at satisfying citizens in the treatment of their diseases. So, the issue revolves around the realization of the right to health in a universal and effective way, especially with regard to the supply of drugs and devices for the treatment of diseases, through the action of the Judiciary Power.

Methods: For this purpose, the realization of this study took place through a bibliographical research, with the use of sources that deal with issues related to health litigation and the role of the Judiciary Power in public policies. The authors analyzed have studies about the judicialization and mobilization of the right in favor of social actors. The most important for our study were, in United States, Frances Zehmans and Michael McCann, and, in Brazil, Luís Roberto Barroso, Werneck Vianna and Maria Tereza Sadek

Results and Conclusion: In conclusion, some parameters, that are related to the adoption of criteria that meet regional needs, through an epidemiological study to be done by Public Power, as well as, the eventual elaboration of a specific policy for inputs, with the use of the data obtained by judicialization, were delimited; which, consequently, could result in a saving of material and institutional resources, for the Judiciary Branch and federal entities, because of the annual revision of the system of free drugs supply in countries which have the prevision of this public policy and high rates of judicialization of public health."

Session Topic: Global Health

Presenter: Jackline, Aridi[1]
Institution: Strathmore University, Nairobi, Kenya
Co-Authors: N. Wafula[1], Mary Adam[2] and Gilbert K'okwaro[1]
[1]Institute of Healthcare Management, Strathmore University
[2]AIC Kijabe Hospital

Kenyan women's preferences for place of delivery: A comparative study between Embakasi North sub-County and Naivasha sub-County, Kenya.

Background: Many sub-Saharan Africa countries over the years have introduced policies aimed at removing barriers to access health service utilization including removal of user-fees. The Kenyan Government in 2013 via presidential decree initiated such a policy with an aim of increasing access to facility based delivery in an attempt to reverse Kenya's high maternal mortality ratio. Despite the new policy women continue to choose to deliver their babies at home and women are also bypassing smaller primary health facilities and having their babies at tertiary facilities. Health system factors related to place of delivery are well studied however women's preferences that drive the demand for certain health facilities over others are not well understood. This study aims to fill this research gap by using a discrete choice experiment to establish the relative importance of attributes that drive women's preferences for a place of delivery to improve the understanding of patterns of maternal health service utilization.

Objectives: The study aims to examine women's preferences for place of delivery and establish the relative importance of attributes of the health facilities that drive women to choose facilities where they deliver their babies. The study will compare attributes of women in a peri-urban context in Embakasi North sub-County with those in a predominantly rural context in Naivasha sub-County in Kenya.

Methods: The study intends to utilize mixed methods framework incorporating both a qualitative study and a quantitative methodology known as Discrete Choice Experiment (DCE) to determine the most important health facility attributes preferred by women when choosing their place of delivery. Household characteristics data for women will also be collected via a cross-sectional survey.

Conclusion: This study hopes to establish the relative importance of health facility attributes valued by women particularly in the two settings in Kenya and use the information to inform policy making both at the devolved county units and National Ministry of Health. This information should be used for resource reallocation to promote health equity and efficient service delivery within health facilities in both urban and rural areas.

Session Topic: Global Health

Presenter: Chaula Godlove
Institution: National Institute For Medical Research- Mbeya Centre, Mbeya, Tanzania
Co-Authors: Emmanuel Sichone[1], Lwitiho Sudi[1], Jonathan Munkai[1], Nyanda Ntinginya[1], Bariki Mtafya[1], Daniel Mapamba[1], Wolfram Mwalongo[1].

[1]NIMR-Mbeya Medical Research Centre, Department of laboratory Sciences- Mbeya-Tanzania

Pathogenic fungi from bat droppings causing histoplasmosis in humans in Southern West Tanzania: Mbeya region. A case study

Background: *Histoplasma* is a genus of dimorphic fungi commonly found in birds and bats fecal materials and *Histoplasma capsulatum* is the causative agent of histoplasmosis which occurs worldwide and should not be overlooked in patients with unexplained pulmonary or systemic illnesses. H. capsulatum has been reported to cause human disease in the coastal areas around the cities of Tanga and Dar es Salaam. After exposure chronic histoplasmosis can resemble pulmonary Tuberculosis.

Methodology: This was a case study conducted at NIMR-Mbeya Medical Research Centre, Bats droppings were collected into falcon tubes, 0.5ml of 0.85%Nacl was used to prepare the inoculum by votexing, few drops were inoculated on two Sabouraud dextrose agar plates, we incubated one plate at room temperature for few days and another at 370c for 24hours. The results were identified macroscopically and microscopically.

Results: Culture at 37°C we observed 2-3mm, wrinkled, moist, heaped and creamy yeast like colonies, Gran stain we observed round, oval budding yeast cells at room temperature we observed white, fluffy mold that turns to brown to buff with age in celotape techniques we observed the mycelium with round microconidia.

Conclusion: We conclude that, the fungi isolated was pathogenic which is the causative agent of Histoplasmosis in human and people should be prevented from exposed spores. The chronic stage of histoplasmosis have similar symptoms like those people who have *M. tuberculosis*.

Session Topic: Global Health

Presenter: Chaula Godlove
Institution: National Institute For Medical Research- Mbeya Centre, Mbeya,Tanzania
Co-Authors: Emmanuel Sichone[1], Lwitiho Sudi[1], Jonathan Munkai[1], Nyanda Ntinginya[1], Bariki Mtafya[1], Daniel Mapamba[1], Wolfram Mwalongo[1].

