

Final Abstract Number: 05.001

Session: Oral Presentations: Public Health & Hackathon Presentations

Date: Friday, March 2, 2018

Time: 10:15-12:15

Room: Retiro A

Type: Oral Presentation

Outbreak investigation of Crimean Congo Hemorrhagic Fever Balochistan Province, Pakistan, 2016

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Background: Purpose of investigation was to investigate cases, assess risk factors and recommend preventive measures.

Crimean Congo hemorrhagic fever (CCHF) is a tick-borne viral severe hemorrhagic disease. It is transmitted to humans through bite of infected ticks or by direct contact with viremic animals or humans. Clustering of cases in Ghaus Abad Quetta was reported through Media. Three member team constituted to investigate

Methods & Materials: Case-control study was conducted in Quetta from January to September 2016. World Health Organization standard case definition was used to identify suspected and confirmed cases. Active case search was conducted in health facilities and community. Matched for age and sex controls were taken with a ratio of 1:2. Data was collected through review of illness history and hospital records and interviews conducted of cases, Medical Superintendent, doctors and nurses concerned. Active contact tracing was undertaken among family, friends and concerned medical staff. Data were analyzed using EpiInfo® version 7.0

Results: 76 cases were identified. 75 % (n=57) cases were from Baluchistan and 25 % (n=19) from Qandahar Afghanistan. Majority of cases were male 71 % (n=54). Mean age 29 years with range 9-86 years. PCR of 84 % (n=64) cases was done and 46 % (n=35) were CCHF Positive. CFR was 18% (14). Statistical associations between disease occurrence and following risk factors were found; slaughtering (*OR 34.35; 95%CI: 4.63-254.59; p < 0.05*), handling meat (*OR 2.0; 95%CI: 1.67-3.73; p < 0.05*), animal waste handling (*OR 11.4; 95%CI 5.79-22.75; p < 0.05*), contact with case (*OR 6.6; 95% CI: 3.56-12.32; p < 0.05*) and farming animals (*OR 7.1; 95%CI 3.82-13.38; p < 0.05*).

Conclusion: Animal contact was most probable cause of outbreak. Close coordination with livestock department is recommended to disinfect animals in province. Awareness sessions regarding animal handling, CCHF prevention and control at each district level planned and implemented. Provision of PCR facility, PPE for medical staff and attendants and other latest equipment at Isolation ward were recommended.

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Date: Friday, March 2, 2018

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High impact of influenza on hospitalisation rates in children with a range of chronic lung diseases: A population-based study

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Background: The impact of influenza is significant in people with certain chronic conditions, yet, there remains a dearth of information on its contribution to burden of disease in children with chronic lung diseases (CLDs). Estimates of influenza burden among children with CLDs are required for baseline data, to monitor burden of disease over time and to evaluate the effectiveness of influenza vaccination program.

Methods & Materials: We performed a retrospective cohort study using population-based linked data for all children born in New South Wales between 2001 and 2010 followed until December 31st 2011. The cohort was divided into five mutually exclusive groups, children with: i) asthma ii) bronchopulmonary dysplasia (BPD) iii) cystic fibrosis (CF), iv) other congenital lung disorders including bronchiectasis, diaphragmatic hernia, trachea-oesophageal fistula, tracheomalacia, congenital malformation of lung and respiratory system and Kartagener's syndrome; and v) all other children without CLDs. The primary outcome was any episode of influenza-associated hospitalisation (ICD codes J.09-J11). Adjusted incidence rates for influenza-associated hospitalisation were calculated for 2001-2011 using Poisson estimation.

Results: Our cohort comprised 888,154 children born between 2001 – 2010, 11,050 (1.24%) had one of the CLDs. The adjusted incidence/1000 child-years (95% CI) of influenza-associated hospitalisation in children with CLD was 3.61 (2.38 – 4.84) and for all other children without CLD was 0.66 (0.45 – 0.87). During 2001 – 2011, the incidence of influenza-associated hospitalisation in children with CLD ranged between 0.20 – 20.66/1000 child-years; the incidence was highest for children aged <2 years of age. The incidence/1000 child – years (95% CI) of influenza-associated hospitalization in children with asthma was 1.1 (0.63 – 1.58), BPD was 5.29 (3.16 – 7.41), CF was 5.44 (1.21 – 9.67) and other congenital lung diseases was 6.42 (4.48 – 8.36). The relative risk of influenza-associated hospitalisation was highest for children with other congenital lung disease compared to children without CLDs and was 10.61 (95% CI 7.94 – 14.18).

Conclusion: This large population-based study suggest a significant burden of influenza in children with a range of CLDs. Further research investigating the influenza vaccine uptake and effectiveness in these children will help design interventions to reduce the disease burden.

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Joint external evaluation of IHR core capacities of the Islamic Republic of Pakistan, 2016

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Background: The Joint External Evaluation (JEE), a voluntary, collaborative process to assess country's capacity under International Health Regulations (IHR) to prevent, detect, and respond to public health threats. Pakistan was the first country in the region to volunteer for JEE. The objectives were to measure country- status in building the necessary capacities to prevent, detect, and respond to infectious disease threats and to establish a baseline measurement of capacities & capabilities.

Methods & Materials: A joint assessment of IHR & Global Health Security Agenda (GHSA) technical core-capacities was conducted during April 27, through May 6, 2016, using GHSA-IHR-JEE tool. The tool covering 19 technical areas, ranging from 1-5 ((1 indicates no implementation; 5 indicates implementation) scoring with color coding. The evaluation was mostly descriptive and qualitative and completed in two stages: self-evaluation by the country and in-country evaluation by multi-sectoral international team. Assessments were based on peer-to-peer model included site visits and discussions with representatives from all relevant sectors.

Results: Legislation, Reporting, Risk-Communication, Points of Entry, National Laboratory System, Chemical Events, Food-Safety, Biosafety-Biosecurity and Immunization, all scored as 2/5. Domestic legislation, policies, administrative arrangements were adjusted/aligned (scored 3/5). Functional mechanism for Coordination, Communication and Advocacy is established (scored as 3/5). Linking Public Health and Security Authorities, Zoonotic disease surveillance and response was scored as 3/5. Indicator/event based surveillance was scored as 3/5 while electronic reporting, data analysis and syndromic surveillance scored 2/5. Workforce Development, human resources availability and existence of epidemiology trainings were scored as 3/5 while workforce strategy as 2/5. Preparedness and Antimicrobial Resistance detection, surveillance, stewardship and Infection control was scored as 1/5. Emergency Response Operations scored 3/5 while Case management & operating procedures/plans as 2/5. Medical Countermeasures and Personnel Deployment scored 4/5 and Radiation Emergencies scored 5/5.

