Final Abstract Number: 01.001
Session: Plenary I: Long-Term Zika Complications
Date: Friday, March 2, 2018
Time: 09:00-09:45
Room: Libertador ABC
Type: Invited Presentation

Long-term Zika complications
V. van der Linden
Recife, Brazil

Abstract text: Congenital Zika Syndrome (CZS) has as a main characteristic the brain impairment, with microcephalus, however it is still little known about this entity and its clinical spectrum that includes newborns with normal head circumference.
In addition to congenital microcephaly and craniofacial disproportion, a range of manifestations have been associated with CZS, including neurologic symptoms, arthrogryposis, hearing and ocular abnormalities.
The neurologic findings of severe affected patients include irritability, hyperexcitability, hypertonia and dysphagia. Regardless of the ophthalmologic impairment, more than a half of the patients with the CZS and severe microcephaly have presented poor interaction with the environment related to cortical impairment.
Epilepsy is frequent, even in patients with normal head circumference at birth. The arthrogrypotic joints did not result from abnormalities of the joints themselves and are likely to be of neurogenic origin.
The pattern of brain images abnormalities in CZS has been fully described. The pattern of calcifications at the junction between cortical and subcortical white matter, in addition to the cortical developmental disorders predominantly on frontal regions confers highly suggestive pattern of CZS. Cerebellar atrophy and malformations of the brainstem may also occur.
Unlike other congenital infections, several patients are developing hydrocephalus between 3 to 18 months. The pathophysiology of hydrocephalus in CZS is still unknown
The complete neurological picture requires the central nervous system maturation and it will only become clear after, at least 18 months, so to a better definition of congenital Zika syndrome we need a longer follow-up.

Final Abstract Number: 02.001
Session: New Approaches to Vaccines for Pneumonia
Date: Friday, March 2, 2018
Time: 10:15-12:15
Room: Libertador A
Type: Invited Presentation

Pneumococcal vaccines
G. Rodgers
Seattle, USA

Abstract text: *Streptococccus pneumoniae* is a major cause of disease and death globally with the highest incidence occurring in children less than 5 and older adults and in low income countries. Development of pneumococcal conjugate vaccination (PCV), against the most common disease-causing serotypes, has been an important advancement in prevention of disease with documented effectiveness for invasive pneumococcal disease, pneumonia and otitis media in countries incorporating the vaccine in their national immunization programs. Additionally, protection of unvaccinated persons (herd protection) by decrease in nasopharyngeal carriage and consequently, transmission of pneumococcus, has expanded the benefits of PCV vaccination of children. Introduction of PCVs into middle income countries, sustainability of PCV immunization programs, particularly in Gavi graduating countries and serotype replacement are key issues that must be addressed in order to continue to benefit from vaccination against pneumococcus, globally. This talk will address novel dosing schedules and new vaccines that may change the pneumococcal vaccine landscape.

Final Abstract Number: 02.002
Session: New Approaches to Vaccines for Pneumonia
Date: Friday, March 2, 2018
Time: 10:15-12:15
Room: Libertador A
Type: Invited Presentation

RSV vaccine

F. Polack
Fundación Infant, Buenos Aires, Argentina

No abstract received!

Final Abstract Number: 02.003
Session: New Approaches to Vaccines for Pneumonia
Date: Friday, March 2, 2018
Time: 10:15-12:15
Room: Libertador A
Type: Invited Presentation

Group B Streptococcus (GBS) vaccine

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Abstract text: Intrapartum antibiotic prophylaxis (IPA) during labor for women identified as having recto-vaginal Groups B Streptococcus (GBS) colonization, has been successful in preventing early-onset invasive (<7 days of age) disease in new-borns in high income countries where implemented. Nevertheless, GBS remains a leading cause of neonatal sepsis in high-income settings, and is now also the leading cause of bacterial meningitis in USA. Also, the incidence of invasive GBS disease remains high in sub-Saharan African countries, where IAP is not feasible, whilst its contribution to neonatal sepsis is uncertain in South Asia. Furthermore, recent data indicate that the burden of GBS associated stillbirths might be similar to that for EOD in some African countries.

Recent advances in the prevention of invasive GBS disease during early infancy, including the potential to prevent late onset disease (7-89 days age) which is not preventable by IAP, is the development of polyvalent polysaccharide protein conjugate vaccines. Recent studies have reported on the safety and immunogenicity of a trivalent (serotypes Ia, Ib and III) GBS polysaccharide protein conjugate vaccine (GBS-3CV). This vaccine elicits immune responses in pregnant women vaccinated during the last trimester, albeit less so among women in whom the pre-vaccination antibody titers were less than the lower detection limit of the assay. The ratio of antibody transfer to the newborns' of these women was approximately 0.5-0.7, indicating less efficient transplacental transfer of polysaccharide targeted IgG than is observed for IgG targeted at protein antigens. Furthermore, vaccination of HIV-infected women, elicited lower quantitative antibody responses than in HIV-uninfected women, suggesting the need for different vaccine schedules in these women. Also, the GBS conjugate vaccine appears to be more immunogenic in African than European/North American women.

The licensure of a GBS vaccine for pregnant women aimed at protection against invasive GBS disease of their newborns will, however, require sample size in excess of 70,000 participants for an invasive disease endpoint. An alternate licensure pathway, as is the case for meningococcal vaccine, could be premised on establishing a sero-correlate of protection against invasive disease and using this to license the vaccine based on immunogenicity and safety.

Final Abstract Number: 02.004
Session: New Approaches to Vaccines for Pneumonia
Date: Friday, March 2, 2018
Time: 10:15-12:15
Room: Libertador A
Type: Invited Presentation

A universal influenza virus vaccine strategy targeting the conserved stalk domain of the hemagglutinin
F. Krammer
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Abstract text: Influenza virus infections remain a significant cause of morbidity and mortality worldwide. Current vaccines show acceptable efficacy against antigenically matched viruses by inducing strain specific antibodies against the membrane-distal globular head domain of the viral hemagglutinin, but fail to protect against drifted and pandemic strains. The membrane-proximal stalk domain of the viral hemagglutinin exhibits a high degree of both sequence and structural conservation across influenza virus subtypes and monoclonal antibodies directed against this region typically show broad neutralizing activity. However, these antibodies are rare and usually not induced/boosted by regular seasonal vaccines. We hypothesize that a vaccine strategy that stimulates a robust immune response towards this region of the hemagglutinin could provide universal influenza virus protection. We developed a universal influenza virus vaccine based on the conserved stalk domain of group 1 and group 2 hemagglutinins. By sequential vaccination of mice and ferrets with chimeric hemagglutinin constructs that share the same stalk domain but have divergent head domains we were able to specifically boost broadly neutralizing antibody titers against conserved epitopes in the hemagglutinin stalk. Animals vaccinated with these constructs were protected from morbidity and mortality induced by infection with a panel of heterologous and heterosubtypic influenza A viruses. Additionally, chimeric hemagglutinin vaccination also impacted on virus transmission in the ferret model. In the light of emerging viruses in Asia it is of note that our vaccination regimen also protected animals from H5N1, H6N1 and H7N9 virus challenges and reduced lung titers upon H10 virus infection. Finally, we showed that stalk-reactive antibodies were boosted in individuals that received an H5N1 vaccine in clinical trials. This supports the hypothesis that exposure to hemagglutinins with divergent heads but conserved stalk induces such antibodies in humans. The present data suggest that this vaccine strategy has the potential to provide broad influenza virus protection in humans and clinical trials are currently ongoing. A universal influenza virus vaccine, which requires a single or only a few immunizations, would represent a major advance towards the control of influenza worldwide and would significantly enhance our pandemic preparedness.

Final Abstract Number: 03.001
Session: How to Manage Antimicrobial Resistance
Date: Friday, March 2, 2018
Time: 10:15-12:15
Room: Libertador B
Type: Invited Presentation

Update - management of drug-resistant gram negative infections
Y. Morinaga
Katsunori Yanagihara, Nagasaki, Japan

Abstract text: Antimicrobial resistance (AMR) has become a global concern and drug-resistant bacteria are commonly observed in the clinical settings. In particular, the expansion of plasmid-mediated drug-resistant genes is an emerging problem among the Gram-negative bacteria. These mobile resistances are often shared between bacteria belong to Enterobacteriaceae. These bacteria have a highly affinity to the intestinal environment, which contains several clinical concerns such as a colonization potential of drug resistance, possibility of possessing multiple drug-resistances, and difficulties in eradication of drug-resistant bacteria. For critically ill patients, infectious diseases caused by these intrinsic bacteria are common problem.
How efficiently manage drug resistance is important for patients and infection control. Recent diagnostic progress can provide advantages in the detection of drug resistances. These developments not only provide rapid detection of drug resistances but also promote de-escalation. In the era of AMR, the microbiological diagnosis is now increasing in importance in the management of infectious diseases. Molecular methods using nucleic acids have become helpful tools for the detection of drug-resistant genes. Several multi-target nucleic acid tests are currently available in the bloodstream infections. In particular, rapid and accurate nucleic tests for bloodstream infections can enhance the prompt and appropriate treatment in critically ill patients. Matrix-assisted laser desorption ionization-time of flight mass spectrometry (MALDI-TOF MS) a rapid tool for identification bacteria but some important β-lactamases can be also detected on the MALDI-TOF MS platform by methodological progress.
Development of new antibiotics does not match with the pace of resistance. In addition to use of new diagnostics, optimizing antibiotic dosing based on pharmacokinetic-pharmacodynamic parameters is also important to manage drug-resistant infections. To preserve antibiotics for human health, it is essential that physicians manage infectious diseases by efficient diagnosis and effective treatment.

Final Abstract Number: 03.002
Session: How to Manage Antimicrobial Resistance
Date: Friday, March 2, 2018
Time: 10:15-12:15
Room: Libertador B
Type: Invited Presentation

Management of drug-resistant gram-positive infections
L. Grayson
Melbourne, Australia

Abstract text: Emerging multi-drug resistance (MDR) among staphylococci and enterococci continues largely unabated, while early evidence of resistance to certain key drug classes among some streptococcal species is of increasing concern. Although improved hand hygiene in hospitals has helped control the spread of methicillin-resistant *Staphyococcus aureus* (MRSA), some strains have developed resistance to daptomycin and linezolid with significant clinical consequences. Furthermore, community MRSA strains are increasing in many countries, often driving increased use of empiric vancomycin therapy for severely ill patients where MRSA sepsis is likely.
Vancomycin-resistant enterococci (VRE) are also increasing substantially – in some countries being more common than MRSA as a cause of healthcare-associated bacteraemia. VanA-VRE predominates in USA, while in Australia and some European countries, VanB-VRE is dominant, but with clonal outbreaks of VanA-VRE increasing, especially among high-risk patients. For these infections there are often limited treatment options due to the emergence of daptomycin resistance and, less commonly, linezolid resistance. Detailed hospital cleaning with bleach or hydrogen peroxide appears to be effective in reducing healthcare-associated VRE transmission, but can be difficult to ensure.
Given the limited new treatment options for most serious Gram-positive pathogens, a return to basic infection control measures is required.

Final Abstract Number: 03.003
Session: How to Manage Antimicrobial Resistance
Date: Friday, March 2, 2018
Time: 10:15-12:15
Room: Libertador B
Type: Invited Presentation

AMS across the surgical pathway in LMICs
E. Charani
Imperial College London, London, United Kingdom

Abstract text: Optimizing antibiotic prescribing across the surgical pathway (before, during, and after surgery) is a key aspect of tackling important drivers of antimicrobial resistance and simultaneously decreasing the burden of infection at the global level. The overwhelming majority of surgical procedures require effectively limited delivery of antibiotic prophylaxis to prevent infections. Evidence from around the world indicates that antibiotics for surgical prophylaxis are administered ineffectively, or are extended for an inappropriate duration of time postoperatively. Ineffective antibiotic prophylaxis can contribute to the development of surgical site infections (SSIs), which represent a significant global burden of disease. The World Health Organization estimates SSI rates of up to 50% in postoperative surgical patients (depending on the type of surgery), with a particular problem in low- and middle-income countries, where SSIs are the most frequently reported healthcare-associated infections. Much of the scientific research in infection management in surgery is related to infection prevention and control in the operating room, surgical prophylaxis, and the management of SSIs, with many studies focusing on infection within the 30-day postoperative period. However it is important to note that SSIs represent only one of the many types of infection that can occur postoperatively.Surgical patients comprise 35-50% of hospital admissions. Historically, LMICs have sub-optimal investment in surgical services, and existing surgical systems are growing too slowly to meet the increasing demand. The success of interventions such as the WHO checklist targeting surgical safety are highly context-dependent and variable, and are influenced by economic, cultural, and social factors, including role identity and hierarchies within healthcare teams. In particular, LMIC hierarchies have a significantly greater impact on the successful adoption of interventions in surgery. Importantly, leadership, flexibility, and teamwork are required for the implementation of checklists to be effective in any setting. This lesson applies to the successful implementation of any patient safety initiative, including interventions aiming to optimize antibiotic use. Interventions in antibiotic use tend to consider and address only *one* point at a time on the patient pathway, and in the case of surgical patients, attention has been focused primarily on prophylactic antibiotic use. Identifying and mapping current actors and actions in the surgical specialty in different healthcare settings will inform interventions that are context-specific and relevant to the local patient population. They will also help ensure greater equity in access to safe surgery on a global scale.

Final Abstract Number: 03.004
Session: How to Manage Antimicrobial Resistance
Date: Friday, March 2, 2018
Time: 10:15-12:15
Room: Libertador B
Type: Invited Presentation

National action plans on antimicrobial resistance in Japan
H. Kawamura
Department of Infection Control and Prevention, , Japan

Abstract text: The healthcare-associated infections spread in Japan, caused by antimicrobial-resistant bacteria including Methicillin-resistant *Staphylococcus aureus* (MRSA) and multidrug-resistant *Pseudomonas aeruginosa*. Furthermore, this growing problem is now increasingly found as community-acquired (CA) antimicrobial-resistant infections including penicillin-resistant *Streptococcus pneumoniae* (PRSP), extended-spectrum beta-lactamase producing Enterobacteriaceae and CA-MRSA. The proportions of antimicrobial resistance (AMR) in MRSA (51% of *S. aureus*) and PRSP (48% of *S. pneumoniae*) are higher in Japan than in other countries and those in carbapenem-resistant *P. aeruginosa* (17% of *P. aeruginosa*) and third-generation cephalosporin-resistant *Escherichia coli* (18% of *E. coli*) maintain levels equal to or lower than those in other countries.
The Government of Japan formulated the National Action Plan on AMR in April 2016. This National Action Plan is structured around goals in the following six areas: (1) Public Awareness and Education, (2) Surveillance and Monitoring, (3) Infection Prevention and Control, (4) Appropriate Use of Antimicrobials, (5) Research and Development, and (6) International Cooperation. This action plan specified the outcome indices; lower the penicillin resistance of *S. pneumoniae* to 15% or less, the methicillin resistance of *S. aureus* to 20% or less and lower the imipenem resistance of *P. aeruginosa* to 10% or less in 2020. In hospital setting, the efforts including the surveillance of AMR, monitoring of the trend of the antimicrobial use, infection prevention and control, and operation of antimicrobial stewardship teams have been initiated. In Japan, it is possible to calculate the additional medical fee of infection prevention by arranging certificated nurse for infection control and promoting antimicrobial stewardship measures including the mandatory pre-authorization or reporting for specified antibiotics use. In 2012, a premium for regional cooperation in infection control was created and regional infection control networks among medical institutions are being established to support infection control of small and medium-sized medical institutions.
The state of antimicrobial use counts 90% of the prescription, among outpatients and residents in nursing care facilities, however, it is unknown about infection control for outpatient departments and nursing care facilities. It is necessary to carry out further surveillance for outpatient departments and nursing care facilities.