[1]NIMR-Mbeya Medical Research Centre, Department of laboratory Sciences- Mbeya-Tanzania

Severe sepsis due to *Chryseobacterium indologenes* a possible organism resistant to multiple antibiotics: a case study. Mbeya Tanzania.

Introduction: *Chryseobacterium indologenes* is a yellow pigmented, Gram-negative rods, oxidase-positive, non-glucose-fermenting bacteria. It is an environmental organism usually an opportunistic pathogen associated with nosocomial infections. This case, affecting a fit, demonstrates that it may be an agent of severe sepsis. *C. indologenes typically* exhibits resistance to multiple antibiotics.

Methodology: We collected a pus from severe sepsis and suspend in a sterile 15ml falcon tube containing 0.85% Nacl and maintained at 2-80C. We inoculated a sample on Muller Hinton agar, Blood agar and incubated for 24hours and observe the morphological characteristics. We identified the organism by Gram stain, oxidase test and API test. We did the Antimicrobial Sensitivity test to the isolated organism per protocol. We analyzed the data using Microsoft excel and presented by table and figures.

Results: We observed, yellow pigmented colonies from Muller Hinton Ager, Beta hemolysis in blood agar, Gram- negative rods microscopically. Biochemically we observed Oxidase positive and in API 20NE the organism isolated was *Chryseobacterium indologenes*. From antimicrobial sensitivity testing, Imipenem and Gentamycin were sensitive, Azithromycin was intermediate sensitive, Amoxicillin clavulanate, Chloramphenicol, Trimethoprim sulphamethoxazole, and Cefepime, Doxycycline, Ceftazidime and Ceftriaxone were resistant to the bacteria.

Conclusion: We concluded that *Chryseobacterium indologene*s shows resistance to many antibiotics.

Session Topic: Global Health

Presenter: Chaula Godlove
Institution: National Institute For Medical Research- Mbeya Centre, Mbeya,Tanzania
Co-Authors: Emmanuel Sichone[1], Jonathan Munkai[1], Nyanda Ntinginya[1], Bariki Mtafya[1], Daniel Mapamba[1], Wolfram Mwalongo[1].

[1]NIMR-Mbeya Medical Research Centre, Department of laboratory Sciences- Mbeya-Tanzania

Infection due to pathogenic fungi isolated from infected skin of a child: A case study. Mbeya Tanzania

Introduction: The extent of skin fungal infections occur worldwide and amount to approximately 34% of all occupational diseases encountered is still a big problem, this diseases affect 21–87 % of children in African developing countries including Tanzania in people with a weakened immunity. The disease is often characterized by hyphae growing in and around blood vessels and can be potentially life-threatening. *Rhizopus stolonifer* is commonly known as black bread mold. It is a member of *Zygomycota* and considered the most important species in the genus *Rhizopus*.

Methodology: We scraped the lesions with a side of glass slid and suspend in falcon tube contain 1ml 0.85% NaCl. We analyzed a sample using Culture media and celotape technique, we inoculated a sample on sabouraud dextrose agar and incubated at 37oC for 24 hours. The colonial morphology were observed macroscopically. A celotape technique was prepared by putting a drop of methylene blue on a clean glass slide, a pure culture from was taken using a piece of white celotape which has glue and was covered on a methylene blue drop. We examined the slide under light microscope using X10 and X40 objectives and an image was taken using a digital camera.

Results: Macroscopically, colonies grew rapidly, they were white to a greyish in color cotton like as the mold matures it begins to turn black. Microscopic, we observed filamentous, branching hyphae that generally lack cross-walls.

Conclusion and Recommendations: We concluded that *Rhizopus stolonifer* is opportunistic agent of human disease like Zygomycosis.

Session Topic: Global Health

Presenter: Chaula Godlove
Institution: National Institute For Medical Research- Mbeya Centre, Mbeya,Tanzania
Co-Authors: Emma Peter[2], Bariki Mtafya[1], Johnisius Msigwa[1] & Nyanda E. Ntinginya[1]

[1]National Institute for Medical Research Mbeya Research Centre, Mbeya, Tanzania; Sokoine
[2]University of Agriculture, Faculty of Veterinary Medicine, Morogoro, Tanzania

Investigation of selected pathogens in raw vegetables: a case study in Morogoro, Tannzania

Background*: Escherichia, Shigella* and *Salmonella* species are Gram negative bacilli, non -motile, non-sporeforming bacteria, belong to the family E*nterobacteriaceae* which cause enteric fever. Leafy vegetables can be contaminated by enterobacteria due to water sources contaminated by faecal derived organisms this has been reported elsewhere.

Methodology: This was a case study whereby a total of 27 samples of *Lettuce sativa, Brassica oleracea* and *Amaranthus hybridus* were collected and transported at room temperature. Samples were washed by sterile distilled water and washed materials were collected and inoculated in culture media SB, BA, MCA and XLD agar for colonial morphology after incubation at 37°C, followed by Gram reaction (Gram stain)and biochemical test; TSI, Sugars and IMVC.

Results: Among 27 leafy vegetable samples 18 (67%) were found to contain *E. coli,* 3 (11%) were found to contain *Shigella* species. Samples were found to be positive by 78% of total samples. Of the *Escherichia coli* infected vegetables, 26% were from Morogoro Municipal markets, 22% from Mji mpya market and 18% Mawenzi market. With regards to Shigala infection, 7% were from Morogoro Municipal market and 4% from Mji mpya market. No Salmonella species was isolated.
Conclusion:This case study observed that leafy vegetables were highly contaminated with the selected pathogens due to the use of manure, stagnant and slow moving water for watering vegetables.