Conclusion: Five major cross-cutting themes emerged from review of 19 areas. This evaluations provided an opportunity to identify strengths & weaknesses, and to prioritize opportunities for preparedness, detection & response, capacity building and resources allocating. Based on the JEE recommendations, Pakistan has developed five year costed National Action Plan aiming to develop a strong public health system with the standards and competencies required for implementing IHR.

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Human-environment interactions impact *Aedes aegypti* abundance in an urban desert setting

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Background: The Sonoran Desert of southwestern North America is naturally hostile to *Aedes aegypti* mosquitoes, but their populations have thrived in Arizona cities since initially reported over two decades ago. With growing concern about the emergence and spread of *Aedes*-borne diseases like Zika, chikungunya, and dengue, there is a pressing need to understand the factors that promote *Ae. aegypti* survival and abundance. Though well studied in more tropical climates, little is known about these factors in arid regions. This study aimed to investigate the multi-level geographic factors that enable *Ae. aegypti* abundance in desert cities.

Methods & Materials: The Maricopa County Environmental Services Vector Control Division collects mosquitoes weekly from ~700 CO₂-baited Encephalitis Vector Survey (EVS) traps distributed throughout Maricopa County, which includes the Phoenix metropolitan area. Weekly counts were reported from each year 2014 to 2016. We used 1m-resolution satellite images from the National Agricultural Imagery Program from 2013 and 2015 to classify microgeographic differences in land cover. We assessed land surface temperature, rainfall, normalized difference vegetation index (NDVI), land cover/use, and human demographic data from the U.S. Census as potential predictors of the presence and abundance of adult *Ae. aegypti* in each trap.

Results: A total of 83,750 female adult *Ae. aegypti* mosquitoes were captured between 2014 and 2016. High-density traps consistently tended to be located in the north-central and southeastern parts of the county. The percent of positive traps and the average number of mosquitoes per trap peaked in October each year, following annual rains from July-September. Nearly all human socioeconomic status variables were inversely associated with the presence of *Ae. aegypti* mosquitoes in crude logistic regression, though the direction and strength of the associations with mosquito counts from negative binomial regression were less consistent. Further model fitting and analyses of geospatial relationships are underway.

Conclusion: Desert urban residents may be susceptible to disease outbreaks where *Ae. aegypti* mosquitoes are abundant. Better knowledge of factors promoting mosquito survival and distribution in these settings will support both long- and short-term control efforts to prevent epidemic and endemic vector-borne disease transmission in arid habitats.

Final Abstract Number: 16.001

Session: Oral Presentations: Hot Topics

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SEAE: Southeast Asia Encephalitis Project

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Background: Meningoencephalitis (ME) can be severe in children or adults, especially in tropical and low-resource settings. Despite extensive laboratory testing, majority of patients remain undiagnosed. Better understanding of ME causes is of crucial public health importance, in order to better inform immunization policies and guide clinical management.

Methods & Materials: A clinical study is conducted in four referral hospitals in Hanoi, Phnom Penh, Vientiane and Yangon. Between July 2013 and May 2017, patients with clinical acute encephalitis syndrome were prospectively enrolled. Laboratory diagnostics consisted of molecular and serological tests targeting ~70 ME-causative pathogens. Only pathogens identified in CSF or blood were considered as a possible etiology.

Results: Of 617 enrolled patients, 57% were male. Median age was 6.3 [0-76] years. When performed, MRI was abnormal in 98% of patients. No etiology was identified in 43% cases. Japanese encephalitis virus, *M. tuberculosis* and Human herpes simplex virus 1 were the most common pathogens detected, identified in 33%, 5% and 4% cases respectively.. Outcome was fatal in 16% and neurological sequelae occurred in 49% of patients. Focal neurological signs and shortness of breath on admission were significantly associated with death ($p < 0.05$). Of identified etiologies, 50% are preventable and 8% curable.

Conclusion: Encephalitis in the Mekong region is associated with high morbidity and mortality. Despite extensive laboratory testing, a little under half of the patients remain undiagnosed. Preventable or curative therapies exist for the most frequently identified causative pathogens. CSF and Serum from a selection of undiagnosed cases are submitted into the pathogen discovery program. This research project has strongly capacitated hospital clinical teams and labs.

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Meta-Analysis of predictive symptoms for Ebola virus disease in West Africa

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Background: One of the leading challenges in the West African Ebola virus disease (EVD) outbreak in 2014/15 was how best to quickly identify patients with Ebola, separating them from those without the disease. This meta-analysis aggregates all available data on symptom predictors for Ebola. This will enable quicker diagnosis of probable cases in resource-limited settings, and earlier stratification of patients as high-risk, permitting appropriate clinical and public health precautions to be taken.

Methods & Materials: Identification of relevant existing literature was performed by an online search in MEDLINE and EMBASE for studies published from 1st January 1946 to 11th September 2017. The MESH headings (keywords) included “ebola” and “symptom*” or “clinical” or “predict*” or “suspect*”. The initial search on MEDLINE and EMBASE produced 4380 results. After exclusion criteria and further review, there were seven papers that met our criteria.

For each predictive symptom investigated, EVD and non-EVD patients were aggregated across studies. We then used a random effects meta-analysis model in STATA. This provided a pooled odds ratio along with 95% confidence intervals and a p-value, for each symptom; with detailed forest plots.

Results: Fatigue was the most predictive for Ebola (OR 3.29, 95% CI 1.89-5.71), with anorexia (OR 3.11, 95% CI 1.40-6.94), confusion (OR 3.04, 95% CI 2.18-4.23) diarrhoea (OR 3.02, 95% CI 1.89-4.85), conjunctivitis (OR 2.99, 95% CI 1.77-5.04), vomiting (OR 2.89, 95% CI 1.79-4.67), fever (OR 2.37, 95% CI 1.33-4.21), hiccups (OR 2.25, 95% CI 1.23-4.08) and dysphagia (OR 2.22, 95% CI 1.18-4.18) all more than twice as likely in Ebola cases. Chest pain, bleeding, and sore throat were not statistically significant predictors of Ebola.