Final Abstract Number: 04.001
Session: CA-RTIs and Reducing Antimicrobial Resistance - can both be achieved?
Date: Friday, March 2, 2018
Time: 10:15-12:15
Room: Libertador C
Type: Sponsored Symposium

Rational use of antimicrobials in upper respiratory tract infections in children
M. Safadi
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Abstract text: Upper respiratory tract infections (URTIs) are one of the most common childhood diseases and are recognised as the main cause of medical visits and prescription of antimicrobials in developed countries.[1,2] Most cases of URTIs in children, however, have viral aetiology, self-limited evolution and are usually benign.[1,2] In spite of this evidence, we have observed an increasing tendency towards antibiotic abuse, particularly broad-spectrum antibiotics, which in the end contributes to increasing antimicrobial resistance rates, and also causes potentially preventable adverse events and unnecessary costs.[1–3] Moreover, emerging evidence links early antibiotic exposure in infants and its impact on the human microbiome with long-term effects in metabolic, immunological and developmental diseases.[4,5]
In this context, the implementation of judicious prescribing strategies, establishing stringent criteria for the diagnosis and therapeutic management of the most common bacterial URTIs, including acute otitis media, bacterial sinusitis and streptococcal pharyngitis, is crucial.[6] These strategies should weigh up the benefits and harms of antibiotics, taking into account quality information on local data of resistance rates of the most likely pathogens associated with these infections and the selection of narrow-spectrum antibiotics at an appropriate dosage and duration of treatment.[6]

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Final Abstract Number: 04.002
Session: CA-RTIs and Reducing Antimicrobial Resistance - can both be achieved?
Date: Friday, March 2, 2018
Time: 10:15-12:15
Room: Libertador C
Type: Sponsored Symposium

Clinical impact of antimicrobial surveillance in the management of infected patients

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CEMIC, Buenos Aires, Argentina

Abstract text: Antimicrobial resistance (AMR) is present in all parts of the world with new resistance mechanisms continuing to emerge and spread globally.[1] The World Health Assembly responded to this crisis by adopting, in 2015, a global action plan on AMR.[2] The goal of this plan is to ensure, for as long as possible, continuity of successful treatment and prevention of infectious diseases with effective and safe medicines that are quality-assured, used in a responsible way, and accessible to all who need them.[2] These aims have been corroborated by the 2016 final report of the UK government-commissioned review on AMR – 'Tackling drug-resistant infections globally'.[3] Recommendations from this review include improving worldwide surveillance of AMR and consumption along with highlighting the vital importance of global co-operation.[3]
Antibiotic susceptibility trends provide indisputable evidence of the progress of AMR and surveillance provides early warning about emerging threats and trends and to provide information to guide appropriate antibiotic prescribing and health policies, which, in turn, can help slow or halt rising resistance levels.[3] Surveillance and the use of local susceptibility data is an important part of appropriate antibiotic prescribing.[4,5] The Survey of Antibiotic Resistance (SOAR) is an international study which was initiated in 2002 to generate up-to-date local susceptibility data for the three most important respiratory tract pathogens: *Steptococcus pneumoniae, Haemophilus influenzae* and *Moraxella catarrhalis*. SOAR continues to expand globally and some recently published results will be presented.[6]
SIREVA (Sistema de Redes de Vigilancia de los Agentes Responsables de Neumonias y Meningitis Bacterianas) is a surveillance study instigated by the Pan American Health Organization (OPS) to provide susceptibility data for pneumococcal pathogens. Eleven countries (Bolivia, Brazil, Ecuador, El Salvador, Guatemala, Honduras, Nicaragua, Panama, Paraguay, Peru and Venezuela) are part of the surveillance network.[7] SIREVA II, 2014[8] is a surveillance study coordinated by OPS, to present susceptibility data from pneumococcal pathogens isolated from invasive infections. Nineteen countries are included (Argentina, Bolivia, Brazil, Chile, Colombia, Costa Rica, Cuba, Ecuador, Mexico, El Salvador, Guatemala, Honduras, Nicaragua, Panama, Paraguay, Peru, Dominican Republic, Uruguay and Venezuela). Results from the most recent reports will be presented.[8]

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Final Abstract Number: 04.003
Session: CA-RTIs and Reducing Antimicrobial Resistance - can both be achieved?
Date: Friday, March 2, 2018
Time: 10:15-12:15
Room: Libertador C
Type: Sponsored Symposium

Management of CA-RTIs - importance of guideline adherence
G. D. Lopardo
FUNCEI, Buenos Aires, Argentina

Abstract text: Respiratory tract infections (RTIs) are a frequent reason for consultation in ambulatory practice and represent the leading cause of antibiotic consumption in the community.[1] Diagnosis is based on clinical practice and the aetiological agent is rarely established; treatment is empirical in most cases. One of the pillars of the appropriate use of antibiotics in clinical practice is the knowledge of local pathogens, their resistance patterns and to adhere to clinical guidelines. Improving antibiotic prescribing has become an urgent public health priority. Reducing antibiotic overuse may achieve various potential outcomes, including slowed evolution of antibiotic resistance, decreased healthcare costs, and fewer adverse drug events.

The progressive growth of bacterial resistance is a concern worldwide and is now considered a global health security threat by the World Health Organization.[2] One of the main factors involved in the escalation of resistance is the irrational use of antimicrobial drugs by prescribing doctors.[3] In Latin America, of equal or greater importance, is the easy access of the population to these drugs which are usually obtained as over-the-counter medication.[4,5]

Primary care is increasingly becoming the focus of antimicrobial stewardship in the fight against the global crisis of antibiotic resistance. This is where the greatest tonnage of antibiotics is prescribed—perhaps three quarters of all used in medical care. RTIs are the group of infections most commonly treated with antibiotics, principally made up of otitis media, sore throat, cough ('acute bronchitis'), rhinosinusitis, and undifferentiated infections.[6]

Interventions aimed to improve antibiotic use are intended to achieve a variety of outcomes, including diminished antibiotic resistance, fewer adverse events, and decreased health care costs. However, long-term studies to evaluate these impacts are largely yet to be done, and studies of antibiotic resistance would need to be conducted in large populations and over long time periods. In the absence of patient-centred outcomes, it has been suggested that the rate of 'inappropriate' prescription of antibiotics would be the best surrogate outcome. But although a number of guidelines define when antibiotic use is warranted, defining and determining 'appropriate' use for study purposes is difficult because determination of appropriateness is subjective and requires both access to adequate patient-level data and clinical knowledge.

The implementation of treatment guidelines for RTIs is a key tool to optimise treatment. A considerable number of guidelines for the management of upper and lower RTIs have been developed. The Infectious Diseases Society of America (IDSA)[7] and the European Society for Clinical Microbiology and Infectious Diseases[8,9] develop guidelines on a regular basis, enabling most countries to facilitate the proper treatment of RTIs. Guidelines combine results of microbiological surveillance with the rational use of antibiotics. However, several studies have shown that GPs do not always follow guidelines. A study recently conducted in Germany showed that there is a big gap between guideline recommendation and actual prescribing, in the decision to prescribe and the choice of antibiotic agent. This gap could be closed by periodic quality circles on antibiotic prescribing for GPs.[10]

Martin Llewelyn, *et al* published in July 2017 in the British Medical Journal an article entitled 'The antibiotic course has had its day'.[11] The authors refer to the relationship between exposure to and the development of resistance to antibiotics, at both the individual and population levels, and promote the reduction of unnecessary use of antibiotics in line with the objectives of the World Health Organization[2]. Global health authorities suggest replacing the term 'complete the course' by taking antibiotics 'exactly as prescribed'. Although evidence supporting the duration of antibiotic treatment is scarce, in recent years a considerable number of publications have shown that short courses of antibiotics are sufficient to obtain clinical and microbiological cure in most outpatient infection.[12-15] The Infectious Diseases Society of Argentina (SADI) has developed recommendations for the treatment of frequent infections in the community to avoid the unnecessary prescription of antibiotics, to use those of reduced spectrum and to prescribe short courses of antibiotics[16-20] and thus considerably reduce the burden of antibiotics to which the community is exposed.

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Final Abstract Number: 06.001
Session: HIV and Hepatitis in the Americas
Date: Friday, March 2, 2018
Time: 10:15-12:15
Room: Retiro BC
Type: Invited Presentation

New antiretroviral treatment options
R. Arduino
Houston, USA

Abstract text: Combination antiretroviral therapy (cART) became the standard of care for the treatment of HIV infection since 1996 when morbidity and mortality among people living with HIV dramatically dropped and the prognosis of HIV infection shifted from almost fatal to a manageable chronic disease. However, Many remaining obstacles may lead to decreased adherence and consequent virological and clinical failure, such as high pill burden, dosing frequency, and drug-drug interactions, and short- and long-term side effects. New antiretroviral treatment options aim to overcome these drawbacks of current antiretroviral drugs. Among them, long-acting injectable nanoformulations of rilpivirine (RPV LA, a non-nucleoside reverse transcriptase inhibitor) and cabotegravir (CAB LA, a new integrase strand transfer inhibitor under development) that allow intermittent intramuscular administration were developed to improve adherence and quality of life among people living with HIV. In addition, several groups are exploring innovative nanochannel delivery systems for the constant and sustained delivery of antiretroviral drugs for HIV pre-exposure prophylaxis and treatment. This technology achieves constant and sustained drug release from an implantable reservoir by nanoscale diffusion, without the need for pumping mechanisms. I will review these new treatment options for HIV prevention and treatment.

Final Abstract Number: 06.002
Session: HIV and Hepatitis in the Americas
Date: Friday, March 2, 2018
Time: 10:15-12:15
Room: Retiro BC
Type: Invited Presentation

Novel strategies for antiretroviral treatment

P. Cahn
Buenos Aires, Argentina

Abstract text: In just 30 years highly-active antiretroviral therapy has evolved from complex, difficult to adhere to, and limited efficacy to current standard of care of potent and convenient single tablet regimens. With the improved potency, tolerability and durability of newer drugs, with higher resistance barrier, drug-sparing strategies have gained increasing interest among HIV researchers. While as a simplification strategy boosted-PI monotherapy has shown acceptable results in selected groups of patients, these simplified regimens failed to achieve non-inferiority when compared to standard of care triple drug combinations in treatment-naïve patients.
We designed a series of dual therapy studies (two randomized, open label boosted-PI based and one pilot trail based on dolutegravir) including lamivudine as second drug.
Our results paved the way for several clinical trials, some of them still ongoing. In this presentation, we will revisit the existing evidence regarding dual therapy as a possible strategy for both treatment-naïve and virologically suppressed patients, the potential benefits and remaining challenges of these regimens.

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Room: Retiro BC
Type: Invited Presentation

Management of HIV-Hepatitis B co-infection
A. Gadano
Buenos Aires, Argentina

Abstract text: HIV infection has a significant impact on the natural history of chronic hepatitis B virus (HBV) infection, with accelerated progression of liver disease and increased liver-associated mortality compared with HBV monoinfection. Liver disease related to infection with hepatitis B virus (HBV) is a frequent cause of morbidity and mortality in these patients.
Since chronic hepatitis B may evolve in an asymptomatic way, early diagnosis by HBsAg screening among people living with HIV could have substantial impact on preventing morbidity and mortality among HIV/HBV co-infected individuals. European and American guidelines on the management of HIV infected patients recommend the initiation of ART in HIV/HBV co-infected patients irrespective of CD4 cell count due to the increased risk of fibrosis progression, cirrhosis and HCC. Nucleos(t)ide reverse transcriptase inhibitors (NRTI) is the mainstream of therapy for HIV-HBV-coinfected patients. The double antiviral activity of NRTI requires coordination and careful selection of treatment for both viruses to avoid selection of resistance mutations and toxicity. All persons with HIV/HBV co-infection should receive ART including either TDF or TAF, which have antiviral activity against HIV and HBV. Stopping TDF- or TAF-containing ART should be avoided in persons with HIV/HBV co-infection because of the high risk of severe hepatitis flares and decompensation following HBV reactivation hepatitis. Drug toxicity (renal, bone density, liver) should be closely monitored during ART. Persons with liver cirrhosis and low CD4 count require careful surveillance in the first months after starting ART in order not to overlook immune reconstitution syndrome and subsequent liver decompensation due to flares of liver enzymes. Because TDF, TAF and possibly also ETV monotherapy can cause HIV resistance mutations, all HBsAg-positive patients should be screened for HIV before these drugs are used in the treatment of HBV infection. Early initiation of HBV-active antiretroviral therapy has substantially improved the natural history of HIV-HBV coinfection but the prevalence of liver disease remains elevated in this population.
Patients with decompensated liver disease should be referred to a liver transplant center.

Final Abstract Number: 07.001
Session: Hot Topics in Travel Medicine
Date: Friday, March 2, 2018
Time: 10:15-12:15
Room: La Pampa
Type: Invited Presentation

Update on travel vaccines

L. G. Visser
Leiden University Medical Centre, Leiden, Netherlands

Final Abstract Number: 07.002
Session: Hot Topics in Travel Medicine
Date: Friday, March 2, 2018
Time: 10:15-12:15
Room: La Pampa
Type: Invited Presentation

Building travel medicine networks in South America
A. Lepetic
GSK, Argentina

No abstract received!

Final Abstract Number: 07.003
Session: Hot Topics in Travel Medicine
Date: Friday, March 2, 2018
Time: 10:15-12:15
Room: La Pampa
Type: Invited Presentation

Emerging infectious diseases and international travelers
A. Wilder-Smith
Atlanta, USA

Abstract text: Epidemic spreading patterns changed dramatically after the development of modern transportation systems. In pre-industrial times, the spread of disease was mainly a spatial-diffusion phenomenon. When the Black Death was spreading through 14th century Europe, it generated an epidemic front that passed as a continuous wave through the continent at about 200 – 400 miles per year. The 1918 influenza pandemic took one year to spread from the US to isolated Pacific islands, while the 1957 flu virus moved around the globe in about six months. In 2003, SARS spread to 5 countries within 24 hours after introduction to Hong Kong. The speed and pattern of the 2009 H1N1 pandemic was even more astonishing with a rapid but patchy propagation pattern shaped by human-mobility networks that allow infected people to travel across continents in one day or less. Through mathematical modeling we are now able to analyze social aggregate states made up of millions of people, taking into account the complexity and non-uniformity of transportation fluxes and population movements. The interconnectedness makes draconian travel restrictions almost impractical and reduces the effectiveness of any containment or mitigation strategies that are limited to a single country.
Factors associated with vulnerability of countries to the emergence of infectious diseases include population density, national and international travel, bio-diversity, land use change, zoonotic reservoirs, weak healthcare and public health systems, and deficiencies in water and sanitation. Information on air travel can help identify the origin of the importation and predict further geographic spread. Examples of the spread of diseases with relationship to travel will include influenza, SARS and MERS, polio, Zika and dengue, antimicrobial resistant pathogens, and viral haemorrhagic fevers. Because of the unique role of travel in emerging infections, efforts are underway to address this factor by agencies such as WHO, CDC, the International Society of Travel Medicine, GeoSentinel and the travel industry.

Final Abstract Number: 07.004
Session: Hot Topics in Travel Medicine
Date: Friday, March 2, 2018
Time: 10:15-12:15
Room: La Pampa
Type: Invited Presentation

GeoSentinel - A surveillance network of returning travelers and migrants

D. Hamer
Boston University School of Public Health, Boston, Massachusetts, USA

Abstract text: GeoSentinel is an emerging infectious disease network created as a joint project between the International Society of Travel Medicine (ISTM) and the U.S. Centers for Disease Control and Prevention (CDC). GeoSentinel has several major objectives including conducting surveillance for emerging infectious diseases; rapidly sharing novel data on emerging infections with participating sites, internet information services (e.g. ProMED), and public health authorities (e.g. CDC, ECDC, Public Health Agency of Canada); and analyzing, presenting, and publishing surveillance results collaboratively with CDC, GeoSentinel sites, and GeoSentinel's two regional subnetworks, CanTravNet and EuroTravNet. The GeoSentinel surveillance network provides robust data that defines the spectrum of illness and its relation to place of exposure for significant health risks facing travelers and migrants. There are currently 70 GeoSentinel sites in 30 countries and 210 Affiliate Members with a presence on every continent except Antarctica. The GeoSentinel database now contains nearly 300,000 patient records; these include 54% post-travel visits, 31% seen during travel, and 15% migrants.

GeoSentinel has successfully identified new outbreaks over the last two decades including leptospirosis in participants in the Borneo Ecochallenge (2000), sarcocystis in travelers to Tionan Island, Malaysia (2010), an outbreak of dengue fever in Angola (2013), schistosomiasis in vacationers in Corsica (2014), and sentinel cases of Zika virus disease in Costa Rica (2016), Vietnam (2016), and several other destinations in Southeast Asia and the South Pacific in recent years. GeoSentinel has also characterized the risk for travelers to countries where major sporting events were planned such as the 2016 Summer Olympics in Brazil.

In summary, GeoSentinel is a vibrant global surveillance system that has made important contributions to the identification of disease outbreaks and trends in infectious disease epidemiology among travelers and migrants. In addition, GeoSentinel has the potential, through the development of a biobank of clinical samples, to collaborate with high level laboratories in academia and government to identify new pathogens responsible for respiratory, gastrointestinal, and systemic infections. GeoSentinel translates clinical and epidemiological data into meaningful evidence that is of critical importance to the containment of the global spread of infection.

Final Abstract Number: 12.001
Session: Plenary II: Global Pandemic Preparedness
Date: Friday, March 2, 2018
Time: 14:00-14:45
Room: Libertador ABC
Type: Invited Presentation

Evolutions in global epidemic and pandemic preparedness
G. Gamhewage
WHO, Geneva, Switzerland

Abstract text: The 21st century poses complex challenges for public health. Our planet is experiencing unprecedented levels of globalization, urbanization and mobility of its 7 billion inhabitants, many of whom live in poverty, conflict or are at risk of natural disasters and suffering from the effects of climate change . Infectious hazards, new and old, threaten the lives and well-being of billions of people across the globe. As the UN's specialized agency for health, WHO investigates around 300 disease outbreaks every year. But detecting and managing epidemic and pandemic-prone diseases is harder than ever.
During the last two decades, several high profile disease outbreaks have had a profound effect on public health's response to epidemics and pandemics. Today, in sharp contrast to the last century, there is an expectation that we detect outbreaks faster and manage them better. The response to health emergencies today is vastly different from previous eras where containment was a pre-dominant strategy. Today, for any outbreak, we need to systematically use the combination of modern epidemiology utilizing the power of technology; new and easy-to -use field-based rapid diagnostic tools; clinical care even in the harshest of conditions, vaccines and other medical counter-measures, rapidly developing them if they don't already exist; real-time training of front-line responders; and effective risk communication and community engagement. This new recognition that we need to marry the social aspects of epidemic and pandemic response with an ever stronger bio-medical response is changing the way disease outbreaks are being managed.
Just in the last decade, lessons learnt from MERsCoV in Saudi Arabia and South Korea; Ebola in West Africa; Zika in South America; Yellow Fever in Angola and the Democratic republic of Congo, several ongoing outbreaks of Cholera and Diphtheria in Bangladesh have created the momentum to re-think disease outbreak management to prevent epidemics or pandemics.
As the science of epidemic and pandemic diseases marches forward, and social science makes its presence increasingly felt, there is an effort to make the response operations more effective, particularly for large-scale epidemics. The introduction of Emergency Operations Centers (EOCs) in countries, and WHO's own reform establishing the use of an incident management system (IMS) have had an impact on how disease outbreaks are viewed and managed. As the current generation of public health experts and personnel, we will undoubtedly write the next chapter in how the epidemics and pandemics of the rest of the 21st century will be managed.