Session Topic: Global Health

Presenter: Olaniran Esther
Institution: University of Lagos, Lagos, Nigeria
Co-Authors: Temitope O. Sogbanmu[1]

[1]Department of Zoology, University of Lagos.

Biomonitoring, physico-chemical, and biomarker evaluations of abattoir effluent discharges into the Ogun River from Kara Market, Ogun State, Nigeria using *Clarias gariepinus*

Background: The discharge of untreated effluents into aquatic ecosystems poses potential adverse effects to aquatic organisms.

Methods: In this study, the physico-chemical characteristics of abattoir effluent from Kara cow market, Ogun state, Nigeria, surface water and sediments from the Ogun River were evaluated. Fish species and macrobenthic fauna diversity in the river were also examined. Acute toxicity, biochemical and histological studies were investigated in *Clarias gariepinus* exposed to sub-lethal concentrations of the effluent over a period of 28 days.

Results: Effluent physico-chemical parameters such as ammonia, conductivity, total dissolved solids and total suspended solids were higher than set limits. Total polycyclic aromatic hydrocarbons (PAHs) in the effluent and sediment were 6.73 mg/L and 8.07 mg/kg respectively. Tetracycline (an antibiotic administered to the cows at the market) levels in the effluent and surface water were 0.23 µg/mL and 0.85 µg/mL respectively. Fish species diversity was lower at the test site compared to the reference site. *Chironomus spp.* and *Tubifex tubifex dominated* the benthic assemblage at the test site. There were significant changes ($p<0.05$) in the biochemical indices but no histological alterations in exposed C. gariepinus after 28 days.

Conclusions: The results demonstrate that the effluent poses potential risks to the aquatic organisms and ecosystem services provided by the river. We recommend that environmental regulatory agencies and stakeholders should establish effluent and solid wastes management systems at the market to prevent environmental and public health epidemics within the framework of the United Nations Sustainable Development Goals 6 (clean water and sanitation) and 14 (life below water).

Session Topic: Global Health

Presenter: Farwa Sajadi
Institution: York University, Toronto, Canada
Co-Authors: Jean-Paul Paluzzi[1]

[1]Department of Biology, York University. Toronto, Canada

Anti-Diuretic Action and Signaling Cascade of a CAPA Neurohormone in the Mosquito Disease Vector, Aedes aegypti

Background: *Aedes aegypti* mosquitoes are vectors of a variety of pathogens leading to illnesses, such as Dengue fever, Yellow fever, and most recently, the Zika virus. Due to environmental changes, such as global warming, there has been an increase in the geographic range of these mosquito-borne diseases. Millions of people are infected each year due to transmitted diseases, thus, there is a greater need to create new control strategies to prevent the outbreak of these tropical diseases becoming pandemic. Female *A. aegypti* mosquitoes face the challenge of excess water and ion intake after a blood meal. To cope with this, *A. aegypti* have a highly active excretory system, including the Malpighian tubules (MTs), which is under rigorous control by neuroendocrine factors to regulate diuresis. Although both diuretic and anti-diuretic roles for CAPA peptides have been found in larval A. aegypti, its role and signaling pathway remains unclear in adults.

Methods: In this experiment, the effects of AedaeCAPA-1 were measured on adult female MTs stimulated with various diuretic factors. The secretion rates and ion concentrations were measured using Ramsay Assay's and ion-selective microelectrodes.

Results: AedaeCAPA-1 specifically inhibits secretion of MTs stimulated by diuretics, 5-HT and DH31. Furthermore, although AedaeCAPA-1 acts as an anti- diuretic, it does not influence the relative proportions of cations transported by adult MTs. In addition, the effects of the second messenger cGMP and PKG/NOS inhibitors were measured in adult MTs indicating 5-HT and DH31–stimulated secretion is strongly inhibited by cGMP, similar to effects seen with AedaeCAPA-1. Additionally, pharmacological inhibition of PKG/NOS signaling abolishes the anti-diuretic activity of AedaeCAPA-1, confirming the role of cGMP/PKG/NOS in the CAPA signaling pathway. Interestingly, although AedaeCAPA-1 has no inhibitory activity on kinin-stimulated fluid secretion, cGMP strongly inhibited fluid secretion by this diuretic hormone, which targets stellate cells specifically, suggesting that another anti-diuretic factor in addition to AedaeCAPA-1 exists and may utilize cGMP as a second messenger.

Conclusions: Studying the excretory system and understanding the underlying mechanisms behind ion balance aids in developing improved pest management strategies, reducing Aedes populations, and thus mitigating their role as a disease vector."

Session Topic: Global Health

Presenter: Jason Naude
Institution: University of Cape Town, South Africa
Co-Authors: Ann Meyers[1], Edward Rybicki[1]

[1]Biopharming Research Unit, Department of Molecular and Cell Biology, University of Cape Town, Cape Town, South Africa

Expression of chikungunya virus proteins in tobacco plants for the development of a diagnostic reagent and a candidate vaccine

Background: Chikungunya virus (CHIKV) is a non-fatal but highly debilitating zoonotic arbovirus transmitted by mosquitos of the Aedes genus. CHIKV is distributed in Africa, Asia and America. There is no cheap, rapid diagnostic test to distinguish CHIKV from similarly-symptomatic viruses which is problematic as prognosis, patient care, and persistent symptoms of these viruses are different. Additionally, no licensed vaccine is available. Virus-like particle (VLP) candidate vaccines using CHIKV proteins such as E2 have been the only approach to make it to clinical trials. However, these VLPs were developed in costly and poorly-scalable mammalian and insect cells. As such, a cheap and rapid diagnostic reagent and a licensed vaccine is desperately needed. We hypothesise that optimising a plant-expression platform to transiently express CHIKV proteins will be a cost-effective and scalable strategy for biopharmaceutical development.