Conclusion: Existing literature fails to provide a unified position on the most predictive symptoms for Ebola. This analysis demonstrates that late presenting symptoms including confusion, anorexia, conjunctivitis and hiccups are predictive for Ebola. However, early non-specific symptoms of fatigue, fever, diarrhoea, vomiting were also highly predictive. These findings will aid effective future clinical assessment, risk stratification tools and emergency epidemic response.

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Impact of 4% deltamethrin-impregnated dog collars on the incidence of human visceral leishmaniasis

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Background: In Brazil, visceral leishmaniasis (VL) is caused by the protozoan parasite *Leishmania infantum*, primarily transmitted by the sand fly *Lutzomyia longipalpis* with the dog as the main urban reservoir. This study aims to evaluate the effectiveness of 4% deltamethrin-impregnated dog collars (DMC) on the incidence of human visceral leishmaniasis (HVL).

Methods & Materials: This is a cluster randomized trial carried out in 6 municipalities in Brazil. In each municipality, two areas were randomly allocated to either (1) culling seropositive dogs + residual insecticide spraying (control area - CA) or (2) culling seropositive dogs + residual insecticide spraying + DMC fitted to dogs every six months during two years (intervention area - IA). The study started in the second semester of 2012. Cases of HVL (n=1167) occurring from 2008 to 2015 were identified from the Brazilian Reportable Diseases Information System and georeferenced to control and intervention areas of each municipality. HVL cases from 2008 to 2012 were considered as occurring in the "pre-intervention" period, and those from 2013-2015 occurring in the "post-intervention" period. We used a mixed-effects Poisson regression model to estimate the effectiveness of the intervention comparing the changes from pre to post intervention periods in the control and intervention areas.

Results: There was a statistically significant reduction in the incidence of HVL in both areas comparing the pre and post-intervention periods. However, the reduction was significantly higher in the intervention area yielding an effectiveness estimate of the DMC of 27% (IC95% 2%-46%, p=0.036).

Conclusion: The use of DMC was associated with a reduction of 27% in the incidence of HVL, suggesting that DMC could be used as an additional strategy for controlling visceral leishmaniasis in Brazil. However, since the estimate of the effectiveness is relatively small and DMC are expensive, a cost-effectiveness analysis should be performed before recommending a large scale introduction of such preventive device.

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Sepsis prevention in neonates in Zambia study: Impact of an infection prevention bundle on neonatal sepsis and mortality

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Background: Sepsis is a major cause of mortality in neonates in sub-Saharan Africa. Bloodstream infections (BSIs), the most common hospital-associated infections in neonates, occur more frequently in resource-limited countries than in industrialized countries and contribute to many in-hospital neonatal deaths. We assessed the efficacy of a novel bundle of low-cost infection prevention and control (IPC) measures targeted to known and suspected risk factors for neonatal hospital-associated BSI. We studied the impact of this intervention bundle on BSI and mortality in a neonatal intensive care unit (NICU) at the University Teaching Hospital (UTH) in Lusaka, Zambia.

Methods & Materials: This prospective observational cohort study of neonates who survived >3 days after NICU admission consisted of a six-month baseline period ("baseline"), two months during which interventions were introduced ("implementation"), and 10 months of intervention assessment ("intervention"). The intervention bundle consisted of IPC training, introduction of alcohol-based hand wash, weekly bathing of neonates >1.5 kg with 2% chlorhexidine, targeted environmental cleaning, and SMS reminders of IPC messages. The outcomes were all-cause neonatal mortality (primary) and suspected sepsis and laboratory-confirmed BSIs (secondary).

Results: From September 2015 through March 2017, we enrolled 2669 eligible neonates. Median maternal age, maternal HIV status, and newborn characteristics were similar in the baseline, implementation, and intervention periods (with the exception of birth weight). Half of neonates had one or more episodes of sepsis, including 549 (41%) who had a positive blood culture. *Klebsiella pneumoniae*, predominantly ESBL-producing, was most common (n=289, 70%); possible contaminants were isolated in most other positive cultures (n=140, 25.5%). All-cause neonatal mortality was lower during the intervention (18.0%) than the baseline period (23.6%), and similar reductions in mortality were seen in all birthweight categories. The incidence density rates for suspected sepsis and BSI with a pathogen were significantly lower in the intervention relative to baseline periods for all birth weight categories, except babies weighing <1 kg.

Conclusion: This bundle of infection prevention measures resulted in reductions in all-cause neonatal mortality, suspected sepsis, and BSI with pathogens. This combination of low-cost measures has potential to be applied in other contexts where hospital-associated sepsis is a major contributor to neonatal mortality.

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Type: Oral Presentation

Genotyping and Sero-Virological characterization of Hepatitis B Virus in blood donors, Southern Ethiopia

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Background: Hepatitis B virus (HBV) prevalence is highest in Sub-Saharan Africa including Ethiopia. HBV genotypes have distinct geographic distributions, also play a role in course of infection and treatment management. However, in Ethiopia there is paucity of information about distribution of HBV genotypes. This study was done to determine genotype, mutation and sero-virological profiles of HBV isolates in Southern Ethiopia.

Methods & Materials: Cross-sectional study was conducted on a total of 103 HBsAg sero-positive samples collected from blood donors visiting Hawassa Blood Bank in May to September 2016. HBV serological markers and biochemical assays were done. Serum viral load was measured using quantitative real-time PCR. Partial HBV S-gene was amplified with nested PCR and sequenced. Bioinformatics tools were utilized to determine genotypes, serotypes and presence of mutations.

Results: Of 103 HBsAg reactive serum samples, HBeAg (14.6%) and HBeAb (70.9%) were detected. The median serum ALT was 21(17-29) IU/L. Ninety-eight samples gave detectable viral load with a median of 3.46 (2.62-4.82) log IU/ml. Eighty five isolates were successfully amplified, sequenced and genotyped into 58 (68.2%) genotype A (HBV/A) and 27 (31.8%) genotype D (HBV/D). HBV serotypes found were *adw2* (74.1%), *ayw2* (24.7%), and *ayw3* (1.2%). In twenty-four (28.2%) samples mutations in the major hydrophilic region (MHR) were observed. Donors infected with HBV/A had higher viral load and more frequent MHR mutation than those infected with HBV/D.