Final Abstract Number: 14.001
Session: HIV - Hot Topics
Date: Friday, March 2, 2018
Time: 15:15-16:45
Room: Libertador B
Type: Invited Presentation

Prospects for cure of HIV
P. Tebas
University of Pennsylvania, Philadelphia, USA

Abstract text: Antiretroviral medications have become less toxic and easier to take; however, we still cannot cure HIV infection. Patients still have to take medicines every day of their lives. Curing HIV represents a substantial challenge that may be very difficult to overcome. A “sterilizing cure” may not even be possible…, although remains the ultimate goal, the *Ithaca* of the long journey to a cure. A “functional cure” may be more attainable. These strategies, although not sterilizing, may allow the withdrawal of antiretroviral therapy without virological relapse and the close monitoring of participants to ensure that the “functionally cured” do not have other long term consequences that would have been prevented with the use of continuous antiretroviral therapy.
How will we get there? It will not be an easy path. First, we need to understand the nature of the HIV reservoir/s and the mechanism/s that maintain it. We must develop tests that accurately and reproducible measure the HIV reservoir/s that could potentially be used as surrogate endpoints for cure, pharmacological or immune strategy trials. We need to evaluate approaches that would make the body resistant to HIV either by using currently available gene therapy or gene editing technologies. In addition, we need to evaluate immunotherapies (humoral, cellular and innate or a combination of them) that will enhance the immune response of the body against HIV by either targeting the reservoir or the emerging virus from latency, including but not limited to therapeutic vaccines, checkpoint antagonists, interferons, TLR7 antagonists, broadly neutralizing antibodies, DARTs and BYTEs. Last, and not least, we need to engage the HIV infected and affected Community so we have a better understanding of their goals and needs and make them real partners in the pursuit of curing HIV.

Final Abstract Number: 14.002
Session: HIV - Hot Topics
Date: Friday, March 2, 2018
Time: 15:15-16:45
Room: Libertador B
Type: Invited Presentation

HIV+/HCV+ donor transplantation

C. Durand
Baltimore, USA

Abstract text: For those living with end-stage organ disease, transplantation provides a clear survival benefit. However, due to a critical shortage of donated organs, many individuals awaiting organ transplantation will die before every receiving an organ offer. As such, innovative strategies to expand the organ donor pool are needed. One such strategy is the use of organs from donors with chronic viral infections. More specifically, the use of organs from HIV-infected (HIV+) donors for HIV+ transplant candidates and the use of organs from hepatitis C virus-infected (HCV+) donors for HCV-uninfected transplant candidates is currently under investigation.
HIV-to-HIV kidney transplantation was pioneered in South Africa in 2010 with good results in a small cohort to date. Inspired by this experience, in the United States the HIV Organ Policy Equity (HOPE) Act was signed in 2013 and reversed the federal ban on HIV-to-HIV transplantation. Pursuant to the HOPE Act, HIV-to-HIV transplants have been allowed within research protocols since 2015. The first HIV-to-HIV kidney and liver transplants were performed at Johns Hopkins in March of 2016 and a national multicenter study of HIV-to-HIV kidney and liver transplantation is ongoing. This session will discuss the potential risks and benefits of HIV-to-HIV transplantation and transplant outcomes to date.
Since HIV remain an incurable illness even with effective antiretroviral therapy, the use of HIV+ donors for those without HIV is not being considered. In contrast, for chronic HCV infection, direct acting antivirals (DAAs) provide a definitive cure for HCV including for transplant recipients. Moreover, in the United States high-quality organs from HCV+ donors are currently underutilized and represent a potential public health resource. Two pilot studies have investigated the use of DAAs as pre-emptive or prophylactic treatment in combination with kidney transplantation from HCV+ donors for HCV- recipients. This session will also review the results of these trials and discuss the potential HCV+ to HCV- transplantation this has to expand organ options more broadly.

Final Abstract Number: 14.003
Session: HIV - Hot Topics
Date: Friday, March 2, 2018
Time: 15:15-16:45
Room: Libertador B
Type: Invited Presentation

Taking on the challenges of an ageing HIV-infected population

W. Powderly
Washington University in St. Louis, Saint Louis, USA

Abstract text: HIV-infected people now have life expectancies comparable to that of HIV-uninfected individuals. As the population living with HIV ages, increased rates of chronic illnesses such as osteoporosis, chronic kidney and liver disease, and in particular cardiovascular disease have been reported among people living with HIV infection. With the aging HIV-infected population, the burden of these comorbid illnesses continue to accrue over time and the risk appears to be greater than in the general population. The causal factors behind these increased rates remain unclear. HIV infection itself, the antiviral medications patients are taking, traditional risk factors that patients already have (*e.g.* smoking, substance abuse, family history), and patients' socioeconomic status have all been implicated, but the relative contribution of each to the over-all risk of developing chronic illnesses over time is less clear. Indeed, the relative role of these factors may differ for each chronic condition. This question becomes more important in aging patients with fully suppressed virus and good immune recovery as a result of the medications they are receiving. Understanding the pathogenesis of age-related diseases in HIV-infected patients may offer novel approaches to the mitigation of these challenges and ensure more successful aging among people living with HIV infection.

Final Abstract Number: 15.001
Session: Infectious Diseases in Vulnerable Populations
Date: Friday, March 2, 2018
Time: 15:15-16:45
Room: Libertador C
Type: Invited Presentation

HIV among indigenous populations: A regional perspective

M. E. Gutiérrez Pimentel
Panama, Panama

Abstract text: Inequity reaches its highest levels when it comes to health issues of indigenous people all around the world. Indigenous peoples face great social disadvantages and poor health compared to the general population. In most Latin American countries, indigenous people have lower life expectancy and higher morbidity and mortality rates than their non-Indigenous counterparts. They also have inadequate access to health services, health prevention and promotion programs. The aforementioned strategies, where they are available, are often designed without taking into account the required intercultural approach.
Regarding HIV among indigenous people, a massive demographic collapse has been foreshadowed by some authors, as it happened with the epidemics brought by the European conquerors. There are numerous socioeconomic and cultural contributing factors that fuel the dissemination of HIV between indigenous people. As a result of that complex interaction, the picture of HIV/AIDS on indigenous people of Latin America is featured by late presentation, many opportunistic infections, affecting very young persons, low adherence to treatment and preoccupying rates of loss of follow up. As well as the international strategies for universal access to treatment, there is urgent need to address the socioeconomic and cultural determinants that make indigenous communities so vulnerable to HIV and other infections. Those efforts should consider inclusion and empowerment of indigenous people as a way to reduce HIV disparities and its fatal impact among them.

Final Abstract Number: 15.002
Session: Infectious Diseases in Vulnerable Populations
Date: Friday, March 2, 2018
Time: 15:15-16:45
Room: Libertador C
Type: Invited Presentation

Meningitis & HIV in Africa
R. Heyderman
University College London, London, United Kingdom

Abstract text: Meningitis in adults is a common reason for hospital admission in sub-Saharan Africa and is associated with a HIV seroprevelence exceeding 80%. Despite the rapid scale-up of antiretroviral therapy (ART), cryptococcal meningitis, bacterial meningitis and tuberculous meningitis remain prominent causes of death and disability in these vulnerable populations. The successes and failures of treatment and adjunctive therapy trials in cryptococcal and bacterial meningitis will be reviewed. The hypothesis that HIV-mediated inflammatory disregulation leading to inadequate microbial control and prominent irreversible tissue destruction occurs early in the evolution of the disease will be explored. Opportunities to prevent meningitis in HIV-affected adult populations through vaccination, ART intensification and antimicrobial prophylaxis will be discussed.

Final Abstract Number: 15.003
Session: Infectious Diseases in Vulnerable Populations
Date: Friday, March 2, 2018
Time: 15:15-16:45
Room: Libertador C
Type: Invited Presentation

Emgering infectious diseases in the Americas

T. Mancero Bucheli
PAHO, Buenos Aires, Argentina

No abstract received!

Final Abstract Number: 17.001
Session: Different Models of Antibiotic Stewardship in Low- and Middle-Income Countries
Date: Friday, March 2, 2018
Time: 15:15-16:45
Room: Retiro BC
Type: Invited Presentation

The role of the 'A' team in the hospital near you

G. Levy Hara
Buenos Aires, Argentina

Abstract text: It is very probably that our hospital has some degree of constrained human and material resources. Implementing an antimicrobial stewardship program (ASP) in these settings is a challenge. Leadership commitment by hospital authorities is important to ensure allocation of the necessary resources to support ASPs. Establishing a multi-disciplinary antimicrobial stewardship team (AST) with full administrative support is essential .Its constitution should be adapted to currently available human resources in every each facility, and all parties´ leaders might be creative despite many barriers that will necessary appear during the implementation process.
The AST is usually composed by a *core group* (physicians, pharmacist , microbiologist) and *supporter members*. The coordinator might be a doctor (e.g, ID specialist or one ¨natural leader¨, respected and with knowledge in the prudent management of antimicrobials) or a clinical pharmacist. The latter has many tasks in the ASP (e.g, review requests of antimicrobials, provide feed-back during ward rounds, detect unnecessary prescriptions). Microbiologists should ideally have some training in clinical microbiology. Doctors from key units (e.g, UCI, Internal Medicine, Surgery) would facilitate the dissemination and adherence to guidelines, generate discussions on antimicrobial prescriptions in his unit and collaborate in the implementation of AMS strategies. Main supporter members could be representatives of the IPC team, nurses, patient safety and information technology.
The AST should design which strategies could better fit, foreseeing the program as a step-by-step dynamic process. For example, in settings with a small AST and without previous experiences in ASP, it would be necessary to implement a pre-prescription authorization strategy for some antimicrobials, accompanying it with targeted education initiatives. Later, once the "*stewardship spirit"* is more disseminated along the hospital, pre-authorization will probably be not necessary, and main strategy could progressively turn to post-prescription audit and feed-back. Education initiatives in multiple forms (e.g, face to face, classes and clinical case discussions) and communication of progresses are also essential. Monitoring the ASP might give an idea of what needs to be emphasized to improve AMS in our hospital.

Final Abstract Number: 17.002
Session: Different Models of Antibiotic Stewardship in Low- and Middle-Income Countries
Date: Friday, March 2, 2018
Time: 15:15-16:45
Room: Retiro BC
Type: Invited Presentation

Non-specialist pharmacists as stewardship champions

D. van den Bergh
Netcare , Johannesburg, South Africa

Abstract text: While experts agree that antibiotic stewardship programmes should ideally be led by a multidisciplinary professional team with specialist training in antibiotics and infectious diseases, resources to constitute these teams, especially in low-and middle-income countries(LMICs) remain a challenge[1]. The use of non-specialist pharmacist as stewardship champions has shown important progress and impact across multiple hospitals in 3 South Africa studies and may offer potential solutions for other LMICs. The first study, aimed to reduce consumption of antibiotics across 47 hospitals, focused on prospective audit of process measures (prolonged duration, multiple antibiotics, and redundant antibiotic coverage) with pharmacist's interventions[2]. Overall antibiotic consumption reduced by 18,1% over 104 weeks using standardised measurement and feedback. The second intervention across 33 hospitals improved compliance to timeliness of antibiotic administration and built important collaboration with nursing colleagues[3]. In the third study, a pharmacist-led strategy involving change management and improvement principles across 34 hospitals reviewed perioperative antibiotic prophylaxis (PAP) guideline compliance and a post-implementation phase of audit, intervention and monthly feedback, facilitated improvements in compliance[4]. There was significant improvement in composite compliance with all process measures from 66.8% to 83.3% representing a 24.7% increase and the SSI rate decreased by 19.7%. Additional studies across public and private sector hospitals are underway to further test this strategy as a model for progressing antibiotic stewardship programmes in lower resource settings.

Final Abstract Number: 17.003
Session: Different Models of Antibiotic Stewardship in Low- and Middle-Income Countries
Date: Friday, March 2, 2018
Time: 15:15-16:45
Room: Retiro BC
Type: Invited Presentation

Nursing leadership in AMS interventions: Lessons learnt worldwide

E. Castro Sánchez
Imperial College London, London, United Kingdom

Abstract text: Among the measures proposed to combat antimicrobial resistance, governments and healthcare organisations have been encouraged to increase funding and participation of health care workers (HCW) in interventions of optimal use of antibiotic. However, by 2035 there will be an estimated shortage of just under 13 million HCWs worldwide.
However, a certain professional group remains under represented and not active in stewardship activities. Nurses are the largest group of health professionals around the world. For example, there were 377,000 nurses in the UK for the 150,000 doctors. Equally, there were just under 1.5million nurses in India in 2011. The impact of engaging and activating just 1% of those professionals could be dramatic for stewardship initiatives. Such increased participation of nurses has been gradually advocated, but still needs to be allowed and encouraged, including at the point of decision-making.
Most examples of advocacy for nurse participation in stewardship have focused on clinical, bedside roles. However, it would be beneficial to consider other aspects such as influencing of other clinicians and patients, leadership of clinical and public health campaigns including vaccination, education of HCWs and citizens, or direction of infection prevention and control initiatives. Additionally, there may be much to learn from novel nurse-focused initiatives developed and conducted in low- and middle-income countries, particularly in clinical areas such as tuberculosis and HIV/Aids, where issues of treatment adherence, increased resistance and complexity are similar to antimicrobial stewardship.
For these and other initiatives to be successful, nurses would have to address existing barriers including foundational (that is, whether nurses think that they should participate in stewardship), 'branding' (where nurses may not know much about stewardship yet may carry out many AMS-related tasks), educational (including limited AMS-related education in undergraduate nursing courses), and leadership (a lack of executive and directive nurses in local, national and international settings aware of the impact of commissioning and service delivery planning to influence AMS interventions).

Final Abstract Number: 18.001
Session: Gorgas Lectures and Case Discussions in Clinical Tropical Medicine I
Date: Friday, March 2, 2018
Time: 15:15-16:45
Room: La Pampa
Type: Invited Presentation

Typhoid fever: A current problem
E. Gotuzzo
Universidad Peruana Cayetano Heredia, Lima, Peru

Abstract text: The Salmonellosis basically more than 2,000 species are zoonotic infections, however there are 2 salmonellas whose only reservoir is the human being: *S. typhi* and *paratyphi.* Internationally, typhoid fever is not a reportable disease in many countries. The estimated number of cases without considering China is 5-20 million annually, mainly in South East Asia, India, China, and Africa, in countries with poor sanitation. .
Latin America, which was one of the major sources of typhoid fever, after the cholera epidemic, (1991) was significantly reduced the number of cases in our countries.
This infection, fecal oral contamination, produces fever, headache, malaise and early gastrointestinal involvement. The frequent complications of digestive bleeding, perforation of the ileum with peritonitis and meningo encephalic compromise (frequent in Asia) are accompanied by an estimated mortality of 1-3%, mainly in children and elderly as well as in pregnant women. The isolation of salmonella in blood and feces is reduced by the previous use of antibiotics and it is used to make bili culture and bone marrow culture.
The treatment with chloramphenicol and/or ampicillin, allowed a high cure rate, but did not prevent relapse or transient or chronic carrier states. The emergence of resistance and epidemic outbreaks forced the use of quinolones such as cirpfloxacin, which has been for years, the drug of choice, both in children and adults. Recent studies show increasing resistance to nalidixic acid in India and Southeast Asia and is associated with a high failure rate with fluorquinolones. The appearance of multiresistant strains have forced the incorporation of azithromycin as the drug of choice for this situation.
Oral and parenteral vaccines have been useful to reduce morbidity and mortality for the next 2-5 years after vaccination, however it does not protect for salmonellosis *paratyphi A* today causes more than 50% of cases in China and part of the South East Asia. A new vaccine: Typhoid conjugate vaccines (TCVs) are innovative products that have longer-lasting immunity than older vaccines, Vaccine has been prequalified by WHOin 2017.

Final Abstract Number: 19.001
Session: New Outbreaks of Cutaneous Leishmaniasis and Management
Date: Friday, March 2, 2018
Time: 17:00-18:00
Room: Libertador A
Type: Invited Presentation

Cutaneous Leishmaniasis outbreaks and management

O. Salomon
National Institute of Tropical Medicine, Puerto Iguazu, Argentina

Abstract text: 'Cutaneous Leishmaniasis' (CL) term includes a broad range of clinical expressions, etiological agents of the genus *Leishmania*, and environmental and epidemiological scenarios, distributed mainly in the inter-tropical belt around the world. The outbreak events involve a couple of unexpected cases to more than 60,000 cases by year. There are 'perfect waves' or eco-epidemiological momenta of interwoven socio-economic, political and cultural, biological and physical causes, and also inter-linked consequences. However, we can figure out a typology of the outbreaks to think on the better strategies to control them, discriminating levels because in the large-long duration ones, climate change, economic trends or immune compromise by malnutrition, require actually structural changes. On the other hand, in space-time scales from foci up to individual exposure two mains processes could be discriminated: the human moving toward the primarily zoonotic cycle or the zoonotic cycle moving toward the humans. In the former case the contact could be: 1) Transient: soldiers, fleeing populations, illegal traffic, forest-related works as deforestation; 2) temporary: soldier, refugees and workers camps as gold miners settled on potential foci; 3) permanent: immigration of susceptible people, peripheral new neighborhoods (deforestation-peaks) or settlements in 'low rent' lands (unplanned urbanization-borders-new endemic areas). The zoonotic cycle toward human outbreaks, even if afterward the cycle become anthroponotic, are usually related to environment modification, vector-reservoir dispersion or exceptional population growth, and frequency of extreme climatic events. Many control measures were assayed for these scenarios as active surveillance, physical and chemical blocking or 'barrier' interventions, reservoir elimination directly or by food deprivation, although there are scarce rigorous impact evaluations. However, the better strategy to control outbreaks is to avoid them wherever possible, each past outbreak is a lesson to learn. Development, urbanization, military and law-enforcement projects should include CL epidemiological risk assessment with forecasting statistical modeling in time and space; the corporate and the state accountability should be explicitly stated and evaluated 'a priori' in terms of cost-community acceptable risk, and if the outbreak happens the system besides treatment, personal protection, and vector-reservoir control should also think in the psychological, social and economic consequences for individuals, families and collectives (refugees).