Methods: Two variants of a recombinant CHIKV E2 envelope gene were synthesised and cloned into a plant expression vector and electroporated into Agrobacterium tumefaciens. Following this, the constructs were transformed into Nicotiana benthamiana leaves via Agrobacterium-mediated small-scale syringe-infiltration. Both constructs were co-infiltrated and co-expressed with constructs encoding either human chaperones CRT and CNX, the plant silencing-suppressor NSs or a combination thereof. Leaves were sampled on 3, 5 and 7 days post-infiltration (dpi), ground up in buffer and levels of recombinant proteins in the crude extracts then assessed by western blotting.

Results: Both E2 variants were expressed transiently in the leaves with one higher than the other. When co-infiltrated with chaperones, expression levels increased significantly, however co-infiltration with the silencing suppressor made no detectable difference. The E2 protein lacking its transmembrane domain showed the highest levels of expression when co-infiltrated with CRT compared to the full-length protein when expressed with its co-infiltrates.

Conclusions: Our findings demonstrate that co-expression of the CHIKV E2 gene lacking its transmembrane domain with CRT results in the highest levels of recombinant E2 expression in plants. This is potentially an alternative, cheaper strategy of biopharmaceutical development and this combination of constructs will be taken further to scale up production of the protein, purify it and characterise it.

Session Topic: Global Health

Presenter: Aryan Lajevardi
Institution: York University, Toronto, Canada
Co-Authors: Mark Brown[2], Jean-Paul Paluzzi[1]
[1]Department of Biology, York University, ON, Canada
[2]Department of Entomology, University of Georgia, Athens, USA

Receptor expression, immunolocalization and physiological activity of a pyrokinin neuropeptide in the mosquito, *Aedes aegypti*

Backgroud: The mosquito, *Aedes aegypti*, is a chief vector responsible for transmitting pathogens causing yellow fever, dengue, Zika virus, and chikungunya. With the rise of these vector-borne illnesses, advancing our understanding of mosquito biology and related physiological processes is imperative in order to develop new methods for vector control. Pyrokinin-related peptides, characterized by a conserved FxPRLamide C-terminal motif, have been shown to exert myotropic effects in some insects, but their functions remain unclear in blood-feeding arthropods.

Methods: In the present study, we deorphanized the pyrokinin-1 receptor (PK1-R) by expression in a heterologous cell system, and profiling its selective and dose-responsive activation by pyrokinins. We further examined receptor expression at both the transcript and protein levels through RT-PCR and whole-mount immunohistochemistry, the latter of which used an antiserum that recognizes antigen sites localized over the third intracellular and extracellular loops of the receptor. We further assessed whether its ligand, AedaePK1, elicits any myotropic actions through hindgut contraction assays, whereby we measured any changes in contractile frequency within the mosquito rectum in response to peptide application. Lastly, we used the Scanning Ion-selective Electrode Technique with Na+-selective microelectrodes to examine whether AedaePK1 influences Na+ transport along the rectal pad epithelia.

Results: Herein, we have functionally deorphanized two A. aegypti pyrokinin-related receptors and examined their differential expression within the alimentary canal (e.g. hindgut) and reproductive tissues in *A. aegypti*. We also screened PK1-R transcript expression in tissues of adults and found the highest level in the posterior hindgut (rectum), suggesting it is a prominent target for pyrokinins. Analysis of pyrokinin innervation and PK1-R localization in this organ with immunohistochemistry showed that cells situated within the rectal pads supported this hypothesis. Based on these expression profiles at the transcript and protein level, we examined prospective physiological roles, however, our first efforts found that pyrokinins did not influence myotropic or ionomodulatory (Na+) activity in isolated recta.

Conclusions: The specific localization of PK1-R in rectal pad cells offers a new model to define how pyrokinin signaling may regulate diuresis and excretion in this important blood pathogen vector species."

Session Topic: Global Health

Presenter: Dr. Mohamed Ali Hind[1]
Institution: University of Khartoum, Soudan
Co-Authors: Eltahir Awad Gasim Khalil[1], Khalid Anan[1,2]
1-institute of endemic disease eltahirk@iend.org
2-Assistant Professor Khalid Enan (PhD)

Hepatitis B Virus (YMDD,YIDD,YVDD)Genes Mutations among sudanese patients

Background: Hepatitis B virus (HBV) infection is a universal health problem, with an estimated 350 million infected individuals worldwide. Chronic infection leads to cirrhosis and even hepatocellular carcinoma.This study was aimed to report and establish taq man probes -real-time pcr-based assay methods for detection of HBV lamivudine resistance genes (YMDD, YIDD, and YVDD) in Sudanese patients.

Methods: Taq man probes were used in a real-time pcr-based assay, Taqman probes were designed to detect (YMDD, YVDD, YIDD) mutations strains of HBV. Serum samples collected from 60 patients with chronic mutant HBV infections were analyzed using this method.

Results: Four samples out of 60 samples the result were positive resistance genes, the variants detection in four samples were 1.6% (1/60) , 3.3% (2/60) ,25% (1/60) FOR (YMDD, YVDD and YIDD) respectively.

Conclusions: We concluded that lamivudine resistance genes (YMDD, YIDD, and YVDD) among chronic HBV patients in Khartoum, Sudan are not common.
We successfully established rapid detection for mutations genes (YMDD, YIDD, YVDD) in HBV by Taqman probes were used in a real-time pcr- based assay, and found significant.