Conclusion: This study illustrated distribution of HBV genotype A and D among blood donors in southern Ethiopia. It also demonstrated occurrence HBV variants that may influence clinical aspects of HBV infection. The study contributes in narrowing the existing gap of HBV molecular study in Ethiopia.

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Type: Electronic/Moderated Poster Presentation

Functional phenotype and role of resident and recruited bone marrow derived exudate macrophages in influenza virus-induced lung injury and repair

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Background: Alveolar macrophages (AM) play an important role in host defense and tissue homeostasis. Even though macrophage polarization has been extensively studied in different disease models, the generation of macrophage phenotypes with specific functional profiles, their lineage relation and particular roles during pathogen-induced acute lung injury (ALI), resolution and tissue repair has not been convincingly elucidated.

Methods & Materials: C57BL/6 mice were infected with influenza virus (IV) PR8 by intra-tracheal (i.t) application. BAL and lungs were harvested during the acute and resolution and repair phases of infection. The polarization profiles of different AM subsets were characterized by FACS during the course of infection. Bone marrow transplantation (BMT) experiments using CD45.2/1 mice were performed to demonstrate lineage-relation between recruited and resident macrophages. Adoptive transfer of BMM with diverse polarization patterns (isolated from IV-challenged wild type mice) into the lungs of IV-infected CCR2^{-/-} mice (lacking BMM recruitment) was performed to address their functional phenotypes during injury, resolution and lung repair. Gene expression profiles in different BMM phenotypes were screened by genome wide transcriptome analysis.

Results: Our flow cytometry analyses demonstrated that alveolar and interstitial BMM show an M1 phenotype in the acute phase and shift to an M2 phenotype in the late phase of infection. BMT experiments revealed that M2 BMM substantially contributed to replenishment of the depleted resident alveolar macrophage (rAM) pool, indicating a high functional plasticity of BMM recruited after infection. In addition, M1 and M2BMM adoptive transfer experiments showed that intra-tracheal transferred M1BMM increased alveolar barrier dysfunction whereas M2BMM preserved the rAM pool and induced alveolar epithelial cell proliferation and barrier repair. Further, our genome-wide transcriptome analysis on flow-sorted M1/M2BMM showed significant up-regulation of a distinct set of growth factors, repair mediators and pro-survival genes in M2 when compared with M1BMM, some of which were found to be central mediators of the beneficial functions of M2BMM in vivo.

Conclusion: These data support that mediators produced by M2BMM contribute to replenishment and preservation of the rAM pool and improved lung barrier function. In summary, our data demonstrate high functional plasticity of BMM during IV pneumonia and highlight these cells as targets for therapeutic approaches.

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Type: Oral Presentation

Detection of Cytomegalovirus in pulmonary samples of critically ill, immunocompetent patients using a real time PCR based method: Preliminary findings of a prospective study

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Background: Human cytomegalovirus (CMV) infection and negative clinical outcome are associated in patients with immunosuppression. However, the association between CMV and negative outcomes in immunocompetent-critically ill patients is controversial. There is data which suggests that CMV reactivation in critically ill patients is linked to adverse outcomes. One of the proposed mechanisms for this possible adverse outcome is CMV direct lung injury.

We aimed to find the frequency of CMV reactivation in pulmonary samples from non-immunosuppressed patients admitted to the intensive care unit (ICU) in a reference hospital.

Methods & Materials: We prospectively detected CMV in pulmonary samples by real-time polymerase chain reaction by using a commercial assay (Cat. Number CMVDNAQT.2G, Diapro, Italy) in a cohort of 23 immunocompetent adults admitted to ICU at Hospital Luis Vernaza in Guayaquil, Ecuador during 2017. Personnel blinded to CMV results evaluated patients' clinical outcomes. Primary endpoints were death and ICU length of stay. In addition, associations among CMV reactivation and other clinical variables were assessed to look for risk factors by using Cox regression analysis, chi-square test, t-test and odds ratios.

Results: We recruited 23 patients. The male/female ratio was 1.88. There were 10 (43.5%) CMV positive cases whose age mean was 49.4 ± 21.9 , whereas CMV negative age mean was 56.5 ± 16.6 years old. Regarding ICU length of stay, there was no significant difference between patients with CMV positive and negative (p -value=0.9682); there were five (62.5%) CMV negative patients and three (37.5%) CMV positive cases who stayed at ICU longer than 30 days. The other endpoint studied was death. Four CMV negative patients versus three CMV positive patients (57.1% vs 42.9%, respectively) died throughout this study. Therefore, we did not find statistical association between death and CMV status. Furthermore, sex, age and transfusions did not affect significantly the probability of dying in this group of patients.

Conclusion: In the present work, we found a high frequency of pulmonary CMV detection in critically ill immunocompetent patients. However, CMV detection in pulmonary samples was not statistically associated with prolonged hospitalization or death in this cohort. We encourage to conduct a larger study to confirm these findings.

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The persistence of the immune response following Ebola infection in Liberian survivors of the 2014-2015 outbreak

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Background: Recent studies suggest that both humoral and cellular immunity are critical for recovery from Ebola virus (EBOV) infection in humans. However, the determinants of a protective immune profile are still not fully understood. We investigated the persistence of immune responses among Liberian Ebola virus disease (EVD) survivors infected during the 2014-2016 West African outbreak.

Methods & Materials: Serum and whole-blood samples were collected from 52 male and female EVD survivors (median age = 34.3 years (range 18.2-53.1), median time from acute EBOV infection 905 days (range 627-957)). Freshly collected blood samples were stimulated with inactivated EBOV, as well as with recombinant EBOV GP₁₋₁₄₉ or SUDV GP (GP₁₋₆₄₉). Cytokine expression levels were assessed by multiplex ELISA after in-vitro whole-blood stimulation. Specific Ebola IgG antibody levels in serum were determined by chemiluminescence ELISA and corresponding neutralization titers by, viral plaque-reduction neutralization (PRNT₈₀).