Final Abstract Number: 19.002
Session: New Outbreaks of Cutaneous Leishmaniasis and Management
Date: Friday, March 2, 2018
Time: 17:00-18:00
Room: Libertador A
Type: Invited Presentation

Cutaneous Leishmaniasis: Treatment needs and combination therapies
B. Arana
Drugs for Neglected Diseases Initiative, Geneva, Switzerland

Abstract text: There is an increasingly number of cases of cutaneous leishmaniosis (CL) reported worldwide. The ideal treatment for CL should be based on the clinical presentation: local therapies for subjects with small/ few lesions; systemic oral drugs for subjects with numerous or large lesions; whilst subjects with leishmaniasis recidivans, diffuse CL or PKDL should be benefit from using an anti-leishmania drug in combination with an immune response modifier to accelerate and enhance a Th-1 type immune response.
Miltefosine is the only oral treatment currently available for treatment of leishmaniasis. In 2014, FDA approved its use for infections caused by *L. braziliensis*, *L. panamensis* and *L. guyanensis*. Despite its limitations due to teratogenicity and gastro-intestinal side effects, miltefosine is a better option than antimonials which are toxic, difficult to administer and its efficacy in many regions is doubtful. Local thermotherapy has also been tested widely. In a meta-analysis of controlled clinical trials comparing thermotherapy with systemic antimonials it was found that the overall efficacy of thermotherapy was 73.9% (95% CI 70.0 - 77.8%) whereas that of systemic antimonials was 72.7% (95% CI 68.7 – 76.6%).
Although DNDi and partners have identified several compounds showing activity against *Leishmania* parasites causing CL, completing the clinical development of at least one of them will take 8-10 years, so the currently available treatments will probably represent the therapeutic arsenal for the coming decade. Hence, DNDi is proposing to explore opportunities to better use the existing approved treatments in combinations, as a short-term solution.
The combined use of thermotherapy (one application, 50^0C for 30 mins) + miltefosine (2.5 mg/kg/day for 21 days) seem to be the best option. The advantages offered by this combination are that a) both approaches are currently recommended for use individually, and there is good information regarding efficacy and safety when used alone; b) combining a topical and a systemic treatment is expected to have an additive effect, since systemic treatment would eliminate circulating parasites or those located in the periphery of the lesion that topical treatment fails to remove; c) it offers the opportunity to increase the current cure rate compared to either treatment used alone and; d) it will reduce the duration and severity of the adverse events associated with 28 days of treatment with miltefosine alone.

Final Abstract Number: 21.001
Session: Hot Topics in Infection and Prevention Control
Date: Friday, March 2, 2018
Time: 17:00-18:00
Room: Libertador C
Type: Invited Presentation

The World Health Organization (WHO) clean care is safer care promotion campaign, 2005-2018

D. Pittet
Director, WHO Program on Hand Hygiene and Safety, Geneva, Switzerland

Abstract text: The World Health Organization (WHO) *Clean Care is Safer Care* global programme is based around a change model. It fosters partnerships and coordinates activities as set out in its programme plan. By May 2016, more than 140 of the 194 United Nations' member states had pledged their support to implement actions to reduce healthcare-associated infections, corresponding to 95% coverage of the world population.
The finalized WHO Guideline on Hand Hygiene in Healthcare was launched in 2009 alongside a field-tested and validated multimodal improvement strategy. The strategy comprises five critical components: 1) system change; 2) healthcare workers' training and education; 3) evaluation and performance feedback; 4) reminders in the workplace; and 5) promotion of an institutional safety climate.
WHO has over this time coordinated more than 50 national campaigns and importantly launched the global annual healthcare worker call to action; the SAVE LIVES: Clean Your Hands campaign to maintain a profile on hand hygiene action at the point of care.
Reasons for the success of *Clean Care is Safer Care* will be reviewed, including those possibly associated with a positive influence on infection rates and patient safety.

Final Abstract Number: 21.002
Session: Hot Topics in Infection and Prevention Control
Date: Friday, March 2, 2018
Time: 17:00-18:00
Room: Libertador C
Type: Invited Presentation

Hand hygiene promotion in Argentina

E. Andión
CEDECEM, Buenos Aires, Argentina

No abstract received!

Final Abstract Number: 21.003
Session: Hot Topics in Infection and Prevention Control
Date: Friday, March 2, 2018
Time: 17:00-18:00
Room: Libertador C
Type: Invited Presentation

The train-the-trainers concept applied in Brazil and Mexico

H. G. Marquez Villarreal
Guadalajara, Jalisco, Mexico

No abstract received!

Final Abstract Number: 24.001
Session: Clinical Applications of Whole Genome Sequencing
Date: Friday, March 2, 2018
Time: 17:00-18:00
Room: La Pampa
Type: Invited Presentation

Whole genome sequencing for diagnosing infectious diseases

P. Brown
University of the West Indies, Kingston, Jamaica

Abstract text: Given the complex nature of diagnostic practices for infectious diseases, the one unifying characteristic of the agents investigated is their possession of a genome. While many molecular diagnostic tests investigate parts of the genome, whole-genome sequencing (WGS) has emerged as a cost-effective and convenient approach for answering the varied microbiological questions that arise. In that regard, four essential tasks are addressed: species identification, phenotypic characterization, e.g., antimicrobial resistance and virulence, evolutionary traits and pathogen tracking.
Some of the benefits already available include, in addition to the ability to fully characterize prospective and retrospective isolates, the ability to be applied directly to clinical samples for simultaneous identification and predicting antimicrobial susceptibilities (even in culture-negative cases); identification in polymicrobial samples; generating regional phylogenomic sublineages; correlation of genomic features with strains of clinical importance; tracking of multidrug resistant organisms in hospitals and communities. These benefits, while largely seen in reports from North America and Europe, are also being observed in Latin America and the Caribbean. Further, WGS allows for estimation of mutation rates among isolates, as well as assessment of the rates and breadth of horizontal gene flow within and between species, the evolution of new virulence traits, and the role of host genetics in host-pathogen interactions, all with the view to develop novel therapeutic interventions.
The main directions of WGS applications include diagnosis and control of local and regional infectious diseases; detection of multidrug resistance (MDR) and virulence characteristics; surveillance of pathogen evolution and transmission dynamics; development of new (portable) diagnostic tests and assays for use in clinics and outpatient facilities; and discovery of novel antimicrobial drugs and therapeutics and assessment of their prevention and control. Given that pathogens occur in complex microbial communities, further elaborations to explore the pathobiome using metagenomics and high-throughput sequencing will assist with the understanding of the forces supporting population structure, including pathogen plasticity.

Final Abstract Number: 24.002
Session: Clinical Applications of Whole Genome Sequencing
Date: Friday, March 2, 2018
Time: 17:00-18:00
Room: La Pampa
Type: Invited Presentation

Genome sequencing to contain viral epidemics
M. Kraemer
Harvard University, Cambridge, USA

Abstract text: Despite many successes in the control of human infectious diseases they continue to pose a considerable risk to human health. Today, the rapid spatial spread of pathogens such as Ebola virus in West Africa, Yellow fever in Angola, and Zika in the Americas is unprecedented in their speed and magnitude. The main drivers are rapidly changing ecological and demographic processes. Traditionally, epidemiologists relied on passive disease case reporting and contact tracing data to inform and direct public health responses. However, advances in high-resolution genomic epidemiology enabled the reconstruction of virus spread and the detection and quantification of importation events that lead to local outbreaks and persistence in human populations. With the right tools, such information can aid epidemiological inference and a unifying formal integration of genetics into epidemiology would ultimately help contain disease faster.

Final Abstract Number: 25.001
Session: Plenary III: Advances and Challenges in the Treatment of Chagas Disease - a Global Perspective
Date: Saturday, March 3, 2018
Time: 09:00-09:45
Room: Libertador ABC
Type: Invited Presentation

Advances and challenges in the treatment of Chagas disease - a global perspective

S. Sosa-Estani
Instituto Nacional de Parasitologia, Buenos Aires, Argentina

Abstract text: Chagas disease, caused by *Trypanosoma cruzi*, is a global problem with an increasing impact on public health. Diagnosis and treatment of infected patients is considered to be key to its control. Current tools for primary and secondary prevention are able to interrupt transmission and control Chagas disease.

The use of benznidazole and nifurtimox as anti-parasitic treatments for Chagas disease is indicated in the following situations: a) All acute phase patients, including congenital transmission; b) Following reactivation of infection by immune suppression; c) Patients up to 18 years of age with chronic disease; and d) Women of childbearing age with *T. cruzi* infection (with contraception during treatment). There is a relative consensus that drug treatment should be offered to adults aged 19–50 years without advanced heart disease, and is optional for those older than 50.

Progress has been bolstered by the generation of clinical evidence on the safety and efficacy of new anti-parasitic treatment regimens from several clinical trials assessing new chemical entities. The BENDITA study (DNDi-Bolivia) is assessing new regimens of benznidazole, as a monotherapy and in combination with fosravuconazole. A trial to assess short regimens of fexinidazole is underway (DNDi-Spain). The MULTIBENZ trial (Berenice project-FP7-EU-Spain-Argentina-Brazil-Colombia); the BENZNIDAZOLE INTERMITTENT trial (HGAEV-INP-FMS-Argentina) and the CHICAMOCHA Trial (COLCIENCIAS-Colombia-Benznidazole-vs-Nifurtimox) are evaluating the efficacy and safety of different regimens of current trypanocides. These trials are all in the chronic phase of infection in adult patients. The CHICO trial (Multicenter trial-Bayer), is evaluating the safety and efficacy of a new paediatric formulation of nifurtimox.

Ongoing clinical studies from DNDi, the NHEPACHA Network, and other groups are identifying and validating potential biological markers of therapeutic response in Chagas disease patients to support clinical development.

Continued progress on these fronts will help ensure that diagnosis and treatment finally reach the over 99% of people with Chagas disease who have thus far been neglected.

In order to reduce the burden of Chagas disease and to eliminate it as a public health issue, it is essential to incorporate diagnosis and treatment into public health strategy, and will be useful for primary, secondary, and tertiary prevention.

Final Abstract Number: 27.001
Session: Diagnosis and Management of Difficult to Treat Fungal Infections
Date: Saturday, March 3, 2018
Time: 10:15-12:15
Room: Libertador B
Type: Invited Presentation

Molecular tools for the detection of azole antifungal drug resistant phenotypes in aspergillus species

G. García-Effron
Laboratorio de Micología y Diagnóstico Molecular. Cátedra de Parasitología y Micología. Facultad de Bioquímica y Ciencias Biológicas. Universidad Nacional del Litoral. Santa Fe. Argentina., Santa Fe, Argentina

Abstract text: Azole drugs are the first-line treatment option for invasive aspergillosis. Over the past few years, azole secondary resistance incidence in *Aspergillus fumigatus* strains is increasing. Similarly, the isolation of naturally azole resistant cryptic species of *Aspergillus* section Fumigati is starting to emerge. These issues became an important clinical concern considering that invasive aspergillosis treatment due to azole-susceptible strains are already difficult. Recently, an expert panel concluded that antifungal susceptibility testing of isolates should be performed if azole treatment is indicated. However, in vitro susceptibility testing by using commercially available or standard procedures takes at least 48 hours. Azole resistance in *Aspergillus fumigatus* is mainly linked with amino acid substitutions at Cyp51Ap or a combination of mutations and overexpression of the CYP51A gene. There are at least 15 resistance alleles described (seven of them molecularly confirmed by gene replacements and/or knockouts experiments) but few are prevalent. Whether or not the mutations at *CYP51A* are confirmed or prevalent it is clear that the nature and position of the substitution influence the pattern of azole resistance. For example, it is now clear that itraconazole/posaconazole resistance and cross-azole resistance are linked with substitutions at Cyp51A glycine 54 (G54) and subtition at leucine 98 combined with a higher *CYP51A* expression due to a tandem repetition of a 34-pb sequence in the *CYP51A* gene promoter, respectively. To circumvent the delays of the available susceptibility testing procedures and taking advantage of the correlation between *CYP51A* mutations and *A. fumigatus* susceptibility patterns, several molecular tools for the detection of azole resistance were developed. The aims of this presentation are: (i) to review the published diagnostic tools describing its advantages and disadvantages, (ii) to discuss the usefulness of these tools as a non-culture based diagnostic methods and (iii) to show our experience in this subject.

Final Abstract Number: 27.002
Session: Diagnosis and Management of Difficult to Treat Fungal Infections
Date: Saturday, March 3, 2018
Time: 10:15-12:15
Room: Libertador B
Type: Invited Presentation

C. auris: What do we know about the emergence of this multidrug resistant yeast?
R. Vitale
Hospital Ramos Mejia, Buenos Aires, Buenos Aires, Argentina

Abstract text: *Candida auris* has been reported as emerging yeast with variable antifungal susceptibility profile and development of antifungal resistance. Infections are associated with a variety of invasive fungal diseases observed in critically ill patients such those with hematological malignances, in intensive care units, with catheter devices, those undergoing invasive procedures. Genetic analysis showed the emergence of separate clades in different geographical regions. *C auris* was reported in Japan, India, South Korea, Pakistan, Oman, South Africa, USA, United Kingdom, Norway, Germany, Spain, Venezuela, Colombia and Brazil. The identification is not easy with conventional diagnostic tools and missidentification was reported since *C auris* is closely related with *C. haemulonii*, *C lusitaniae* and others. However it is important to have a suspition if an isolation of a yeast that forms pink to beige colonies in chromogenic agar, growing at 42 C but not in the presence of cycloheximede, microscopic oval to elongated yeast without pseudohyphe, is encountored. There is not a breakpoint for *C auris* and reduce susceptibility were reported for fluconazole, voriconazole, itraconazole, isavuconazole, amphotercin B. Echinocandins are proposed to use, although due their more widespread use, some isolates were reported with low susceptibility. In vitro the new 1-3 B glucan inhibitor SCY-078 has been demonstrated potent activity. Suggested therapy include echinocandins, combination of amphotericin B plus flucytosin, micafungin plus voriconazole, depending the site of infection. Thus, it is important to have the knowledge about the emerging of this yeast that becomes a potential dominant opportunistic pathogen in immunocompromised hosts.

Final Abstract Number: 27.003
Session: Diagnosis and Management of Difficult to Treat Fungal Infections
Date: Saturday, March 3, 2018
Time: 10:15-12:15
Room: Libertador B
Type: Invited Presentation

Epidemiology of Fusarium, a significant emerging group of human opportunistic infections
M. Nucci
, Brazil

Abstract text: Fusarium species are plant pathogens widely present in nature, which cause disease in immunocompetent and immunocompromised hosts. Onychomycosis and keratitis are the most frequent diseases in immunocompetent individuals, whereas immunocompromised patients typically develop a disseminated disease with positive blood cultures, metastatic skin lesions and a frequently fatal outcome. In this presentation we will show some epidemiologic data that suggest that the incidence of fusariosis has increased in South America. We will speculate about the origin of this increase in the incidence, and the clinical implications of these observations. We will also discuss briefly data of molecular typing of Fusarium isolates that may have clinical and epidemiologic relevance.

Final Abstract Number: 27.004
Session: Diagnosis and Management of Difficult to Treat Fungal Infections
Date: Saturday, March 3, 2018
Time: 10:15-12:15
Room: Libertador B
Type: Invited Presentation

Current trends and future perspectives in infections due to emerging yeasts and molds difficult to treat
J. Afeltra
Hospital J.M Ramos Mejía, Buenos Aires, Argentina

Abstract text: A immunosuppressed patients has resulted in increasingly frequent diagnoses of invasive fungal infections, including unusual yeasts. The incidence of non-albicans species of *Candida* is increasing compared with that of *Candida albicans*. *Trichosporon* species are common cause of fungaemia in oncohaematological patients with poor prognosis. *Rhodotorula* cause catheter-related fungaemia, sepsis, and invasive disease in severely immunosuppressed patients. Other uncommon yeasts that can cause invasive disease include *Geotrichum, Hansenula, Malassezia*, and *Saccharomyces*. Diagnosis can be challenging and relies heavily on traditional cultures of blood and other sterile sites. Infections caused by filamentous fungi represent a major burden in inmmonocompromised patients. Invasive aspergillosis is emerging in non-neutropenic individuals with predisposing conditions. Diagnosis is challenging because the signs and symptoms are non-specific, and initiation of additional diagnostic examinations is often delayed because clinical suspicion is low. Isolation of an *Aspergillus* species from the respiratory tract in critically ill patients, and tests such as serum galactomannan, bronchoalveolar lavage 1-3-β-d-glucan and specific PCR should be interpreted with caution. Mucormycosis is a rare, but increasingly prevalent disease that occurs mainly in patients with uncontrolled diabetes mellitus, immunocompromised individuals or previously healthy patients with open wounds contaminated with Mucorales. Control of underlying predisposing conditions, rapid surgical resection and administration of liposomal amphotericin B are the main therapeutic actions. Although rare fungi are emerging as opportunistic human pathogens, diagnosis remains challenging and treatment suboptimal.