Session Topic: Global Health

Presenter: Niven Mubarak Mursi Mohammed[1]
Institution: University of Khartoum
Co-author: Muzamil Mahdi Abdel Hamid[*2]

1.Department of Molecular Medicine,Institute of Endemic Disease , University of Khartoum
2.Department of Parasitology, Institute of Endemic Disease , University of Khartoum

Molecular docking and mutation analysis of Artemisinin resistant k13 gene: an *in silco* approach

Backgroud: Plasmodium falciparum has developed drug resistance to Artemisinin, which is firmly established in Asia with little information in Africa .artemisinin resistance posing a great challenge for malaria control program worldwide. Artemisinin remain the most effective drug in most African countries, but few studies reported resistance therefore monitoring of resistant should be performed. kelch protein have been identified as the common target of artemisinin resistant. In Sudan, there is little data on status of K13 mutations.

Methods: K13 Sequence were obtained from previous drug follow up study and aligned with reference genome. Homology model of the mutated protein was obtained from Raptor X. Docking of target proteins and drug ligands (Artemisinin, Artemether and Curcumin) using LEED IT.

Results: Non-synonymous single nucleotide polymorphism (SNP) was found (A621V) with frequency (0.03571) not associated with resistance. Homology modeling showed the structure of the mutated protein two chain of (α and β-strand) with p-value 1.07e-12 for one domain containing 233 amino acid. Docking results of the Three ligands with kelch A621V using LEED IT showed no effect on the binding of ligands to kelch (A621V) with docking score (-13.20,-13.38) for Artemisinin and Artemether, Furthermore curcumin showed highest score (-26.14).

Conclusions: In conclusion, a non-resistant SNP is observed in Sudan. The reported functional mutation K621I is not found in the present study. Artemisinin remain effective against P.falciparum malaria. Further *in vitro* and *in vivo* studies should be done to confirm Curcumin as anti-malarial drug.

Session Topic: Global Health

Presenter: Dr. Kirtika Patel
Institution: Moi University, Eldoret, Kenya
Co-Authors: K. Patel, G Vila-Nadal, J. Shah, M. Shamji, L Swan, S.R. Durham, K. Patel, I. Skypala

The prevalence of Pollen Food Syndrome in adults with Irritable Bowel Syndrome

Background: Pollen food syndrome (PFS) is a common food allergy which presenting in those who have seasonal allergic rhinitis. The UK prevalence of PFS is 2%, but a retrospective study found that 33% of IBS patients reported PFS, perhaps expected due to the known high level of reported allergic rhinitis in IBS patients. However, what is less clear is whether PFS is responsible for symptoms rather than IBS. Our prospective study aimed to accurately determine PFS prevalence in IBS subjects, and compare the symptom severity, quality of life, reported food triggers and allergen sensitisation patterns in IBS subjects with and without PFS.

Methodology: Subjects with IBS diagnosed using the Rome IV criteria were prospectively recruited. They completed a validated PFS diagnostic questionnaire, the results of which were compared to a control group of age and sex matched hospital outpatients with congenital heart disease. The IBS group also completed further validated questionnaires on IBS symptoms and the diagnosis and severity of SAR. They also underwent allergy testing to aeroallergens and foods.

Results: Of the 35 adults with IBS (30 female, mean age 34), 29% (10) had PFS, compared to 0% in a group of 35 age and sex-matched controls with congenital heart disease ($p<0.001$). In the whole of the IBS group, 57% of subjects (20/35) had a diagnosis of SAR. There was a significant correlation between PFS and SAR severity ($p<0.05$) and between PFS and IBS symptom severity ($p<0.05$). Those with PFS were also significantly more likely to have positive SPT to potato (raw and cooked), semolina (wheat), hazelnut, tomato, grass and Silver birch ($p<0.05$). The majority also had positive tests to the main birch allergen Bet v 1 and birch cross-reacting allergens in hazelnuts, peanuts, apples, peaches and kiwifruit.

Conclusion: These data confirm that IBS patients have a greater prevalence of SAR, which might explain why their level of PFS is well above the population average. Those with PFS were also more likely to have more severe SAR and IBS symptom scores. It is unknown whether sensitisation to certain foods indicates that IBS symptoms are linked to food allergy

Session Topic: Global Health

Presenter: Sujana Pokhrael
Institution: Tribhuvan University, Kirtipur, Nepal
Co-Authors: Tuladhar R., Manandhar R.

Detection of Panton-Valentine Leukocidin (pvl) gene and SCCmec typing in MRSA

BACKGROUND: Panton-Valentine Leukocidin (pvl) gene - synergohymenotropic toxin gene - encoded by Community Associated Methicillin Resistant Staphylococcus aureus (CA-MRSA) strains are highly virulent; causes skin and soft tissue infection in healthy individual and also a marker of CA-MRSA.This study was conducted to detect a pvl gene and characterize SCCmec typing that aids in providing epidemiological evidence about MRSA and its harbored gene.

METHODS: In a cross-sectional study, a total of 160 growth positive strains were collected from the patients admittimg to the various wards of the hospital and from the 85 S. aureus strains, 40 of these had been confirmed as MRSA by cefoxitin disk diffussion method. Multiplex PCR was used to detect pvl genes among the MRSA isolates. Only selected MRSA isolates were subjected to SCCmec tyoing by multiplex PCR. Antibiotic susceptibility test among the MRSA and MSSA isolatea were analysed.