Results: Chemiluminescence ELISA against viral proteins: GP₁₋₆₄₉, NP, VP40 and VP30, revealed that 84.6% of the survivors tested positive for two or more of the viral proteins and had neutralizing activity in the sera, as demonstrated by PRNT₈₀. Cytokines measured with multiplex ELISA demonstrated significant increases in the levels of IL-1 β , IL-6, IL-8 and TNF α , but not IL-10 after stimulation with EBOV GP or inactivated EBOV, as compared with baseline unstimulated levels. There was no difference in any of the cytokine levels between survivors with and without demonstrated neutralizing capacity. Furthermore, humoral and cell-mediated cross reactivity to recombinant SUDV- GP₁₋₆₄₉ was observed (increase in IL-10, IL-1 β and IL-8), and some participant sera also demonstrated cross-reactivity to MARV GP.

Conclusion: In conclusion, both cellular and humoral immune responses in Ebola virus survivors demonstrate persistent recognition of relevant antigens, indicating immune memory. Furthermore, our findings of cross-reactive immune recognition suggest the potential of developing panfiloviral vaccines.

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Maternal immunity and antibodies to dengue can promote Zika virus-induced microcephaly in fetuses

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Background: Zika virus (ZIKV), a recently emerged flaviviral pathogen, has been linked to microcephaly in neonates. Yet, it is not understood why some fetuses develop severe microcephaly due to maternal ZIKV infection while others do not. The risk for ZIKV-induced microcephaly is greatest during the first trimester of pregnancy in humans, yet this alone cannot account for the varied presentation of microcephaly observed. Given the antigenic similarity between ZIKV and closely related dengue virus (DENV), combined with the substantial immunity to DENV in ZIKV target populations in recent outbreaks, we hypothesized that maternal antibodies against DENV were a risk factor for ZIKV-induced microcephaly.

Methods & Materials: Using immune-competent mice, we developed a mouse model of maternal to fetal transmission of ZIKV infection. Mother mice were infected on embryonic day 7 (E7), an equivalent fetal developmental stage to the first trimester of human pregnancy. Microcephaly was assessed in the fetuses by measuring head circumference and cortical thickness on E18, near full-term. ZIKV replication was measured in the mothers and fetuses by real-time quantitative PCR, negative-strand PCR, and immunohistochemistry for multiple ZIKV proteins. To test the influence of DENV immunity on fetal infection, mothers that were DENV immune or that were given the flavivirus cross-reactive monoclonal antibody 4G2 were infected with ZIKV and their fetuses were examined. Mice deficient in the neonatal Fc receptor (FcRN), which is known to carry maternal antibodies into the fetus, were used to determine its role in vertical transmission of ZIKV infection.

Results: We observed disproportionate microcephaly and reduced cortical thickness in the fetuses of ZIKV-infected mothers, which was greatly enhanced by DENV immunity or 4G2-injection of mother mice. ZIKV infection was also enhanced by DENV-specific antibodies both in fetuses and in the mothers' spleens. Use of FcRN-deficient mice showed that there was significantly increased trans-placental infection in an FcRN-dependent manner, leading to a greater incidence of microcephaly in the fetuses of DENV-immune mothers.

Conclusion: We show that DENV-specific antibodies in expectant mothers results in a severe microcephaly like-syndrome during ZIKV infection. Furthermore, fetal infection was promoted by FcRN. Our results raise caution since ZIKV epidemic regions are also endemic to DENV.

Final Abstract Number: 22.002

Session: Oral Presentations: Arboviruses

Date: Friday, March 2, 2018

Time: 17:00-18:00

Room: Retiro A

Type: Oral Presentation

Neurodevelopmental delays arising from in utero exposure to Zika virus in Salvador, Brazil

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Background: Since 2015, Brazil has experienced an unprecedented Zika virus outbreak. A devastating consequence of this viral infection is congenital Zika infection (CZI), which is transmitted from pregnant women to newborns. Most descriptions and publications regarding CZI focus on the clinical presentation of newborns and infants with microcephaly. Scarce information is available concerning children without microcephaly born from infected mothers.

During 2016, in the city of Salvador (Bahia, Brazil), a cross-sectional study enrolled 103 pregnant women who reported an exanthematous disease during pregnancy. Of these, 69 (67%) presented anti-Zika antibodies at the time of delivery. A total of 7 (6.8%) newborns were diagnosed with microcephaly, while 96 (93.2%) were classified as newborns without microcephaly.

Methods & Materials: In June 2017, we began a prospective follow-up of these infants without microcephaly exposed to Zika Virus *in utero* by evaluating neurodevelopment delays, performing neurological examinations and applying the Bayley Scales of Infant Development III (BSID-III), Mental Development Index (MDI) and Bayley-III cognitive and language scales. Auditory evaluations were performed by Otoacoustic emissions (OAE) and Brainstem Auditory Evoked Potential (BAEP).

Results: To date we have evaluated 18 infants, mean age 1.7 years. Of these, 55.6% are male and 61% were delivered by C-section. Anti-Zika IgG serology was positive in 75% and three (16.6%) presented positivity for Zika by PCR on urine samples within 24h of birth. Based on head circumference (HC) at time of birth, all were classified as normal by the Intergrowth scale and currently fall within normal HC percentiles. Cognitive delay was identified in five (33%) infants, language delay in four (26.6%) and motor delay in two (13.3%).

Conclusion: Our preliminary results indicate that *in utero* exposure to Zika virus could be associated with neurodevelopmental delay, even in children born without microcephaly at birth. Currently, only microcephalic infants are referred to specialized care, while normocephalic children are maintained in primary health care. We believe that all newborns exposed to Zika *in utero* should be referred to specialized centers for the early detection of neurodevelopmental delays and timely intervention.

Final Abstract Number: 22.003

Session: Oral Presentations: Arboviruses

Date: Friday, March 2, 2018

Time: 17:00-18:00

Room: Retiro A

Type: Oral Presentation

Neutralizing and binding antibody response specific to Chikungunya with a natural infection of Chikungunya virus in children from India

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Background: Chikungunya virus (CHIKV) infection has gone global, now we see CHIKV outbreaks emerging in new areas and re-emerging in previously exposed geographical regions thus making it a major public health concern. Chikungunya infection, especially in children are clinically unapparent, which poses challenge to vaccine testing and evaluation. During infection CHIKV-specific antibodies are produced and play crucial role in control of CHIKV infection. The goal of antibodies is to neutralize the liberated virus from an infected cell before it enters an uninfected cell.