Final Abstract Number: 28.001
Session: New World Arenaviruses
Date: Saturday, March 3, 2018
Time: 10:15-12:15
Room: Libertador C
Type: Invited Presentation

Epidemiology and virology of New World Arenaviruses
A. Sinchi
Pergamino, Argentina

Abstract text: Arenaviruses are members of the family Arenaviridae that consists of two different genera (Mammarenavirus and Reptarenavirus). They are enveloped viruses that carry single-stranded, bi-segmented RNA genomes. The mammarenaviruses are divided into two groups: Old World (OW) and New World (NW), and circulate mostly in rodents. Both groups contain Hemorrhagic Fever causing pathogens. The pathogenic OW mammarenaviruses include Lassa (LASV), Lymphocytic Choriomeningitis (LCMV) and Lujo (LUJV) viruses. The NW include Junin (JUNV), Machupo (MACV), Chapare virus (CHPV), Guanarito (GTOV), and Sabiá (SBAV) viruses, which cause Argentine (AHF), Bolivian, Venezuelan, and Brazilian hemorrhagic fever, respectively. All cause severe human disease. AHF is unique among these viral hemorrhagic fevers because it is the only arenavirus that has an effective treatment and a vaccine against this disease. Infusion of immune plasma derived from survivors (passive immunity) is a well-established means of treating acute human infection; when provided within 8 days of illness, it decreases the case fatality rate from 15%–30% to less than 1%. Candid#1 is a live-attenuated Junin virus vaccine with a proved efficacy of 95.5 %.
Since the implementation of vaccination with the Candid #1 vaccine, a significant reduction in incidence was achieved and risk patterns were modified. Classically, the disease affected mostly men who worked in rural areas. Currently there has been an increase in the percentage of women among confirmed cases and the proportion of patients among rural workers has decreased. The number of confirmed cases has increased in people who develop other economic activities and residents in urban areas. There has also been identifying three transmission scenarios: classic, emergent-reemergent, and traveler. All these changes must be taken into account both for the diagnostic suspicion and for the design of health education and vaccination strategies.

Final Abstract Number: 28.002
Session: New World Arenaviruses
Date: Saturday, March 3, 2018
Time: 10:15-12:15
Room: Libertador C
Type: Invited Presentation

Mechanisms of Candid #1 vaccine attenuation
S. Paessler
University of Texas Medical Branch, Galveston, USA

Abstract text: Junin virus (JUNV) is the etiological agent of Argentine hemorrhagic fever (AHF), a severe self-limiting acute disease with an at-risk population of over 3 million individuals in the pampas region of Argentina. While treatment options for AHF are limited, an effective live attenuated vaccine strain of JUNV (Candid #1) was developed through serial passaging of the parental XJ strain in mouse brain tissue and is currently administered to at-risk individuals with a high degree of success. We have previously demonstrated that the GPC of Candid #1 is the primary determinant of the attenuation of Candid #1 in the guinea pig model of AHF. We have shown that the GPC of the Candid #1 strain expresses higher amounts of pre-cleaved G1/G2 and less cleaved G2 than the virulent wild-type GPC in cell culture. The accumulation of pre-cleavage G1/G2 is most directly associated with an amino acid substitution in G1 (T168A), which eliminates an N-linked glycosylation motif that is utilized by the protein. We show that the absence of the glycosylation motif results in detectable accumulation of GPC in the ER and the eventual aggregation of improperly processed GPC through the formation of inter-chain disulfide bridges, ultimately leading to a decrease in surface expression of the GPC compared to wild-type protein. In support of these findings, the ER stress-associated marker BiP is upregulated, and the ER chaperone PDI increases significantly over time in the presence of GPC expressing the T168A substitution. An increase in LAMP-1 and a decrease in total GPC occurs in response, indicating that infected cells are utilizing autophagy to resolve a folding issue that exists in GPC expressing the T168A substitution. Cleaved caspase 3, caspase 7, and PARP become detectable after 36 hours post-infection, indicating that the ER is incapable of resolving a perceived folding issue caused by the T168A substitution. These ER stress-related responses do not occur during infection with the wild-type GPC, suggesting that the decreased surface expression and degradation of Candid #1 GPC could play a significant role in the attenuation of Candid #1.

Final Abstract Number: 28.003
Session: New World Arenaviruses
Date: Saturday, March 3, 2018
Time: 10:15-12:15
Room: Libertador C
Type: Invited Presentation

Clinical management of Arenavirus infections
D. G. Bausch
Naval Medical Research Unit-6, Lima Peru, Callao, Peru

Abstract text: Although there are certainly differences between New and Old World arenavirus infections, it appears likely that there are is enough overlap between these diseases so that findings from one group shed valuable light on the other. The relatively low incidence of many arenavirus infections—especially in the New World where some are recognized only in outbreak form—as well as historically undeveloped research infrastructure and civil unrest in many areas where arenavirus are endemic has impeded clinical study. The natural history of disease and underlying pathophysiology remain poorly understood. Nevertheless, there is reasonable evidence of efficacy of the guanosine analogue ribavirin and convalescent immune plasma for these viruses, although further study employing more modern techniques and standards is certainly warranted. In addition, there are concerns regarding availability, toxicity, and ease of administration of ribavirin and immune plasma. New approaches are needed. The end of some of the civil conflicts in endemic areas for Lassa fever in West Africa, followed by the large 2013-16 outbreak of Ebola virus disease in the region that served to refocus attention on viral hemorrhagic fevers, especially Lassa, has renewed interest and, to a degree, resources, for more in-depth study of Arenaviruses, including efficacy of new drugs. Interest is particularly high in the RNA polymerase inhibitor favipiravir, for which promising pre-clinical data are available. Establishing newer more efficacious and safer treatments of Arenavirus infection will require continued investment in both pre-clinical and clinical study, including development of the required infrastructure for clinical trials in West Africa. It will be important to conduct more systematic clinical observation of patients with arenavirus infection to better understand the pathogenesis of disease and identify logical points of intervention. Lastly, while difficult to quantify, it is likely that much could be gained in terms of reducing mortality simply by enhancing infrastructure required to deliver modern quality supportive care in the endemic areas for arenaviruses, which include many of the world's poorest regions.

Final Abstract Number: 30.001
Session: New Approaches for the Diagnosis of Invasive Infections
Date: Saturday, March 3, 2018
Time: 10:15-12:15
Room: Retiro BC
Type: Invited Presentation

Etiological diagnosis of bloodstream infection: Direct molecular diagnosis from blood
M. van der Brand
Amsterdam, Netherlands

Abstract text: Sepsis is one of the most common severe infections and is associated with high morbidity and mortality. Several studies have underlined the importance of rapid initiation of adequate antimicrobial therapy. This is hampered by growing antimicrobial resistance and the long turnaround time of blood culture. Rapid and accurate diagnosis of the causing pathogen directly in blood together with its associated resistance genes would be highly valuable to improve survival. In this presentation an overview of important aspects of the direct detection of pathogens in blood including blood volume, method of isolation and detection, turnaround time and workflow is provided. Currently available commercial assays (SeptiFast, IRIDICA, T2 Sepsis Solution) are discussed as well as assays still in development. In addition, attention is given to specific patient populations as neonates, ICU patients and neutropenic patients. An important additional benefit of molecular detection could be the quantification of bacterial DNA. This bacterial DNA load can be used as a marker of severity of infection and for monitoring of treatment and will be illustrated with several examples. Despite the large number of studies investigating the molecular diagnosis of sepsis directly in blood, it is still not part of routine practice in many laboratories. Factors that are hampering its introduction in clinical practice (costs, suboptimal sensitivity, contamination and implementation) are presented in the last part of the presentation which includes future prospects.

Final Abstract Number: 30.002
Session: New Approaches for the Diagnosis of Invasive Infections
Date: Saturday, March 3, 2018
Time: 10:15-12:15
Room: Retiro BC
Type: Invited Presentation

Blood culture pellets coupled to MALDI TOF & gram staining to improve fast and accurate microbial diagnosis of bloodstream infections

O. Opota
Lausanne, Switzerland

Abstract text: Bloodstream infection is a life-threatening disease, for which early detection of the incriminated microorganisms and accurate determination of their antimicrobial susceptibility is paramount to reduce both mortality and morbidity. Blood culture remains among the best approach to identify the incriminating microorganisms and to further perform an antimicrobial susceptibility test when a bloodstream infection is suspected. Therefore, many efforts have been made during the last decade to reduce the turnaround time of pathogen identification from positive blood culture. In particular, several subculture-independent methods have been developed. Numerous rapid molecular tests for microbial identification directly from positive blood culture are now available. Most of these molecular methods also detect some major resistance genes. Another subculture independent approach is based on the rapid preparation of a bacterial pellet from a positive blood culture. This method consists in the removal of non-microbial material and on microbes concentration by centrifugation and have been shown to provide sufficient amount of biomass for identification using matrix-assisted laser desorption ionization time-of-flight mass spectrometry (MALDI-TOF/MS) technology. Recently a new approach based on atomic force microscopy applied on bacterial pellet have been shown to provide rapid antimicrobial susceptibility test from positive blood culture. The performance and benefit of these rapid microbial diagnostic strategies from positive blood cultures as well as the most anticipated technologies of this field will be discussed.

Final Abstract Number: 30.003
Session: New Approaches for the Diagnosis of Invasive Infections
Date: Saturday, March 3, 2018
Time: 10:15-12:15
Room: Retiro BC
Type: Invited Presentation

Metagenomics for the diagnosis of exotic infections
R. Schlaberg
Salt Lake City, USA

Abstract text: Next-generation sequencing-based metagenomics provides a powerful tool for hypothesis-free detection of unexpected and exotic pathogens. While proof-of-concept has been well established, the performance of metagenomics compared to traditional approaches is less well understood. We have demonstrated in retrospective studies that metagenomics can improve diagnostic yield compared to culture and PCR-based tests, especially in patients with complex healthcare needs. Results from metagenomics testing of patients with respiratory tract infections, fever of unknown origin, and encephalitis/meningitis will be discussed.
Performing metagenomics in diagnostic laboratories with controlled and consistent quality remains challenging. While lessons can be learned from NGS testing in other disciplines, many challenges pertaining to specimen processing, data analysis, and reference sequence databases are unique to the field of microbiology. We have developed and validated a metagenomics-based test for detection of respiratory pathogens. This test makes extensive use of internal and external controls and was validated using both, real and virtual patient samples. Current challenges and potential solutions will be reviewed.

Final Abstract Number: 30.004
Session: New Approaches for the Diagnosis of Invasive Infections
Date: Saturday, March 3, 2018
Time: 10:15-12:15
Room: Retiro BC
Type: Invited Presentation

Improving the outcome of invasive fungal diseases: Early diagnosis of invasive Aspergillosis
M. Nucci
, Brazil

Abstract text: The outcome of invasive aspergillosis has improved in the last 15 years, attributed to the development of new antifungal drugs and, especially, to an early diagnosis. Early diagnosis of invasive aspergillosis allows clinicians to start treatment with a lower fungal burden. The challenges for early diagnosis, however, are that since the disease is at an earlier stage, clinical manifestations radiologic images are non-specific. The use of fungal biomarkers, especially galactomannan, is a key element in early diagnosis of invasive aspergillosis. In this presentation we review the pathogenesis of invasive pulmonary aspergillosis, the images that appear very early in the disease process, and how to use fungal biomarkers to early diagnose invasive aspergillosis. We will present in detail the clinical scenario in which invasive aspergillosis occurs, the “non-specific” images in chest computed tomography that represent bronchial involvement and dissemination which are typical of the early phase of invasive aspergillosis, the usefulness of the detection of galactomannan in the serum and bronchoalveolar lavage, and the potential usefulness of other fungal biomarkers.

Final Abstract Number: 31.001
Session: Gorgas Lectures and Case Discussions in Clinical Tropical Medicine II
Date: Saturday, March 3, 2018
Time: 10:15-12:15
Room: La Pampa
Type: Invited Presentation

Medical conisderations before international travel and infections in returning travelers

D. Freedman
University of Alabama at Birmingham, Birmingham, AL, USA

Abstract text: The pretravel office visit with an adult traveler to the developing world should follow a structured approach.
Perform Risk Assessment
• Ascertain the exact itinerary, including regions within each country to be visited, dates of travel to assess risk of seasonal diseases, age, past vaccination history, underlying illness(es), current medications, pregnancy status, allergies, purpose of trip, risk exposures—blood, body fluids, adventure or extensive outdoor exposures, urban versus rural travel, type of accommodations, level of aversion to risk, and financial limitations that may necessitate prioritization of interventions
Administer Vaccinations
• Routine vaccinations that are not up to date
• Indicated routine travel vaccines, including hepatitis A, hepatitis B, typhoid, and influenza
Indicated specialized vaccines, including yellow fever, rabies, polio, meningococcal, and, tick-borne encephalitis and cholera
Provide Malaria Chemoprophylaxis (if indicated)
Educate on personal protection against arthropods.
Educate on Travelers Diarrhea Prevention and Self-Treatment
• Prescribe and educate on standby therapy with azithromycin, and advise on use of loperamide and oral hydration if needed.
Teach Preventive Behaviors
• Most travel-related health problems, including vaccine-preventable diseases, can be avoided through simple behaviors initiated by the traveler.
Major syndromes in returned travelers include fever, diarrhea (acute or persistent), skin problems, and eosinophilia.
Tropical Diseaes with positive peripheral blood films are:
• Malaria, babesiosis, filariasis, African trypanosomiasis, American trypanosomiasis, relapsing fever, bartonellosis
Evaluation of Significant Tropical Fever
Consider the possible incubation periods of major tropical diseases in relation to possible exposures in formulating the initial differential diagnosis. Any hemorrhagic manifestations? If viral hemorrhagic fever is possible, isolate and call public health authorities; consider meningococcemia, rickettsiosis, sepsis, dengue.
• Is malaria possible? If there is end-organ damage, initiate empirical therapy.
• Utilize a “rule out malaria protocol,” and use empirical therapy if no local expertise is available.
• Are there localizing findings? Go to syndromic approach and differential diagnosis.
• Are there no localizing findings? Consider typhoid, dengue, rickettsiosis, human immunodeficiency virus infection, leptospirosis, schistosomiasis (eosinophilia), amebic disease.
• Consult a reference source for constellations of exposures and clinical presentations suggestive of particular diagnoses in returned travelers.
• Eosinophilia is caused by tissue-invasive helminths and is proportional to the degree of tissue invasion

Final Abstract Number: 36.001
Session: Plenary IV: Enteric Infections in Under-resourced Countries – From Research to Clinical Practice
Date: Saturday, March 3, 2018
Time: 14:00-14:45
Room: Libertador ABC
Type: Invited Presentation

Enteric infections in low- and middle-income countries-from research to prevention and the clinic
G. Kang
Christian Medical College, Vellore, India, Vellore, India

Abstract text: Diarrhoeal diseases are a major health problem in developing countries and are also a high risk to travellers who visit these countries. Although the total number of deaths is still unacceptably high and disproportionately affects the poorest in low-income countries, there has been a substantial reduction in the past three decades.
In addition to acute illness, repeated infections can lead to acute or chronic malnutrition and consequent effects on physical and mental development of children that may eventually translate into impairment of productivity in adults. Moreover, outbreaks of cholera, shigellosis and typhoid most often occur in resource-poor countries, adding to the burden of disease among the most vulnerable sub-populations. In December 2015, the World Health Organisation (WHO) published its first global estimates of the burden of foodborne diseases, reporting 420,000 annual deaths, with 125,000 occurring in children under the age of 5 years, mainly in the low-income countries in Africa and south-east Asia.
Research for prevention has examined the role of water and sanitation, and highlighted the remarkable impact of engineering solutions to safe supply and limiting contamination, as well as the challenges in sustaining behavioral change. Preventive efforts have resulted in the production of vaccines for cholera, typhoid and rotavirus, and several bacterial and viral targets such as Shigella, Campylobacter and noroviruses have vaccines in different stages of evaluation.
Although the mainstay of treatment of acute gastroenteritis is rehydration, therapy aimed at the infectious agent is important in some enteric infections, such as typhoid. Attempts at anti-viral therapy have been limited, but the increasing importance of antimicrobial resistance has led to greater interest in appropriate treatment of enteric infections, particularly typhoid and travellers' diarrhea. While probiotics and modification of the microbiome are being explored, more conventional efforts to develop and implement targeted therapies have been hampered by the wide empirical, mainly inappropriate, use of antimicrobial therapies for the clinical syndrome of diarrhea in children and adults. The importance of making a diagnosis to direct or withhold antimicrobial therapy is not often recognized, but cheap, effective, widely available diagnostics could impact not just patient care but also public health.

Final Abstract Number: 37.001
Session: A Planetary Health Approach to Emerging Infectious Diseases
Date: Saturday, March 3, 2018
Time: 15:15-16:45
Room: Libertador A
Type: Invited Presentation

How climate, species interactions, and global change drive infectious disease dynamics
J. Caldwell
Standford, USA

Abstract text: Understanding the climatic conditions that drive vector-borne disease emergence and spread is critically important for understanding current infectious disease dynamics and predicting how they may shift with climate change. Temperature, rainfall, and humidity can influence vector abundance, distribution, and vectorial capacity (the number of infectious vector bites per person) by affecting a variety of vector traits, including survival, reproduction, and development. Using dengue and chikungunya as examples, I will discuss how climate factors impact the abundance of the *Aedes aegypti* mosquito vector and disease transmission. Often temperature, rainfall, and humidity influence mosquito traits differently across their environmental ranges. For instance, the relationships between temperature and multiple mosquito traits are unimodal, which has led to the prediction of an intermediate optimal temperature for disease transmission, which is lower than previously expected. We are incorporating these climate-driven traits into mathematical models to better understand how climate affects dengue and chikungunya transmission in Africa and South America, using field entomology and epidemiology data from Kenya and Ecuador. These models can help us predict disease transmission in the near future and understand how global climate change is likely to shift transmission in space and time in the longer term. Further, these results have implications for understanding where other *Aedes aegypti*-vectored diseases could circulate, including currently known diseases of concern such as Zika and yellow fever, as well as emerging pathogens such as Mayaro virus.