RESULTS: Out of 85 S. aureus isolates 40(47.5%) were confirmed as MRSA. pvl gene was detected in 10(25%) of the total S. aureus isolates. From 12 MRSA isolates 9(75%) possessed SCCmec type V and 3(25%) possessed SCCmec type IV.

CONCLUSION: The surveillence, screening, monitoring, isolation and identification of the MRSA isolates along with the molecular approach is emergence for effective diagnosis and minimizing the PVL-SA wound infection case in the patients.

Session Topic: Global Health

Presenter: Eric Berenger Tchoupe
Institution: University of Yaounde, Yaounde, Cameroon
Co-Authors: Palmer MASUMBE NETONGO*1,2,3, Eric TCHOUPE1,3, Séverin KAMDEM1,4, Jean Paul Chejou3, Wilfred MBACHAM2,3

1Molecular Diagnosis Research Group, Biotechnology Centre-University of Yaounde I (BTC-UY-I), Cameroon,
2Department of Biochemistry, Faculty of Science, University of Yaounde I (UY1), Cameroon
3Laboratory for Public Health Research Biotechnologies, Department of Biochemistry, Faculty of Science, University of Yaounde I (UY-I), Cameroon
4Cytokines and Diseases Group;International Centre for Genetic Engineering and Biotechnology (ICGEB), Cape Town, South Africa

Evaluation of a homemade saliva kit for the stabilization of plasmodium DNA at room temperature

Background : Malaria diagnostic methods require blood collection that is fraught with challenges such as the need for skilled personnel, the risk of contracting blood borne pathogens. Saliva from Malaria-infected individuals contains trace amounts of Plasmodium DNA, and therefore, could be used as an alternative specimen for diagnosis and research. Molecular methods such as PCR showed great benefit using saliva; however, conserving parasite DNA in saliva is still problematic especially when it comes to cost. We designed current study to evaluate the effectiveness of a homemade non-invasive kit to stabilize plasmodium DNA in saliva at room temperature.

Methods: Concurrent blood and saliva samples were collected from 33 febrile patients. Saliva samples were collected in two separate kits: OMNIGENE•DISCOVER (OM-501) kit as the standard kit and a newly formulated homemade kit as the test kit. Samples were stored at room temperature for 12 months. Blood samples were analyzed using microscopy to detect Plasmodium blood-stage parasites. Plasmodium DNA was extracted from saliva by the Chelex method and molecular detection of the parasite DNA was based on nested Polymerase Chain Reaction (nPCR) amplification of the multicopy 18s rRNA gene. Products were separated on 2.0 % agarose gel stained with ethidium bromide and visualized under UV light.

Results: The frequency of malaria in this study was 78 % using microscopy. Saliva PCR-f1 detected 21 positive malaria samples whereas saliva PCR-so detected 18 positive malaria sample infections. When microscopy was used as gold standard, the sensitivities of PCR-so and PCR-f1 were all recorded at 100%; however the specificities were at 80%, and 85%, respectively. PCR-f1 had a “very good” agreement (kappa 0.81) compared to PCR-so (kappa 0.64).

Conclusion: Homemade kit could be effective in transportation and preservation of malaria parasite DNA in saliva at room temperature.

HotDocs

Saturday, Feb. 9, 2019.

Timeslot: 9:20 – 9:35 am

Presenter: Atiyya tul Munim
Institution: Moi University, Eldoret, Kenya
Co-Authors: Ian Omwoyo, Amara Daniel

HIV and stigma: a descriptive study

HIV-related stigma and discrimination refers to prejudice, negative attitudes and abuse towards people living with HIV/AIDS. There is a cyclical relationship between stigma and HIV: people who experience it are marginalized and made more vulnerable to HIV, while those living with HIV are more vulnerable to experiencing it.

Myths and misleading information increase the stigma and discrimination surrounding the disease. Some people living with HIV and other key populations affected are shunned by family, peers and the wider community, while others face poor treatment in educational and work, rights, and psychological damage. These all limit access to HIV testing, treatment and other services.

Saturday, Feb. 9, 2019.

Timeslot: 12:20 - 12:45 pm

Presenter: Bahati Ernestine Hategekimana[1]
Institution: Moi University, Eldoret, Kenya
Co-Authors: Istarlin Abdi[2]
[1] 4th year, School of nursing, Moi University, Eldoret, Kenya.
[2] Community worker, Kakuma, Kenya.

Period poverty at Kakuma Refugee Camp

Background: Period poverty refers to having a lack of access to sanitary products due to financial constraints. Around the world, only 12% of young people with periods have access to the products they need. In Kenya, 65% of people don't have enough money to buy menstrual projects. When we get to Refugees and Asylum seekers, the statistics are even higher. These women face various challenges while on their menses such as limited to no resources to menstrual hygiene (this includes pads, underwear, soap, water, toilets). In some communities' women and girls are isolated during their periods. Girls end up missing school because of this as well. If a girl misses school every time she has a period, she is set 145 days behind her fellow male students. In times of need, sanitary needs become secondary or even tertiary to finding food and shelter as is the case in Refugees and asylum seekers

Methods: This study centers on women and girls living at Kakuma Refugee Camp, Kenya. To obtain data, focused group discussions were employed as well as one on one interviews with interviewer administered questionnaires. Open ended questions were utilized. Personal, social, academic and economical aspects of period poverty were explored to try and ascertain the effects of period poverty among the refugee women and girls within the camp as well as the possible causes and solutions. Consent was obtained from all the participants.