Methods & Materials: We evaluated binding(IgG) and neutralizing antibody response specific to in-house recombinant E2(T) protein and whole CHIKV in paired serum samples from 35 CHIKV infected and 35 non CHIKV infected (other febrile illness) children. We also analyzed how well do binding(IgG) antibodies correlate to neutralizing antibodies.

Results: Our results showed significant difference ($p=0.0004$) between acute and convalescent phase sera, from Chikungunya infected children. However, no significant difference ($p=0.3085$) was observed in Chikungunya uninfected (OFI) children. We similarly evaluated IgG antibody response specific to whole CHIKV in Chikungunya-infected and Chikungunya-uninfected (OFI) children and found similar observation. We assessed effect of prior exposure to CHIKV infection during natural infection. Our result showed, 52.94% and 77.78% Chikungunya infected study subjects from study population had IgG antibody specific to E2(T) in their acute phase of infection. Interestingly, the E2(T) specific binding antibody titers moderately correlated with titers of Chikungunya specific neutralizing antibody titers and statistically found significant in acute ($r=0.6912, p<0.0001$) and convalescent phase ($r=0.3851, p=0.0223$) of infection, respectively. Similarly, CHIKV specific binding antibody titers showed positive correlation with neutralizing antibody ($r=0.6012, p=0.0001$) and ($r=0.4024, p=0.0166$) in acute and convalescent phase of infection, respectively.

Conclusion: Our results demonstrated that our E2(T) protein may have diagnostic potential to diagnose CHIKV infection. Acute and convalescent phase serum from children infected with CHIKV showed significant differences in neutralizing and binding antibody capacities. Neutralizing and binding(IgG) antibody titers showed positive correlation in serum of Chikungunya infected subjects. More studies are needed to establish the role of binding and neutralizing antibody during the infection of CHIKV; this information may be useful for development of candidate vaccines and their evaluation.

Final Abstract Number: 22.004

Session: Oral Presentations: Arboviruses

Date: Friday, March 2, 2018

Time: 17:00-18:00

Room: Retiro A

Type: Oral Presentation

Neurological complications associated with arboviruses during Zika outbreak in Salvador, Bahia-Brazil
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Background: An unprecedented and concurrent outbreak of Dengue (DENV), Chikungunya (CHIKV) and Zika (ZIKV) virus happened in Brazil in 2015. Approximately 18.372 cases of an acute exanthematous illness were notified in Salvador, Bahia and several cases of Guillain-Barré Syndrome (GBS) raised.

Methods & Materials: We started a hospital surveillance for GBS and other neurological syndromes in two general hospitals in Salvador, northeastern Brazil.

Results: Twenty-seven cases were included, of which 18 (66%) were female. The mean age was 40 years and 26 (93%) of them had acute symptoms suggestive of arbovirus infection before the onset of neurological symptoms. The main symptoms were skin rash, pruritus, myalgia, and fever. The median time between onset of acute symptoms and neurological symptoms was 10.5 days. Seventeen cases (63%) were classified as GBS, 3 (11%) as acute encephalitis, 2 (7%) as opsoclonus-myoclonus ataxia syndrome (OMS), 2 (7%) as myelitis, 1(4%) as Carpal tunnel syndrome and 1 (4%) as acute disseminated encephalomyelitis (ADEM). GBS cases presented in a variety of clinical spectrum, with 8 (47%) as acute ataxic neuropathy, 5 (29%) as classic GBS, 2 (11%) as bifacial weakness with paraesthesias, 1 (5%) as paraparetic GBS and 1 (5%) as classic Miller-Fischer syndrome. Twelve (44%) patients were admitted to semi-intensive or intensive care units and none died. The arbovirus diagnosis was established in 21(77.8%) of the cases. Serological evaluation by ELISA singly detected IgM-specific DENV antibodies in 3 cases (2 SGB and 1 Myelitis), IgM-specific CHIKV antibodies in 4 cases (3 SGB and 1 myelitis) and IgM-specific ZIKV antibodies in 3 cases (SGB). Six cases had both anti-ZIKV and anti-DENV (2 SGB, 2 encephalitis, 1 ADEM, 1 OMS) with a presumptive ZIKV diagnosis. One case of OMS had a coinfection by CHIKV and DENV-4 established by RT-PCR.

Conclusion: Herein, we describe 28 cases of GBS and other neurological syndromes associated with arboviruses. Besides GBS, we also identified cases of encephalitis, ADEM and OMS, a rare syndrome characterized by chaotic eyes movement and ataxia. Thereafter, clinicians and health care providers should be aware of the potential severe neurological complications associated with arbovirus infection in epidemic areas.

Final Abstract Number: 22.005

Session: Oral Presentations: Arboviruses

Date: Friday, March 2, 2018

Time: 17:00-18:00

Room: Retiro A

Type: Oral Presentation

Projecting the end of the Zika epidemic in Latin America: a modelling analysis

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Background: Zika virus disease emerged in Latin America in early 2015, which had serious implications for population health. In 2016, the World Health Organization declared a cluster of neurological disorders and neonatal malformations associated with Zika cases a Public Health Emergency of International Concern. 2017 incidence has declined, and future disease incidence in Latin America remains uncertain due to gaps in our understanding of the natural history of infection, considerable variation in surveillance and a lack of a comprehensive collation of available data from affected countries.

Methods & Materials: This analysis combines publically available data on Zika virus incidence across most Latin American countries and a spatio-temporal dynamic transmission model for Zika virus infection to determine key transmission parameters and likely future incidence in 87 cities. Seasonality was determined by spatio-temporal estimates of *Aedes aegypti* vector capacity. Country and state-level data are used to infer key model parameters using Monte-Carlo methods, different movement models were tested against the data and the best-fitting parameter combinations were used to estimate incidence within each city.

Results: We predict that the highest incidence in 2018 will be observed in Colombia and some Brazilian States (Parana, Sao Paulo, Rio de Janeiro and Minas Geras), but the estimated number of infections will be no more than a few hundred and the incidence risk ratio will be below 0.05. There was limited transmission in 2015, but for most cities 2016 and 2017 provided a sufficient opportunity for ZIKV transmission and populations have been depleted of susceptible individuals.

Conclusion: The findings suggest that much of the ZIKV-associated morbidity will be in neonates and children that are born up to the end of 2017. The findings present a challenge to planned ZIKV-specific interventions such as phase III vaccine trials, as we predict substantially lower numbers of infections in 2018.