Final Abstract Number: 37.002
Session: A Planetary Health Approach to Emerging Infectious Diseases
Date: Saturday, March 3, 2018
Time: 15:15-16:45
Room: Libertador A
Type: Invited Presentation

Modeling the impact of environmental change on infectious diseases
R. Lowe
London School of Hygiene & Tropical Medicine, London, United Kingdom

Abstract text: Vector-borne infectious diseases are highly sensitive to environmental change, such as variations in climate and land-surface characteristics, which impact developmental rates and survival of both the vector and pathogen and the availability of vector breeding sites. Infectious disease emergence and spread is also exacerbated by anthropogenic activities, such as deforestation, mining, urbanisation and human mobility. For example, the global expansion of dengue fever and the recent spread of chikungunya and Zika viruses to the Americas, has been attributed, in part, to international travel, poor urban infrastructure and ineffective vector control.
Innovative epidemiological modelling tools can help understand how environmental conditions interact with other disease risk factors, such as socio-economic status and human mobility, to determine the risk of disease transmission and spread. In recent years, disease modelling has benefited from computational advances in fitting complex mathematical models and the increasing availability of environmental, socio-economic and disease surveillance datasets. At the same time, the ability to understand and model the climate system has steadily improved, providing accurate forecasts of climate conditions in certain locations and seasons. Thus, climate forecasts at seasonal time scales provide an opportunity to anticipate potential outbreaks of vector-borne diseases several months in advance.
In this talk, I will present a Bayesian spatio-temporal model framework, which quantifies the extent to which environmental and socio-economic indicators can explain variations in disease risk. The framework is designed to disentangle the impacts of climate from other risk factors, using multi-source data and random effects, which account for unknown spatial, seasonal and inter-annual variation. I will provide examples of combining disease models with seasonal climate forecasts to produce real-time probabilistic dengue early warnings in Brazil, during a mass gathering event, and in southern coastal Ecuador, following a major El Niño event. This flexible model framework can be adapted to predict any climate-sensitive disease at various spatio-temporal scales and in diverse ecological settings. I will show how incorporating seasonal climate forecasts in disease prediction models could support public health decision-makers in targeting timely disease control and prevention strategies to mitigate the risk of imminent disease epidemics and emerging disease threats.

Final Abstract Number: 37.003
Session: A Planetary Health Approach to Emerging Infectious Diseases
Date: Saturday, March 3, 2018
Time: 15:15-16:45
Room: Libertador A
Type: Invited Presentation

Anthropogenic global defaunation and its consequences for planetary health
S. Morand
CIRAD, Bangkok, Thailand

Abstract text: The Convention on Biological Diversity has set the 20 Aichi targets for biodiversity by 2020. However, almost all indicators of the Aichi targets show negative trends. Anthropogenic pressure (human appropriation of biological productivity), biodiversity (Living Planet Index), biodiversity benefits (domesticated breeds, Red List of pollinators) show decline with negative consequences on resources and ecosystem services. Many academic studies and reports conducted by international organizations stressed that biodiversity loss is affecting ecosystem resilience but also health and well-being. However, we still lack a framework that could link socio-economics, ecosystems, biodiversity and health.
The social-ecology approach links ecological and biological metabolism with social metabolism, where social systems are seen as hybrid systems between cultures, socio-economics (exchanges and flows) and environments (metabolic exchanges). Human societies can then be characterized by stocks and flows that involve: population and its demography, biophysical stocks and trade/production, land and its biological productivity. An important parameter is HANPP (Human Appropriation of the Net Primary Productivity). HANPP has doubled in the 20th century and scenarios suggest that this appropriation will continue to increase considerably in the coming decades. HANPP is an appropriate indicator for research into the impact of human intervention on biodiversity and can link human appropriation of environmental metabolism with ecological theories on biodiversity, like the species-energy hypothesis.
We used the conceptual framework of social-ecology that links “drivers” (food consumption, energy), “pressures” (land use, HANPP), “states” (biodiversity change), “impacts” (reduction of the quality of ecosystem services) and “responses” (governance, land planning, conservation). This conceptual framework makes it possible to address the link between biodiversity and health.
We tested this social-ecology framework using several databases at the nation level. We confirmed the species-energy hypothesis by showing a positive correlation between HANPP and declining biodiversity. The hypothesis of a reduction in ecosystem services for the regulation of infectious diseases appears also to be confirmed with an increase in zoonotic disease epidemics with the increase in HANPP at the world nation level. The incorporation of health components in social-ecology might provide governance tools for global biodiversity conservation and planetary health.

Final Abstract Number: 38.001
Session: Alternative Strategies to Deliver Affordable Treatment for Hepatitis C Patients
Date: Saturday, March 3, 2018
Time: 15:15-16:45
Room: Libertador B
Type: Invited Presentation

HCV - global challenges
M. Silva
Buenos Aires, Argentina

Abstract text: Hepatitis C virus (HCV) infection is the leading cause of chronic liver disease worldwide and is a serious health burden that requires urgent attention. It is estimated that around 2.5-3.0% of the world's population is chronically infected, which equates to a total of 130-170 million people.
Annually, HCV infection causes 350,000-500,000 deaths worldwide, constituting approximately 1% of the total annual deaths. The large increase in its mortality, which surpassed that of HIV, indicates a worrying lack of action across countries. HCV is also the leading cause of cirrhosis, HCC and of liver transplantation.
Since a large proportion of patients with HCV remain undiagnosed and untreated, it becomes clear that the vast majority of them remain uncured.
Understanding barriers to diagnosis care and cure is critical for improvement of HCV disease burden. These barriers usually arise at the patient, provider, payer, and/or government level.
Finally, national health systems, governments and payer, are critical for overall HCV management. They should recognize HCV infection as an important public health threat and make resources available for implementation of effective programs.
Although most healthcare systems in the world are different, in many ways, they share common challenges. Most have poorly coordinated care and are paying for volume and not for value. Good management requires proactivity in terms of prevention of early detection, and access to cure. Fragmentation of care, lack of quality and safety in healthcare systems and disconnections with occupational health emerge as necessary areas of improvement. Countries with effective HCV programs have comprehensive rather than focusing on a single intervention.
These programs are dependent on the uninterrupted supply of quality-assured, medicines, diagnostics and other health care commodities. Robust procurement and supply management systems are required to ensure that the right products are selected, purchased at a reasonable price and efficiently delivered to the point of care. The demand for affordable treatment for HCV requires price reduction strategies not only for medicines, but also for diagnostics and health commodities.
Often, countries that have a program do not reinforce it with an adequate budget for an appropriate implementation.

Final Abstract Number: 38.002
Session: Alternative Strategies to Deliver Affordable Treatment for Hepatitis C Patients
Date: Saturday, March 3, 2018
Time: 15:15-16:45
Room: Libertador B
Type: Invited Presentation

Affordable Treatment Approaches for HCV with Sofosbuvir plus Ravidasvir Combination
G. Diap
Drugs for Neglected Diseases Initiative, Geneva, Switzerland

Abstract text: The treatment of hepatitis C (HCV) around the globe is limited by the absence of effective, affordable, pan genotypic treatments. The cornerstone of a public health approach to HCV will be ensuring the availability, accessibility, and affordability of an all-oral, easy-to-use, efficacious, and safe treatment that will, to the greatest extent possible, enable the same regimen or regimens to be used for all patients, regardless of genotype, liver disease stage, HIV co-infection, or source of infection.
Develop new, affordable, pan-genotypic treatments for a Public Health Approach to HCV Simplify HCV test and treat strategies and develop innovative models of care to support scale up Improve access (IP, regulatory, pricing, etc.) and affordability to HCV treatments in countries**.**
DNDi works with HCV stakeholders in countries to influence regions. A ravidasvir plus sofosbuvir clinical program is being implemented in seven countries on four continents. Progress in countries will be presented during the session
The clinical development plan for ravidasvir with sofosbuvir is designed to demonstrate its pan-genotypic profile in HCV treatment-naïve and experienced, cirrhotic & non-cirrhotic patients, HIV-HCV coinfected and PWUD, with genotypes 1 – 6 Hepatitis C virus infection. These efforts include partnering with HCV stakeholders to evaluate simplified testing algorithms; pan genotypic treatment regimens; and how to address treatment failure, interruption and resistance. Key strategic elements to move from small-scale pilots to larger scale programs will be provided.
Funding sources:
Médecins Sans Frontières, Unitaid, Department for International Development - UK, Swiss Agency for Development and Cooperation, and Starr International Foundation

Final Abstract Number: 38.003
Session: Alternative Strategies to Deliver Affordable Treatment for Hepatitis C Patients
Date: Saturday, March 3, 2018
Time: 15:15-16:45
Room: Libertador B
Type: Invited Presentation

Addressing IP barriers to the elimination of HCV as a public health problem in Latin America

F. Viegas Neves da Silva
DNDi, Rio de Janeiro, Brazil

Abstract text: Treatment of HCV has evolved from injection-based regimens with severe side effects to DAAs with cure rates of 95%. However, due to patent monopolies high prices are charged and pose a major barrier to access, especially in Latin America, which precludes countries to access more affordable generic DAAs. While DAA patent holders have developed voluntary licensing schemes, with a view to offer more affordable prices to developing countries, too many middle income countries and most Latin America are excluded from it. As a result, countries are facing prices, that range from $12,000 to $6,212 for DAA treatment, which are unsustainable to reach HCV elimination targets.
To face this challenge, DNDi has developed a HCV public health approach that, besides developing a new affordable and pangenotypic treatment, aims to seize the opportunity of the new DAAs available to advocate for its expansion of treatment widely. This strategy will require governments to take active steps to increase access and affordability, including by making use of IP flexibilities, allowed under international trade law, to overcome high prices and patent barriers. To enable this environment, DNDi seeks to work with governments, civil society, patients and other stakeholders to overcome IP and regulatory barriers to an affordable pan-genotypic treatment, particularly to countries in Latin America that are facing high prices and that are excluded from voluntary schemes. Recently, DNDi has welcomed Malaysia´s leadership and example to developing countries facing high prices of DAAs to issue a government-use license to source generic sofosbuvir, in order to accelerate access to affordable sofosbuvir in its public hospitals.
Seizing the public health potential of DAAs to ensure the elimination of HCV as a public health problem in Latin America will require strong leadership from Ministries of Health, governments, active involvement of treatment providers and patient’s groups to advocate for the implementation and strengthening of pro-access policies, overcoming IP and regulatory barriers, to allow for scale up of diagnostic and treatment of HCV in Latin America.

Final Abstract Number: 39.001
Session: Infection Prevention and Control - Controversies and New Perspectives
Date: Saturday, March 3, 2018
Time: 15:15-16:45
Room: Libertador C
Type: Invited Presentation

Applicability of infections and prevention control guidelines in Low- and Middle-Income Countries
S. Mehtar
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Abstract text: Most of the guidelines are written by high income countries such as the CDC, European and UK guidelines. In recent years the Global Unit for IPC, WHO has published several IPC evidence based guidelines which have global application including low to middle Income countries (LMICs). Good quality publication from LMICs are limited and therefore are not usually reflected in the systematic reviews (SR) which are the basis of such guidelines.
Weak health systems and IPC structures in LMICs require considerable infrastructure support to be able to implement guidelines. The WHO Core Components (2016) strongly recommends these as part of implementation programmes. IPC should be a recognized specialty and practitioners should be well trained and able to do their job. In many LMICs (and some HIC) this is not the case.
The surgical site infection guidelines (2016) assume a robust infrastructure such as reliable operating theatre ventilation and validated methods of decontamination. In most LMICs these are weak, and therefore here “surgery associated infections” should be considered as a more appropriate term. In many instances, single use devices are recycled and poorly reprocessed using inappropriate chemical disinfectants. Sterilizers are unreliable and often not validated. The staff running the sterilization areas are usually not adequately trained.
When conducting surveillance for healthcare associated infection (HAI), access to a microbiology laboratory which reliably tests for antimicrobial sensitivity (AST) is required. In Africa, AST is limited to approximately ¼ of the countries and many do not have any access to such facilities. To establish the presence of carbapenem-resistant enterobacteriacae (CRE). Multi drug resistant *Pseudomonas aeruginosa* and *Actinetobacter baumannii* are usually neither detected nor recorded, making it not only difficult to treat, but also to establish antimicrobial stewardship based on local evidence or to influence WHO guidelines.
Implementation strategies for WHO guidelines are usually multimodal strategies, such as hand hygiene, require infrastructure, good basic and advanced training in IPC to ensure the best results.

Final Abstract Number: 39.002
Session: Infection Prevention and Control - Controversies and New Perspectives
Date: Saturday, March 3, 2018
Time: 15:15-16:45
Room: Libertador C
Type: Invited Presentation

Isolation - duration; universal vs selective isolation

G. Bearman
Virginia Commonwealth University, Richmond, VA, USA

Abstract text: Contact Precautions have limited impact on endemic Multidrug Resistant Pathogens (MDROs) and their use of the control of endemic pathogens is generally backed by weak evidence. Considerations when instituting contact precautions in endemic settings include potential harmful effects and poor adherence. Alternative approaches may exist for control of endemic MDROs. In general a horizontal infection prevention program should be the standard platform for the control of all pathogens transmitted via the same mechanism-contact. Universal gloving may be used as an adjunct. Contact Precautions should be used selectively and based on local needs and resources.

Final Abstract Number: 41.001
Session: Gorgas Lectures and Case Discussions in Clinical Tropical Medicine III
Date: Saturday, March 3, 2018
Time: 15:15-16:45
Room: La Pampa
Type: Invited Presentation

Leprosy
P. Legua
Lima, Peru

Abstract text: Leprosy is a disease associated with great stigma due to the deformities it can produce. It is caused *by Mycobacterium leprae*. In 2008 a new mycobacteria, *M. lepromatosis* was recognized as the agent of Lucio leprosy.
It is not known how leprosy is transmitted. Only infected people with a defect in their cell-mediated immunity, which is specific for *M. leprae*, develop the disease. Those with still high immunity will develop tuberculoid leprosy (TT), with a single skin lesion and no detectable bacilli; those with no CMI will develop lepromatous leprosy (LL), with areas of skin infiltrated by foamy histiocytes filled with leprosy bacilli. In between are the borderline patients, borderline tuberculoid (BT), mid-borderline (BB), and borderline lepromatous (BL), with decreasing levels of CMI and increasing bacillary load.
For therapy, according to the WHO, patients are divided in paucibacillary (PB) (negative slit-skin smears, i.e. Indeterminate, TT, and BT) and multibacillary (MB) (positive slit-skin smears, i.e. BB, BL, and LL). PB patients are treated with six months of dapsone plus rifampicin; MB patients are treated with 12 months of dapsone plus rifampicin plus clofazimine.
Two types of hypersensitivity reactions may occur, type 1 and type 2. Type 1 reaction is considered to be due to a change in the CMI and only happens in borderline patients (BT,BB,BL). It produces inflammation of the skin lesions and/or nerves; the drug of choice for it is prednisone. Type 2 reaction is considered to be due to antigen-antibody deposition in tissues, and only happens in BL and LL patients. The most common presentation is erythema nodosum leprosum, but it may present with fever and inflammation of several organs. The drug of choice for a severe reaction is thalidomide, but in a woman of child-bearing age it is contraindicated and prednisone should be used.
Leprosy is a disease that can be easily diagnosed, and with appropriate early therapy can be cured with no sequelae.

Final Abstract Number: 42.001
Session: Pandemic Preparedness
Date: Saturday, March 3, 2018
Time: 17:00-18:00
Room: Libertador A
Type: Invited Presentation

Innovative disease surveillance
J. Brownstein
Childrens Hospital, Boston, USA

Abstract text: Over the past fifteen years, Internet technology has significantly changed the landscape of public
health surveillance and epidemic intelligence gathering. Disease and outbreak data is disseminated not only through formal online announcements by government agencies, but also through informal channels such as social networking sites, blogs, chat rooms, Web searches, local news media and crowdsourcing platforms. These data streams have been credited with decreasing the time between an outbreak and formal recognition of an outbreak, allowing for an expedited response to the public health threat. Collectively, these online sources create an image of global public health that is fundamentally different from the one produced by traditional public health surveillance infrastructure.
Dr. Brownstein will discuss the current capabilities and future directions in the use of the nontraditional data sources for the purposes of public health surveillance and rapid detection of emerging infectious diseases.

Final Abstract Number: 42.002
Session: Pandemic Preparedness
Date: Saturday, March 3, 2018
Time: 17:00-18:00
Room: Libertador A
Type: Invited Presentation

Critical care considerations and pandemic preparedness

P. Tambyah
National University Hospital, Singapore, Singapore

Abstract text: Critical care units are a vital component of pandemic preparedness. In a severe pandemic of a respiratory viral illness, it is likely that critical care resources will be stretched tremendously. Even for non-respiratory illnesses such as encephalitis or one of the hemorrhagic fever syndromes, there will be a significant demand for mechanical ventilation, hemodynamic monitoring and all the other elements of a modern critical care unit. While critical care is costly and resource intensive, it can result in dramatic “cures” which have enormous intangible benefits for healthcare worker morale. In addition, there is no doubt that safe and effective critical care can improve outcomes, encourage sick individuals to seek medical attention early and mitigate the devastating consequences of a severe pandemic. At the same time, it is important to realise that in a setting with vulnerable patients who may be immunocompromised, a high intensity of medical device use and stretched staff, there are significant risks of nosocomial transmission of either the pandemic pathogen or other infectious agents. It is thus vital that basic infection control practices are not compromised in critical care units even in the face of a pandemic. Ultimately, good planning that incorporates training, education and resource allocation prioritization will be important to ensure that all healthcare systems are prepared for the pandemics that we might face in the near future.

Final Abstract Number: 44.001
Session: Optimized Antibiotic Use
Date: Saturday, March 3, 2018
Time: 17:00-18:00
Room: Libertador C
Type: Invited Presentation

Individualized antibiotic use - an introduction

U. Theuretzbacher
CEFAIA, Vienna, Austria

Abstract text: Most antibiotics were developed many decades ago on a trial-and-error basis. Usage patterns and dosing regimens are often not appropriate for individual patients. Especially critically ill patients with altered pharmacokinetics or patients infected with less susceptible pathogens need optimised dosing of antibiotics. This session provides basic information about the impact of the patient factors linked to pathogen susceptibility (pharmacokinetics/pharmacodynamics) and its relevance for selecting dosing regimens. Optimised dosing for the individual patient may improve clinical outcome, reduce the probability of emergence of resistance and minimise toxicity. Clinical examples will illustrate how the principles of dosing optimisation can be applied to individual patients.