Results: The data obtained indicated that though there are agencies supplying sanitary towels irregularly, the supply is barely meeting the menstrual needs of the women and girls at the camp. It is reported due to this insufficiency, the women and girls have been forced to find themselves other alternatives. The women and girls have reported to make rags that they use during their menses. Young girls in school reported to abscond school during this time to avoid embarrassment. Women with work also report that they will remain in the house during this time and not go to work as well. Feelings of frustration and shame were reported during their menses because of the unavailability of sufficient sanitary pads.

Conclusion: Alternative and more durable methods of menstrua hygiene management should be explored. Also, efforts should be made to educate the young girls as well as the young women on the basics of menstrual management as it seems to be an area that has been largely neglected.

Saturday, Feb. 9, 2019.

Timeslot: 12:20 - 12:45 pm

Presenter: Jakub Szczupak
Institution: Poznan University of Medical Sciences, Poznan, Poland

Life of a dentistry student from PUMS

This video showcases my perspective as a dental student. The daily life and what we do. You will notice how in majority of this video, I am surrounded by friends that help me go through these studies, help me in time of need and be there for me when I truly need them.

“The single most valuable asset in any dental practice is the dentist and the dental team. Optimal health and work-life balance aren't the buzzwords of the week or touchy-feely luxuries; rather they are essential to the maintenance of the person(s) without whom the practice would cease to exist!” That is straight from the ADAs (American Dental Association) website. It teaches us to help each other in this time of our lives. We all know med/dental school is tough. We can make it easier by being there for each other. These relationships help us navigate these difficult times in our lives. Who said that we need to go through this alone.

Sunday, Feb. 10, 2019.

Timeslot: 9:15 – 9:30 am

Presenter: Dr. Hellina Kassahun
Institution: St. Paul's Hospital Millennium Medical College, Ethiopia

BlueRoots Med Tech Accelerator

The St.Paul's, BlueRoots and iceaddis MedTech Accelerator ('the MedTech Accelerator'/'the Accelerator') will provide financial investment, and technical and business support to twenty Ethiopian start-ups and SMEs targeting the production of medical equipment for commercial sale to the Ethiopian (and wider African) market.

Our model is designed to maximize the success rate of venture capital in the country by reducing the development period for Ethiopian medical-tech start-ups and, mitigating the downside risk of early stage investment into Ethiopian start-ups for private sector investors. Grass roots origination of twenty high potential start-ups from across the country will take place in close collaboration with local universities, Technical and Vocational, Education and Training (TVET) institutes and public-sector partners across the education and healthcare sectors. Once screened and selected, the twenty successful teams will begin the process of developing and manufacturing products with a focus on those locally producible, medical equipment solutions for which there is a clear healthcare demand, and sufficient commercial opportunity.

The MedTech Accelerator will catalyse development of the Ethiopian health sector by building upon the existing Ethiopian manufacturing ecosystem and establishing additional capacity across selected technologies. The Accelerator is strongly aligned with the Ethiopian government's core policy frameworks: the Growth and Transformation Plans (2010-2015 and 2016-2020), which target industrialisation of the Ethiopian economy, and also the National Strategy for Pharmaceutical and Medical Supplies Manufacturing (2015-2025), which targets 50% local production of medical equipment (by 2025). The Accelerator will provide a simple yet effective solution to a common range of issues which affect many African start-ups in the medical-technology sector including: high start-up costs; limited access to capital; an absence of engineering expertise and training; and poor and limited access to technological infrastructure.

Sunday, Feb. 10, 2019.

Timeslot: 11:50 – 12:15 pm

Presenter: Esther Anyango
Institution: University of Nairobi, Kenya

BSI Nairobi at Kabete Rehab Centre

There is a power in reading books that words may not be able to fully express. Reading books for children is associated with improved communication and language skills. Furthermore, it is associated with increased creativity and imagination. Books are useful in rehabilitation programs when positive role models and cultivation of good behaviours are desired. They can inspire and motivate children who find themselves in trouble due to poor decisions.
Kabete Rehabilitation Centre is found in Nairobi County, Kenya. It hosts a population of 78 students; with students from class 5 to 8, the breakdown of the students per class is as follows Class (8 – 19 STDs, 7 – 23 STDs, 6 – 24 STDs and 5 – 12 STDs) these are special children who are on the verge of change from their past life.
The Beyond Sciences Initiative - Nairobi Chapter, saw it fit to establish a library for Kabete Rehab. We had an amazing time establishing the library on the 8th June 2018. This was done in partnership with Story Moja Africa-Start A Library (SAL) team.
This video aims to reveal the impact the library has had on the personal lives, behaviours, and attitudes of the boys at the Centre.

Sunday, Feb. 10, 2019.

Timeslot: 11:50 – 12:15 pm

Presenter: Atiyya tul Munim, Pavanraj Singh Chana
Institution: Moi University, Eldoret, Kenya
Co-Authors: Pavanraj Singh Chana

Reproductive health and education for street adolescents and women in Eldoret, Kenya

Background: Reproductive health is a state of complete physical, mental and social well-being, and not merely the absence of reproductive disease. Reproductive health education deals with reproductive processes, functions and system at all stages of life, and should address harmful practices, unwanted pregnancy, abortions, infertility, nutrition, sexually transmitted infections (STIs), HIV/AIDS, reproductive tract cancers and gender-based violence.

Currently in Kenya, 18% of adolescent girls between 15-19 years are mothers and nearly one in three of them have experienced physical/sexual violence committed by their husband/partner. The challenges are more intense among certain groups, including street adolescents and women, based on social, cultural and biological factors.