Final Abstract Number: 22.006

Session: Oral Presentations: Arboviruses

Date: Friday, March 2, 2018

Time: 17:00-18:00

Room: Retiro A

Type: Oral Presentation

Seroepidemiology of Arbovirus in pregnant women participating in Cohort study in Jundiaí, SP, Brazil:
Preliminaries results of Cohort Zika - Jundiaí

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Background: Arboviruses are transmitted by arthropods. The most common in Brazil, are: Yellow Fever, Dengue and recently Chikungunya and Zika. Zika has emerged associated with cases of fever, arthralgia, Guillain-Barré syndrome and congenital malformation. Beyond, cases of microcephaly in newborn were associations with ZIKV infections. Further studies are needed to confirm this association.

Methods & Materials: From May 2016 to date, 757 pregnant women are being followed up in a cohort study. Blood, saliva and urine were collected from pregnant women and newborns. In the first sample of the mothers the ELISA was performed to detect IgG immunoglobulins anti ZIKV, CHIKV and DENV. The ELISA was performed in 728 (96.2%) of this women.

Results: ZIKV ELISA was performed in 350 pregnant women: 15 (4.2%) positive, 334 (95.4%) negative and one (0.3%) undetermined. Among ZIKV negative cases, 48 (14.4%) were ZIKV positive by RT-qPCR. Of the positive cases, 3 (0.9%) were also ZIKV positive by RT-qPCR. CHIKV ELISA was performed in 709 pregnant women, 63 (8.9%) positive, 629 (88.7%) negative and 17 (2.4%) undetermined. DENV ELISA was performed in 253 pregnant women, 55 (21.7%) positive, 195 (77.1%) negative and 2 (0.8%) undetermined. The diagnosis for three arboviruses were performed in 168 women: Four (2.4%) were ZIKV positive, 4 (2.4%) CHIKV, 31 (18.5%) DENV, 3 (1.8%) ZIKV and DENV and one (0.6%) CHIKV and DENV. Nine (5.4%) of these mothers were ZIKV positive by RT-qPCR. Two (1.2%) mothers had children ZIKV positive by RT-qPCR. Three (1.8%) newborns with microcephaly were detected; one positive for DENV and the other two were negative for any Arboviruses studied.

Conclusion: The individually diagnosis, detected high occurrence of ZIKV (14.4%) and DENV (21.7%) and lower occurrence of CHIKV 63 (8.9%). Cases of co-infection can be detected, at lower levels. The number of patients with complete diagnosis is small, yet. But IgG ELISAs will be performed on remaining mothers and all newborns and IgM ELISA will be performed for all participants.

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Session: Oral Presentations: Bacterial Infections and Antimicrobial Resistance

Date: Saturday, March 3, 2018

Time: 10:15-12:15

Room: Retiro A

Type: Electronic/Moderated Poster Presentation

An investigation of plasmid-mediated colistin resistance mechanism, MCR in *Escherichia coli* of human, veterinary and environmental origin in Bangladesh

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Background: Colistin is considered the last resort antibiotics in human medicine and recently new plasmid-mediated colistin resistance (MCR) mechanism has been emerged and reported in many countries. This study was designed to reveal the existing situation of its occurrence in Bangladesh.

Methods & Materials: A total of 810 samples were collected from human (N=100), cattle (N=50), goat (N=100), poultry (N=250), poultry farm environment (N=150) and street foods (N=160) of Chittagong Division. After obtaining *Escherichia coli* isolates following standard bacteriological method they were screened against 7 antimicrobials of six groups using disc diffusion technique. Finally, colistin-resistant isolates were investigated for the presence of *mcr-1* and *mcr-2* genes using PCR. Epidemiological data were analyzed using univariable and multivariable logistic regression to assess the risk factors associated with the emergence of colistin resistant isolates.

Results: The results revealed that 358 samples were positive with *E. coli*, representing 44.2% prevalence. Antimicrobial resistance profiling of the isolates showed the highest resistance against Amoxicillin (84.45%) followed by Tetracycline (79.9%), Ciprofloxacin (61.2%), and Cephalexin (50.3%) whereas the highest sensitivity was recorded against Colistin (84.1%) followed by Gentamycin (58.9%), and Sulphamethoxazole-trimethoprim (49.2%). Notably, 70.9% isolates showed resistance to ≥ 3 groups of antimicrobials (MDR). The prevalence of *E. coli* showing resistance to colistin was 15.9% with highest from poultry (30.8%). MCR-1 and MCR-2 positive *E. coli* strains were detected only from 3 and 2 of the isolates of poultry and street foods, respectively, and all other *E. coli* strains from other samples were negative for those genes. None of the strain had both genes, but all the 5 strains having MCR were MDR. After univariable analysis, the source factor "Healthy Poultry" itself was positively associated with *E. coli* showing resistance to colistin compared with other sources. However, after multivariable analysis only one variable (poultry farm environment) was found to have negative impact on its prevalence.

Conclusion: Plasmid-mediated colistin resistance genes are circulating in food samples (poultry and street foods) of Bangladesh which can be transferred to human leading to an inevitable public health crisis.

Final Abstract Number: 29.002

Session: Oral Presentations: Bacterial Infections and Antimicrobial Resistance

Date: Saturday, March 3, 2018

Time: 10:15-12:15

Room: Retiro A

Type: Oral Presentation

Current situation of antimicrobial stewardship programs in Argentina

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Background: The implementation of Anti-Microbial Stewardship (AMS) Programs have an impact on the improvement of patient care and health care outcomes; and has also shown to limit the emergence and transmission of antimicrobial-resistant organisms. In Argentina, there is little information about the implementation of AMS programs in Healthcare Institutions (HCIs). The aim of the study was to determine the degree of implementation of different strategies recommended for AMS in Argentina.

Methods & Materials: We evaluated the availability of AMS programs by means of the Composite Index of Adequate Antimicrobial Use (ICATB in French); and analyzed the AMS situation in a representative sample of large HCIs from the biggest cities of Argentina. ICATB is a survey that scores HCIs across 12 different domains related to AMS activities; which allows to classify HCIs according to their degree of use of different AMS strategies or activities.