Final Abstract Number: 44.002
Session: Optimized Antibiotic Use
Date: Saturday, March 3, 2018
Time: 17:00-18:00
Room: Libertador C
Type: Invited Presentation

Bring your tablet - individualized antibiotic dosing with interactive case studies
S. Wicha
Univ. of Hamburg, Hamburg, Germany

Abstract text: In the second presentation of this session, the pharmacokinetic-pharmacodynamic concepts conveyed in the first presentation are utilised to derive individualized dosing suggestions. The participants will use an open-access, web-based, precision dosing software (www.TDMx.eu) to learn the techniques of Probabilistic dosing and Bayesian dosing in interactive case studies with aminoglycoside and beta-lactam antibiotics. Participants are encouraged to bring their laptop or tablet computer (smartphone screens are usually not large enough), supplied with internet access to work ‘hands-on’ with the case examples.

Final Abstract Number: 47.001
Session: Plenary V: The Human Microbiome
Date: Sunday, March 4, 2018
Time: 09:00-09:45
Room: Libertador B
Type: Invited Presentation

The human microbiome
D. Relman
Stanford University, Standford, USA

Abstract text: Recent advances in the study of human-indigenous microbial communities have highlighted the diversity of these communities, features of individuality, conserved as well as personalized predicted functional attributes, and the intimate relationship of these communities to host physiology. Yet, questions remain about the ecological processes that establish and maintain the human microbiota throughout life, as well as the features of this ecosystem that are associated with stability, recovery after disturbance, protection against disease-causing microbes, and other aspects of health and disease. As with other ecosystems, early stages of assembly may have disproportionate impact on later aspects of function. The human microbiome in adults at baseline is dynamic but also displays features of stability. Short, pulse disturbances, such as those caused by antibiotics or abrupt changes in diet may cause at least transient alterations in structure and function; compounded or sustained disturbances may lead to persistent, alternate states. Some examples will be discussed. We need to be able to describe the current ecological fitness landscape in an individual and the kinds of forces necessary to induce shifts towards ecological states associated with health. Our long-term goal is a predictive understanding of the microbiome and the mechanisms that underlie resilience, as well as well-informed strategies for its manipulation, so as to maintain or restore health, and avoid or mitigate disease.

Final Abstract Number: 48.001
Session: Zika: Regional Experiences in Neurological Diseases and Severe Cases
Date: Sunday, March 4, 2018
Time: 10:15-12:15
Room: Libertador A
Type: Invited Presentation

Neurological complications of Zika virus: Experience in French Polynesia
D. Musso
Institut Louis Malardé Tahiti, Tapeete Tahiti, France

Abstract text: Zika virus (ZIKV) was discovered in 1947 in Africa. From its discovery to 2007, less than 20 human infections have been reported. ZIKV emerged for the first time in the Pacific in the Federated States of Micronesia in 2007, emergence was limited to Yap Islands and severe complications were not described. The second emergence in the Pacific occurred unexpectedly in French Polynesia (FP) in 2013, where ZIKV caused a large outbreak with about 30.000 symptomatic infections. During this outbreak the first complications of ZIKV infections and the potential for non vector-borne transmission of ZIKV (materno-fetal, sexual, and transfusion) were described. From FP, ZIKV spread throughout the Pacific and subsequently emerged in Latin America in 2015.
The first case of Guillain-Barré syndrome (GBS) occurring immediately after a ZIKV infection was reported in FP on December 2013. During the following three months additional 41 GBS cases were reported. The increase by 20 fold of the usual incidence of GBS in FP quickly led to an overload of the neurology and the intensive care units (ICU) (16 patients were hospitalized in the ICU and 9 of them required mechanical ventilation). A case-control study conducted in FP demonstrated the link between ZIKV and GBS. The estimated incidence of GBS during the FP outbreak was 0.24 per 1.000 ZIKV infections.
Neurological complications are common features of flaviviruses infections, but GBS complicating ZIKV infection had never been reported before the FP outbreak. Other neurological diseases such as myelitis, encephalitis and meningoencephalitis were also reported during the FP outbreak. The increase in GBS and other neurological diseases incidence and also congenital abnormalities (including microcephaly) related to ZIKV infection was further described at the time ZIKV emerged in the Americas.
FP was the first country to face a large ZIKV outbreak and clinical complications of ZIKV infection were unexpected. One of the lessons learned from this outbreak is that once a new pathogen starts causing large outbreaks, even in small countries, the scientific community should be prepared to the worst case scenario.

Final Abstract Number: 48.002
Session: Zika: Regional Experiences in Neurological Diseases and Severe Cases
Date: Sunday, March 4, 2018
Time: 10:15-12:15
Room: Libertador A
Type: Invited Presentation

Zika congenital syndorme: experience in Brazil
K. G. Luz
Hospital Giselda Trigueiro, Natal, Brazil

Abstract text: The zika virus infection reached a catastrophic dimension in Brazil. It was the first country in the world where there was a large non-immune population. The cases began in the Northeast of the country and continued to affect people to the North and South. It is believed that about one and a half million cases including adults and children occurred in the country. Cases of Guillain Barré Syndrome were recorded very frequently during the epidemic and in the second half of 2015 cases of microcephaly were evidenced. The country very quickly faced this new and serious challenge. Medical guides were drawn up, care services for children and mothers were established. Diagnostic criteria, radiological findings characteristic of the congenital syndrome were reported and the most important was the establishment of the management of the affected children. Management of feeding, neurological conditions and support for early stimulation. This conference will present the main clinical and radiological findings of the congenital syndrome, such as the diagnosis of suspected, probable and confirmed cases. And finally how to make the intrauterine diagnosis and manage the prevention of maternal infection.

Final Abstract Number: 48.003
Session: Zika: Regional Experiences in Neurological Diseases and Severe Cases
Date: Sunday, March 4, 2018
Time: 10:15-12:15
Room: Libertador A
Type: Invited Presentation

Severe, atypical and fatal cases of Zika virus infection: Experience in Colombia

A. J. Rodriguez-Morales
Universidad Central de Venezuela, Caracas, DC, Venezuela

Abstract text: Zika virus, a flavivirus, have arrived to Latin America in 2013, but being evident causing epidemics since 2015 beginning in Brazil and later in other countries in the region, with a higher peak in 2016, when World Health Organization, based on cumulated evidence on its association with Guillain-Barré syndrome and microcephaly and other birth defects (also the congenital Zika syndrome, CZS), declared for a period of almost a year, an international public health emergency (PHEC). Epidemics in the region caused around 1 million cases with also additional complications beyond SGB and the CZS, which in patients with comorbidities lead to deaths. Cases with severe and atypical manifestations presented, particularly involving neurological disease. In a recent systematic review and meta-analysis of observational studies, we identified over 84 fatal cases of Zika virus infection in the Americas, especially during epidemics. Until 2015, in general, Zika was not considered to be a dangerous pathogen or a serious public health threat, but after the first death, reported by our group in Emerging Infectious Diseases 2016, an increasing number of fatalities have been published in the literature. Although the pathogenicity of severe infection is poorly understood; based on vitro and animal evidence, it is possible that antibody dependent enhancement (ADE) has a role in its development. Among the events studied in the region, a number of cases with arboviral coinfections/codetection (dengue and chikungunya), were described and published beginning in Colombia and later in Brazil. In addition to that, cocirculation and ADE are challenges for physicians and public health authorities, given the implications for clinical manifestations and serological diagnosis in patients with previous exposition to other flaviviruses. As part of this situation multiple networks of research for Zika virus infection have been generated in order to assess this situation and prepare the bases for strategies of prevention and control, combining methods, as well multisectoral approaches, finally also consider the setting of the development of vaccines. In this conference, particularly severe, atypical and fatal disease, considering physiopathological and immunological aspects, will be discussed regard the experience generated in Latin America around Zika.

Final Abstract Number: 48.004
Session: Zika: Regional Experiences in Neurological Diseases and Severe Cases
Date: Sunday, March 4, 2018
Time: 10:15-12:15
Room: Libertador A
Type: Invited Presentation

Risk factors, comorbidities and coinfections with Zika virus infection

J. Cardona-Ospina
Universidad Tecnológica de Pereira, Pereira, Colombia

Abstract text: The emergence of Zika virus (ZIKV), in a region confronting the challenge of vector control, showed the risk of sustained ecological and social suitability for the settlement of *Aedes sp.*-transmitted arboviruses. The lack of proper previous mosquito control, the highly interconnected world by travel, and the difficulty detecting asymptomatic infections, allowed a broad and rapid distribution of ZIKV in Latin America infecting communities with previous exposure to other flaviviruses, and a more diverse population facing aging and co-morbidities. In this scenario, previously unseen atypical and severe cases started to be reported as well as fetal compromise when infection happened during pregnancy. Moreover, co-circulation with other arboviruses, each one with different implications in terms of morbidity, mortality, and chronic burden, and the cross-reactivity with dengue and yellow fever, highlighted the need of adequate diagnostic tools for rapid assessment of etiologic agent in acute febrile patients from tropical areas. And the report of co-infections with other arboviruses and other infectious agents, like bacteria, broaden the clinical spectrum of the disease. Then, a previously considered benign febrile disease turned into the spotlight of scientists. The aim of this conference is to briefly introduce some of the social and ecological aspects that probably facilitated ZIKV spread in the Americas, and to show how comorbidities, co-circulation and co-infections probably helped to modify the disease course leading to the emergence of severe and fatal disease, and to adverse fetal outcomes. A recent systematic review conducted by our group during epidemics found that co-morbidities would be a risk factor for atypical disease. Current efforts in our group are turned to the description of the entire clinical spectrum of ZIKV infection, the importance of differential diagnosis in terms of follow up, the role of previous dengue exposure shaping adaptive immune response and acting as a risk factor for adverse prenatal and postnatal outcomes, and the effect of co-infection in terms of modification of immune response and the clinical severity in patients from an endemic area in Colombia.

Final Abstract Number: 49.001
Session: Infectious Diseases Transplant and Immunocompromised Hosts
Date: Sunday, March 4, 2018
Time: 10:15-12:15
Room: Libertador B
Type: Invited Presentation

Parasitic infections in SOT

W. Clemente
Federal University of Minas Gerais, Belo Horizonte, Minas Gerais, Brazil

Abstract text: Transplantation is increasing throughout the world, at the same time immigration and travel to and from developing countries and tropical areas are bringing new challenges for the management of transplant recipients. Parasitic infections (PI) can have a significant impact on donor and candidate screening, donor allocation and recipients infections and prophylaxis. Independent of where the transplant procedure is done, or the location of donors and recipients at the time of transplant, these infections represent a potential risk in the post-transplant period. Additionally, common parasitic infectious diseases in SOT recipients are frequently underestimated, and remain one of the most understudied groups of diseases with few prospective trials and no randomized studies in this setting. The most relevant diseases in this context will depend on the impact on the recipients outcome and the prevalence of the disease in the general population (e.g. Leishmaniasis, Chagas Disease, Malaria and Strongyloidiasis). It is necessary to discuss the main recommendations for screening donors and candidates aiming to achieve balance between minimizing the risk of disease and improving transplant activity with quality, cost-effectiveness and safety. It should be stressed that screening procedures recommendations should evaluate the epidemiological risk, the strengths and limitations of screening tests, and the rates of transmission or reactivation and consequences of these diseases to the recipient. On the other hand, if transmission or reactivation occurs one should provide adequate management warranting for a better outcome.

Final Abstract Number: 49.002
Session: Infectious Diseases Transplant and Immunocompromised Hosts
Date: Sunday, March 4, 2018
Time: 10:15-12:15
Room: Libertador B
Type: Invited Presentation

Emerging viral infections in transplantation

L. Pierrotti
University Sao Paulo, Sao Paulo, Brazil

Abstract text: Emerging virus pathogens are defined by newly discovered pathogen or the increase or threatening to increase in incidence of previously known viruses. In this lecture, the most relevant and current emerging and reemerging virus pathogens in the transplantation will be review.
In transplant scenario, an emerging viral infection may also have a broader impact, causing an atypical or more severe presentation in immunocompromised transplant recipients, as well prolonged viremia and virus shedding sometimes, such as Hepatitis E virus.
On the other hand, some of these new viruses identified during the last decades thanks to the new laboratorial techniques are not necessarily related to a disease, even among immunocompromised patients; an example is the newer polyomaviruses, which are not associated with recognized diseases.
Target antiviral therapy is not available for most diseases. Therefore, reduction of the immune suppression, combined with supportive measures, remains the cornerstone of therapy for most of the cases of severe viral infection among transplant patients.
There are also issues regarding prevention of these infections. Although some are vaccine-preventable illnesses, some vaccines are prepared with live-attenuated viruses, such as the yellow fever vaccine, and, therefore, are not recommended for the immunosuppressed patient.
In addition, the epidemic spread of an emerging viral pathogen in the general population may increase the risk of donor derived virus infection, and may cause a negative impact on the transplant activity. Examples of these scenarios are the emergence of West Nile fever in North America or the Chickungunya outbreaks in Italy and Puerto Rico. The prevention strategies, however, should take into account the epidemiologic scenario and need for continuous updated. The strategies may differ among endemic and non-endemic regions. Risk stratification of the potential donor based on clinical data and laboratorial screening may help to mitigate this hazard. Nevertheless, the limitations of the performance of the screening strategy must be considered in order to appropriately balance the mitigation of the risk of donor-transmitted infection and the adverse consequences of organ shortage for patients who are in the waiting list for transplantation.

Final Abstract Number: 49.003
Session: Infectious Diseases Transplant and Immunocompromised Hosts
Date: Sunday, March 4, 2018
Time: 10:15-12:15
Room: Libertador B
Type: Invited Presentation

Viral respiratory infections in BMT - A common cold is not just a cold in transplant recipients

O. de la Cruz
Virginia Commonwealth University , Richmond, VA, USA

Abstract text: Community acquired respiratory viruses (CARV) are an important cause of morbidity and mortality among Hematopoietic Stem Cell Transplant recipients (HSCT). Reported incidence of CARV in HSCT varies from 4% on early days of antigen testing to ~40% using PCR based detection. Most commonly detected viruses are Rhinovirus/enterovirus (22-34%), followed by Influenza, Respiratory Syncytial Virus (RSV) and Parainfluenza on similar range. Less frequently, with important morbidity associated are Coronavirus (3-11%), Adenovirus and Human metapneumovirus (HMPV).
Influenza pneumonia have attributable mortality in HSCT ~ 12%. Progression to lower respiratory tract infection (LRTI) can occur in one third of patients. However, perceived less aggressive viruses can progress to LRTI with equally precarious outcomes. For example, RSV have attributable mortality ~ 15%, with some series describing mortality around 80% in untreated patients. Adenovirus disseminated infection has been reported around 50% in small series, with mortality ranging 23%. Associated risk factors for LRTI progression include age greater than 65, lymphopenia, neutropenia, unrelated donor and chronic graft versus host disease.
Bacterial coinfection, bronchiolitis obliterans and decline in pulmonary function are complications frequently described after CARV infections. Allograft related shortcomings remained an important area of research.
General preventive measures are recommended to reduce infection related complications. Great example is Influenza vaccination and antiviral prophylaxis in specific scenarios. Immunization for several other CARV remains in development and not commercially available. Impact of contact and respiratory precaution at level of health care has been documented in several studies and should be followed. Other interventions like palivizumab for RSV in adults still lacking enough data and difficult implementation due to cost.
Therapeutic options are narrow given limited antiviral agents approved for the wide range of CARV. Influenza therapy is known to improve outcomes. Ribavirin (RBV) with or without IVIG has reported to beneficial for RSV, PIV and anecdotic reports for HMPV. RBV IV or inhaled (teratogenic and only FDA approved) administration poses a logistic challenge and associated to several side effects. Cidofovir for Adenovirus, ALN-RSV01 (RSV), DAS-181 (PIV), specific T-cell immunity therapies, among others, should accumulate more data to be suited for general use.

Final Abstract Number: 50.001
Session: Diagnosis and Management of Difficult to Treat Bacterial Infections
Date: Sunday, March 4, 2018
Time: 10:15-12:15
Room: Libertador C
Type: Invited Presentation

New diagnostic techniques applied to infection control
F. Pasteran
Buenos Aires, Argentina

No abstract received!

Final Abstract Number: 50.002
Session: Diagnosis and Management of Difficult to Treat Bacterial Infections
Date: Sunday, March 4, 2018
Time: 10:15-12:15
Room: Libertador C
Type: Invited Presentation

New and “recycled” antimicrobials
M. Stryjewski
CEMIC, BUENOS AIRES, Argentina

No abstract received!

Final Abstract Number: 50.003
Session: Diagnosis and Management of Difficult to Treat Bacterial Infections
Date: Sunday, March 4, 2018
Time: 10:15-12:15
Room: Libertador C
Type: Invited Presentation

Therapeutic efficacy of antimcrobials in critically ill patients

E. Nannini
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Abstract text: At any time, 50 % of patients in intensive care units are receiving antibiotics. Source control and early and appropriate antibiotics administration along with other measures are vital interventions for patients with sepsis. Dose optimization is one critical tool that should be use by clinicians to improve outcomes in critically ill patients. Adequate dosing of these patients not only can improve clinical outcomes but also can impact positively in the emergence of bacterial resistance in the unit. Patients with sepsis and systemic inflammatory response (SIR) suffer from hemodynamic changes such as increased cardiac output, reduced peripheral vascular resistance, changes in the volume of distribution, and fluid shifts. In this setting, other systemic changes frequently take place such as hypoalbuminemia, hepatic impairment, and acute modification of renal function (e.g., augmented renal clearance and acute kidney injury). All these physiological adjustments to SIR lead to changing drug concentrations in serum and at the infection site of the antibiotics prescribed for the underlying infection. In this regard, doses of antibiotics usually administered to non-critically ill patients are probably inadequate in most of those patients with sepsis or SIR. Knowing the pharmacokinetics and pharmacodynamics characteristics of each antibiotic is essential to optimize drug treatment in this setting. Individualizing dosing based on patient clinical status and antibiotic properties should be encouraged. Loading dose, continuous infusion of time-dependent antibiotics, therapeutic drug monitoring, and direct administration at the infection site are among the tools that could improve antimicrobial use in critically ill patients. Discussion of optimization options for most commonly used antibiotics in ICU will be presented.