Methods: A descriptive cross-sectional study, using mixed methods, was carried out at the OSCAR Centre in Moi Teaching and Referral Hospital (Eldoret, Kenya) to determine sexual and reproductive health behaviors among street adolescents and women. The centre offers sexual and reproductive health services, education, counselling, prevention, detection and rehabilitation services, especially for the street population. Data was collected through interviews with fixed and open-ended questions, and focus group discussions with the adolescents and women. Interviews were also held with staff at the centre. Education sessions were then given on physiological developments, coping mechanisms in adolescence, personal and menstrual hygiene, physical/sexual violence and sexually transmitted infections.

Results: Despite the services offered at OSCAR, a high percentage of women were involved in risky sexual behavior: many had multiple sexual partners; engaged in prostitution; poor contraceptive use; and had high HIV rates, with many on antiretroviral therapy and having infected children. For the adolescents, there were cases of sexual intercourse before the age of 15 years mainly with older partners. Cases of assault and violence, unsafe abortion, and drug use were high among both groups.

Conclusion: From the evidence obtained, there is need for comprehensive reproductive education to ensure that these adolescents and women are equipped with the information they need to achieve healthy sexual and reproductive lives, to avoid negative health outcomes and engage prongs of elimination and prevention of mother-to-child transmission.

Acknowledgements

The BSI International Remote Conference: Science and Society is made possible through the efforts of the following groups and individuals:

BSI Conference and Tech Committee:
Anastasiya Muntyanu* (University of Ottawa, Canada), Prof. Eleanor Fish*, Kate Friesen, Ashton Trotman-Grant*, Justin Lau*, Jastaran Singh, Stefan Divic*, Conor Vedova*, (University of Toronto, Canada), Phillip Chen* (Trinity College Dublin, Ireland), Ruth Anyango, Ashwinder Bhamra, Pavanraj Chana, Bahati Ernestine, Atiyya Tul Munim, Dr. Nicholas Kisilu (Moi School of Medicine, Kenya), Emilia Surzyn (Poznan School of Medicine, Poland), Samuel Ahuno* (KNUST, Ghana), Esther Anyango (University of Nairobi), Dr. Sergey Yegorov (Suleyman Demirel University, Kazakhstan), Milica Tanic* (McMaster University, Canada), Glauco Vitiello (Londrina State University, Brazil), Ivana Bogado Martinez (Univesidade Unigranrio, Brazil), Dr. Bola Hanna*, Dr. Payam Zarin*, Dr. Silvia Pena Galvan (Harvard Medical School, USA). (*denotes Conference Steering Committee)

BSI KNUST Ghana:
Samuel Ahuno, Dr. Alexander Kwarteng

BSI at Moi University, Kenya:
Ruth Anyango, Ashwinder Bhamra, Pavanraj Chana, Ahmed Ali Dawood, Bahati Ernestine, Deborah Jakait, Daniel Amara, Laventa Obare, Dr. Bernard Ochieng, Dr. Kirtika Patel (Moi School of Medicine, Kenya) and Dr. Nicholas Kisilu (Chandaria Cancer Center, Moi Teaching and Referral Hospital).

BSI Nairobi, Kenya:
Esther Anyango, Adrianne Ochanyo, Rosemary Njogu, Grace Mwarage, John Njenga (University of Nairobi, Kenya)

BSI ICB/USP Organizing Committee:
CCEx-ICB: Dr. Maria Inês Nogueira (President), Dr. Gustavo P. Amarante-Mendes (USP, Brazil)

BSI at National Institute of Immunology (NII), India:
Shubhendu Trivedi, Robin Kumar, Akansha Singh, Deepak Yadav, Alka Gupta, Vijay Bajwa, Sayan Chakraborty, Avinash Kumar Singh (Nantional Institute of Immunology, India), Dr. Swarnendra Singh (Imperial Life Sciences, India)

We also acknowledge the support and efforts of the following groups and individuals:

Dr. Martina Sassone Corsi, Dr. Alborz Karimzadeh, Shannon Marie Haas, Kumba Seddu, Dr. German Spallanzani, Dr. Sims Kochi (Dept. of Microbiology and Immunobiology, Harvard Medical School), Dr. Deepali Raval (Harvard Infectious Diseases Consortium) Adrian Fester (MEDizzy), Kristin Hendricks, (McGill University, Canada), Dr. Behrouz Moemeni (BeMo), Rutvij Khanolkar, Dr. Nana Lee, Dr. Richard McAloney (University of Toronto) Dr. Suraj Varkhande (University of Salzburg, Austria), Simran Ghoman (University of Alberta, Canada), Daniel Udenwobele, Farzan Pavri (Schulich School of Medicine), Dr. Clive Gray (Immunopaedia.org.za), Alicja Surzyn (ASF, Mexico), African Academy of Sciences, Medical Student Association of Kenya (Kenya), Dr. Bruno Silva-Santos (Instituto de Medicina Molecular Lisboa, Portugal), Dr. Yury Rubtsov (Lomonosov Moscow State University, Russia), Dr. Navid Nouri (Genentech), Farzin Shamloo (Perdue University, USA), Elijah Oladipo (LAUT, Nigeria), Sohail Mahmood. BSI is also grateful for help from Medizzy and BeMo Academic Consulting for Conference Marketing.

BSI is also grateful for financial support from the Department of Immunology and Trinity College at the University of Toronto (Special thanks to Prof. Mayo Moran, Prof. Michael Ratcliffe, Prof. Juan-Carlos Zúñiga-Pflücker), Janice Wright, and BioLegend for generously sponsoring the Awards Program.