Final Abstract Number: 52.001
Session: Gorgas Lectures and Case Discussions in Clinical Tropical Medicine IV
Date: Sunday, March 4, 2018
Time: 10:15-12:15
Room: La Pampa
Type: Invited Presentation

Emerging infectious diseases of the skin

F. Bravo
Universidad Peruana Cayetano Heredia, Lima, Peru

Abstract text: One of the most exciting subjects in infectious dermatology is the surge of new entities. Many of them are not truly new but their knowledge was restricted to few areas around the world. Expanding medical care in developing countries, the increased traveling around the world, the growing popularity of certain gastronomic delicatessens , all have influenced the occurrence of infectious diseases in places where their existence was never thought about it. We will present 3 samples of such entities
Non-neoplastic cutaneous manifestations of HTLV-1 are almost unhear of outside the endemic countries, such as Jamaica, Peru and Brazil. Since the original description of Infective Dermatitis (ID) by Sweet in Jamaica in 1961, took many years for medicine to make the connection between this rather particular form of eczema affecting children and the coexistence of an otherwise asymptomatic infection by the Human T cell Lymphotropic Virus type 1 (HTLV-1).
For non-dermatologists , eczema is quite a tricky concept ; pediatricians may be familiar with the most prevalent eczema on children , thus is , atopic dermatitis. When the first cases of infective dermatitis were identified in Lima, dermatologist were astounded: how could one missed such a particular type of eczema: their distribution on areas of the body such as the scalp and intertriginous areas, their tendency to be always covered by honey crusting, the complete resolution after the solitary administration of antibiotics , their tendency to recur after the cessation of therapy. ID is now known and recognized by many dermatologist in South America, and new countries now known they have the viral infection in their population because they have correctly identified the disease. In the last years, ID is been reported in Africa, and most likely many countries in that continent will start identifying the disease as a clue to the presence of the virus.
An interesting topic regarding emerging infectious diseases is the relationship between gastronomic preferences and the surge of parasitic disease. A few years ago, only few countries in the world would have a preference for eating raw fish , either as sushi, sashimi or ceviche. The habit of eating raw fish have expanded to many places around the world; add to that the increasing business and tourist traveling through continents; it is likely that you may encounter a patient with a migratory cellulitis and blood eosinophilia .The diagnosis of gnathostomiasis , from the clinical picture to the histology and the behavior of the parasite to oral therapy will also be reviewed.
Last but not least, on the basis of the large experience on the infection by free living amebas, and more specifically, *Balamuthia mandrillaris*, that the group at Universidad Peruana Cayetano Heredia has, we will review the clinical findings (large asymptomatic plaque on the face or knee), the histological findings (ill defined granulomas with abundant giant cells in the skin biopsy) and the particular experience we have regarding treatment, including the current experience the group has with the combined administration of fluconazole, albendazole and miltefosin.
Nowadays, in our world of today , the word exotic has lost a big chunk of its meaning. You never known what will come up to your clinic tomorrow.

Final Abstract Number: 53.001
Session: Plenary VI - New Frontiers in our Approaches to Antimicrobial Resistance
Date: Sunday, March 4, 2018
Time: 14:00-14:45
Room: Libertador B
Type: Invited Presentation

Plenary VI: New frontiers in our approaches to antimicrobial resistance
A. H. Holmes
Imperial College London and Imperial College Healthcare NHS trust, London, United Kingdom

No abstract received!

Final Abstract Number: 54.001
Session: Point of Care Technology for Infectious Diseases Management and Applications in Low- and Middle-Income Countries
Date: Sunday, March 4, 2018
Time: 15:15-16:45
Room: Libertador A
Type: Invited Presentation

Individualized approaches to infection management
T. M. Rawson
Imperial College London, London, United Kingdom

Abstract text: Artificial intelligence and biosensor technology may facilitate truly individualised approaches to antimicrobial selection and dose optimisation. However, the technology must be applicable to all healthcare situations whether high or low/middle income.
Artificial intelligence provides the potential to support the move from guideline driven decision making to more individualised antimicrobial prescribing, through better utilisation of available data. These work on the basis that the majority of antimicrobial prescribing is done by individuals who are not experts in infection management and often have a limited understanding of antimicrobials, including the evidence around antimicrobial resistance. Therefore, if machines can be trained to act as experts, perhaps these can help to bridge the observed gaps in knowledge and understanding. Different machine learning tools have been incorporated into a web-based user interface that directly links to electronic health records within the hospital. This allows data to be presented to the end user in line with their normal decision-making pathway, whilst also providing individualised prescribing recommendations using a case-based-reasoning approach. Supervised machine learning algorithms have been trained on over 200,000 patient profiles to predict the likelihood of microbiology sample growth and most likely site of culture growth to further support decision making. This work focuses on limiting the number of variables required to allow systems to easily adapt to a range of situations.
Equally as important as antimicrobial selection is optimisation of the dose of antimicrobial to maximise bacterial killing, whilst minimising the harmful consequences of antimicrobial therapy. This includes toxicity and development of antimicrobial resistance. With increasing evidence for the wide pharmacokinetic variability across most classes of antimicrobial, the role of dose optimisation tools is now being explored. However, a major barrier to these interventions is the challenging nature of drug monitoring. Currently available therapeutic drug monitoring protocols provide sporadic data with dosing often altered in line with population estimates for optimal concentrations. With development of minimally invasive biosensor technology we may now be able to facilitate real-time monitoring of changing antimicrobial concentrations. This technology is now being translated into low-cost, low energy, point of care devices for deployment and testing in challenging clinical circumstances.

Final Abstract Number: 54.002
Session: Point of Care Technology for Infectious Diseases Management and Applications in Low- and Middle-Income Countries
Date: Sunday, March 4, 2018
Time: 15:15-16:45
Room: Libertador A
Type: Invited Presentation

Advances in point of care testing technologies
J. Rodriguez Manzano
Imperial college london, London, United Kingdom

Abstract text: Available rapid diagnostic tests (such as immunoassays) are qualitative, have limited sensitivity and generally cannot provide subtype information. Molecular methods are quantitative and can give the high specificity, sensitivity and speed required, but existing efforts using fluorescence techniques are too expensive, require labelling, suffer from inherent noise, and cannot be miniaturized into a small form factor device. There is an urgent need for connected, rapid, portable, ultra-sensitive platforms to be developed for infectious diseases and antimicrobial resistance (AMR) at the point of care (POC) that can be deployed in the community, in homes and in doctors' offices. The importance of diagnostics in the battle against AMR has been recognised in the challenge set by the £10M Longitude Prize and the $20M Prize proposed by the US' National Institutes of Health and the Biomedical Advanced Research and Development Authority. Both aiming to develop a new rapid, POC diagnostic test which would allow clinicians to make better informed decisions, thereby conserving antibiotics and limiting their use to those cases where they would be efficacious. The Centre for Bio-Inspired Technology at Imperial College London has pioneered the use of microhip technology as molecular biosensors for lab-on-a-chip diagnostics technology, which represents an effective and affordable alternative to conventional optical-based sensors. This microchip technology provides the capability for nucleic acid detection through pH changes produced during amplification reactions such as LAMP and PCR below 30min, and have already been demonstrated in full genome sequencing and label free point-of-care diagnostics. Our aim now is to evolve this technology into a portable and connected diagnostic test which will tackle the challenge of infectious diseases and AMR.

Final Abstract Number: 54.003
Session: Point of Care Technology for Infectious Diseases Management and Applications in Low- and Middle-Income Countries
Date: Sunday, March 4, 2018
Time: 15:15-16:45
Room: Libertador A
Type: Invited Presentation

Point-of-care diagnostics for Tuberculosis: Where are we?
M. E. Balcells
Santiago, Chile

Abstract text: Tuberculosis (TB) constitutes a substantial burden on global health, particularly in developing countries. Estimates indicate that only 60% of TB cases are detected and notified, and therefore earlier finding of the missing TB and MDR-TB cases is one of the key WHO priorities to achieve global targets for TB elimination. For that purpose, faster, reliable and simple point-of-care triage and diagnostic tools are urgently required, including non-sputum based tests given the large proportion of patients unable to produce sputum or having extrapulmonary disease. In the last decade, an explosive number of new potential biomarkers have emerged, although only a few of them have reached the requirements for validation. This session will address the most recent and promissory studies reporting on new TB diagnostic tests suitable for point-of-care, that may impact on patient care.

Final Abstract Number: 55.001
Session: Dengue, Chikungunya and Yellow Fever
Date: Sunday, March 4, 2018
Time: 15:15-16:45
Room: Libertador C
Type: Invited Presentation

The human antibody response in Dengue and Zika virus infection

G. Screaton
Univ. of Oxford, Oxfprd, United Kingdom

Abstract text: Dengue is a mosquito borne virus infection occurring in tropical and subtropical countries. There are estimated to be around 400 million infections annually of which approximately one quarter are clinically apparent. The majority of these result in a self-limited, but non the less unpleasant febrile illness, dengue fever. 1-5% of infections lead to a more severe disease, dengue haemorrhagic fever, which is characterized by a severe vascular leak, hypovolaemia and in extreme cases shock and haemorrhage. Dengue exists as four highly divergent serotypes differing in sequence by some 30-35%; infection with one serotype does not provide protection against the other three. In endemic areas serotypes frequently co-circulate and repeat infections are common. Interestingly, severe disease is much more common in secondary as opposed to primary infections, implying a role of the acquired immune system in disease pathogenesis. Understanding this immune enhancement of disease is crucial for the design of safe and effective vaccines. Through clinical collaborations in Thailand and Vietnam we have been studying the immune response to dengue in cohorts of infected children. We will describe the antibody response to the two virion surface glycoproteins prM and E and discuss the E dimer epitope (EDE), a novel site bridging the 90 basic head to tail envelope dimers making up the virion surface and also crossreacts against Zika virus.

Final Abstract Number: 55.002
Session: Dengue, Chikungunya and Yellow Fever
Date: Sunday, March 4, 2018
Time: 15:15-16:45
Room: Libertador C
Type: Invited Presentation

Drivers of spread of Aedes aegypti-borne infections in Latin America
J. Torres
Tropical Medicine Institute, Caracas, Venezuela

Abstract text: While environmental conditions and vector behavior shape the potential distribution and magnitude of *Aedes*-borne diseases, socioeconomic and demographic factors determine the level of human exposure and the recognized transmission risk. As in other mosquito-borne diseases, variation in wealth has been linked to human exposure in multiple disease systems across resource-wealthy and resource-poor nations. This is partially explained by changes in mosquito breeding habitats around the home, land cover, access to public health infrastructure, and access to education and to intervention strategies. The population structure can also influence exposure to vector-borne disease via age, sex, or even pregnancy-related differences in human behavior. Unfortunately, current distribution maps highlighting the transmission risk of DENV, CHIKV and ZIKV, fail to incorporate these relevant factors.
In addition to the existing drivers of vector-borne diseases, such as seasonal weather variation, socioeconomic status, vector control programs and environmental changes, climate change and variability are highly likely to influence their epidemiological behavior. Such effects are likely to be expressed in many ways, from short-term epidemics to long-term gradual changes in disease trends. Although the contribution of all the factors affecting disease transmission and clinical outcomes should be taken into account, there are currently few available data that provide such information; therefore, the fraction of changes in vector-borne diseases attributable to climate change remains uncertain. Whereas the impact of climate variability on vector-borne diseases is relatively easy to detect, this is not the case of climate change because of the slow rate of change.
As climate change has far-reaching consequences that go beyond health, it is a factor that should be rated high among those that affect human health and survival. In some regions, such as South America, *A. aegypti* may be sensitive to climate change and greater efforts and resources will be required to contain the expected change in disease epidemiology. Furthermore, climate variability, unlike any other epidemiological factor, has the potential to precipitate simultaneously multiple disease epidemics and other types of disasters.
Thus, predicting the risk of *Aedes*-borne diseases transmission in novel regions would require understanding the relative importance of the environmental and iological determinants of transmission potential and the interactions among them and the socioeconomic and demographic predictors of human exposure

Final Abstract Number: 55.003
Session: Dengue, Chikungunya and Yellow Fever
Date: Sunday, March 4, 2018
Time: 15:15-16:45
Room: Libertador C
Type: Invited Presentation

Yellow fever
P. Vasconcelos
Ananindeua, Brazil

No abstract received!

Final Abstract Number: 56.001
Session: Malaria - Hot Topics
Date: Sunday, March 4, 2018
Time: 15:15-16:45
Room: La Pampa
Type: Invited Presentation

Plasmodium vivax: It is complicated
A. Siqueira
Fiocruz, Brazil

Abstract text: With malaria elimination back in the agenda there has been increasing interest regarding *Plasmodium vivax* infection. Apart from the dismissal of the benign status previously attributed to this parasite – due to the description of associated clinical complications from several endemic areas – this infection presents significant challenges for treatment and control. Being the second most common human malaria parasite, *P. vivax* shares with *P. ovale* the capability of causing relapses through the activation of dormant forms, the hypnozoites. This results in a naturally infected individual to be subjected to several episodes of malaria even if not exposed to further infective bites, resulting in a considerable burden and rendering additional difficulty in controlling its transmission. Primaquine is the only licensed drug with anti-relapse activity and its use faces many challenges, from the long course it must be administered to the risk of severe haemolysis in glucose-6-phosphate dehydrogenase deficient individuals. Many factors impair the adequate measurement of primaquine effectiveness; from the lack of definition of primaquine resistance to the difficulty in differentiate relapses from recrudescence (due to resistance to the schizontocidal drug) and reinfections. Recent developments, however, have added new perspectives in the management of *P. vivax* relapses. The first is the association of CYP2D6 host phenotypes that result in slow primaquine metabolisation with higher risk of relapses, shedding light regarding the mode of action and clarity over the interpretation of treatment failures. The results of the Tafenoquine trials, an 8-aminoquinoleine, with long half-life is also a major development, as it will allow for *P. vivax* to be treated in three days instead of the WHO-recommended 14-days regimen. These topics will be addressed under the light of the most recent studies related to *P. vivax* management.

Final Abstract Number: 56.002
Session: Malaria - Hot Topics
Date: Sunday, March 4, 2018
Time: 15:15-16:45
Room: La Pampa
Type: Invited Presentation

Update on the management of multidrug resistant falciparum Malaria

E. Ashley
Myanmar Oxford Clinical Research Unit, Yangon, Myanmar

Abstract text: Rising numbers of failures of the frontline artemisinin-based combination therapies (ACTs) in Southeast Asia threaten regional and global malaria control. While there are a number of novel antimalarials in development, they are still some years away from being registered. New ways of using existing drugs are being explored to fill the gap before new treatments become available. Prolonging the course of existing ACTs has been evaluated in a limited number of patients with some success, either by adding on extra doses of the combination treatments, or supplementing the course with extra doses of artesunate monotherapy. A newer approach, evaluated in a large multicentre trial in Asia and Africa, has capitalised on the apparently opposite selection pressures exerted on parasite populations by a) amodiaquine and lumefantrine, or b) piperaquine and mefloquine, by adding a third drug to existing fixed dose artemisinin based combinations. These triple artemisinin based combinations (TACTs) could buy time for malaria patients in Southeast Asia, but their potential role to delay the emergence of artemisinin resistance and preserve these precious drugs in high burden countries in sub-Saharan Africa should also be considered.
The impact of artemisinin resistance on the efficacy of parenteral artesunate to treat severe malaria is still unclear since severe malaria case numbers in areas with high levels of resistance remain low. Studies are needed to answer this question.

Final Abstract Number: 56.003
Session: Malaria - Hot Topics
Date: Sunday, March 4, 2018
Time: 15:15-16:45
Room: La Pampa
Type: Invited Presentation

Correlates of protection from Controlled Human Malaria Infections (CHMI) in semi-immune Kenyan adults

F. Osier
KEMRI, Nairobi, Kenya

Abstract text: The need for a highly effective malaria vaccine remains urgent but the correlates of protection in humans are still poorly defined. Controlled human malaria infections (CHMI) provide a rapid means to compare immune responses between vaccinees with variable parasite growth post-challenge. This strategy may enable the identification of antigens that could be prioritized for vaccine development. We aim to use the CHMI platform as a new tool for the identification of correlates of protection against malaria. To achieve this we are screening 2000 volunteers to identify 200 participants with a range of antibody responses to malaria antigens. These 200 volunteers will undergo CHMI by direct venous inoculation (DVI) with aseptic, purified, cryopreserved *Plasmodium falciparum* (Pf) sporozoites (Sanaria® PfSPZ Challenge), and then admitted to a facility to be closely monitored clinically and for emergence of blood stage parasitaemia by PCR. Pre-CHMI antibodies will be screened using a newly developed custom protein microarray (KILChip v1.0) containing ~120 Pf merozoite antigens to investigate how they affect the outcome of CHMI. To date 129 Kenyan adults have undergone CHMI. Parasite growth rates have varied from the log-linear pattern seen previously in malaria naïve volunteers, through negative growth rates following emergence from the liver, to undetectable parasitaemia throughout monitoring. Pre-CHMI antibody levels against total parasite schizont extract and multiple merozoite antigens have varied from low or undetectable through intermediate to high. Analyses of these data are ongoing and preliminary outcomes with regards to the antibody correlates of protection will be presented.