Results: We evaluated 33 large HCIs from the 6 biggest cities in Argentina. Only 3 HCIs scored below recommended: Category E (0-10 ICATB): 6.1% and Category D (10-30 ICATB): 3.0%. Most HCIs scored favorably: Category C (30-70 ICATB): 27.3%, Category B (70-90 ICATB): 48.5%, and Category A (90-100 ICATB): 15.2%. Regarding specific domains of ICATB evaluation: 18.2% of HCIs does not have a Committee for AMS. Antimicrobial use surveillance is performed by 84.9% of HCIs, but only 36.4% audits on antimicrobial prescription. While only 54.6% of HCIs have some kind of digital records, 45.5% have computer-based prescription. Only 39.4% have education of new prescribers; and 45.5% have restrictions on antimicrobial prescription.

Conclusion: Large HCIs in Argentina have a fair AMS performance. However, we observed improvement opportunities for Information Technology. Half of the HCIs evaluated have not implemented any kind of digital AMS, and a complete computerization could be beneficial to facilitate activities and to improve data analysis to have a better impact on AMS. Educational activities should also be improved by the HCIs. Further studies are needed to evaluate the impact of these programs on optimization of antimicrobial use and resistance and health care outcomes, including mortality and costs in Argentina.

Final Abstract Number: 29.003

Session: Oral Presentations: Bacterial Infections and Antimicrobial Resistance

Date: Saturday, March 3, 2018

Time: 10:15-12:15

Room: Retiro A

Type: Oral Presentation

Fecal contamination hotspots in low-income households in Bangladesh

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Background: Diarrheal diseases continue to be major causes of morbidity and mortality in developing countries. Infectious Diarrhea is often related to fecal pathogen exposure via drinking water. Little is known about the other fecal contamination hotspots within the household and especially in the kitchen environments in overcrowded low-income setting. Current study intended to perform quantitative analysis of fecal contamination in food and domestic surfaces.

Methods & Materials: Fecal contamination was surveyed in routine swabs from four household environmental sites: cutting knife (n=169), food plate (n=165), latrine door knob (n=169), and drinking water pot surface (n=165) among 32 households for 1 year period in a low-income area, Arichpur, Dhaka. Moreover, 137 left over food samples were taken. All the samples were analysed for total thermotolerant *Escherichia coli* count and the presence of *Vibrio cholerae* by molecular method. Fisher's exact test was used to compare the fecal contamination level in different surface locations. A subset of samples was assessed for the genomic presence of diarrheagenic *E. coli* by PCR.

Results: Results revealed that *E. coli* contamination level was highest on food plates with a geometric mean (GM) of 3.08 cfu/cm² and the least contaminated site was latrine door knob (GM=0.06 cfu/cm²). Food samples were found heavily contaminated with fecal *E. coli* (GM=13.32 cfu/gm, with counts ranges from 0 to 6400 cfu/gm). The level of fecal contamination is 4.7 times higher ($p<0.05$) in cutting knife than latrine door knob surfaces and 0.3 times lower ($p<0.05$) in latrine door knob than drinking water pot surfaces. *V. cholerae* contamination was also most predominant in food plate swabs. Genes of enterotoxigenic *E. coli* (ETEC), enterohaemorrhagic *E. coli* (EHEC) and enteropathogenic *E. coli* (EPEC) were detected in surface samples among them ETEC was the most prevalent (46% samples were found positive).

Conclusion: This study presents new dynamics of in-house components in transmission of fecal bacteria via food and kitchen utensils thus, proves the vulnerability of the kitchen environment of low-income urban settings in Bangladesh. Results of the study will enable an update of the diarrhea risk factors for early prevention of disease progression in risk groups.

Final Abstract Number: 29.004

Session: Oral Presentations: Bacterial Infections and Antimicrobial Resistance

Date: Saturday, March 3, 2018

Time: 10:15-12:15

Room: Retiro A

Type: Oral Presentation

Parental knowledge, attitude and practices regarding antibiotic usage among children under five in Pakistan

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Background: The emergence of anti-microbial resistance (AMR) is a serious global public health threat. General public and medical practitioners has the key role in development of AMR. This study was designed to determine knowledge, attitude and practice among parents towards antibiotic use for Under-5 Children in Pakistan.

Methods & Materials: A cross-sectional survey using questionnaire was conducted during July to October 2016 and 270 parents of <5 years age children presented in outpatient pediatric departments of Pakistan Institute of Medical Sciences Hospital, Islamabad were randomly enrolled. The information was taken regarding demographics, Antibiotic Usage, Side effects and resistance. Lickert scale was used for scoring responses (1=Strongly-disagree, 2=Disagree, 3=Neutral, 4=Agree, 5=Strongly-Agree). The knowledge was categorizes as Low (0-5 correct responses), Moderate (6-7 correct responses) and High (8-11 correct responses). Attitude was also divided in two parts; Negative (0-3 correct responses) and Positive (4-7 correct responses). Median score with Inter quartile Range (IQR), Correlation-coefficient (r) and Person Chi-square test were calculated.

Results: More than half (n=164, 60.7%) of the respondent have low knowledge, more than one quarter (n=75, 27.8%) of the respondents have moderate level knowledge and only 11.5% (n=31) respondents showed high level knowledge regarding antibiotic usage for under-5 children. Median score for knowledge remained 05 (IQR 5-4). Three quarters of the study participants (n=200, 74%) thought antibiotics are effective for cough. Seventy Percent (n=189) respondents used antibiotics as self-medication. More than half of the respondents (n=162, 61%) has used leftover medicines and 30% (n=81) shared other siblings medicine. Knowledge remained a predictor for positive attitude (r=0.07, p<0.05). Only nearly one quarter (n=60, 21.9%) of the respondents showed positive attitude towards antibiotics usage for their children under five years of age. The median score for attitude was 02 (IQR 3-2). Agreement that doctors often prescribe antibiotics to meet the patient's expectation remained 36% (n=97). Low Education Level, Non-Medics families and poor had low knowledge and negative attitude (p<0.05).

Conclusion: Based on the study findings, there is immense need to initiate public awareness campaigns and wide range interventions across the sectors to overcome irrational use of antibiotics and emergence of resistance in Pakistan.

Final Abstract Number: 29.005

Session: Oral Presentations: Bacterial Infections and Antimicrobial Resistance

Date: Saturday, March 3, 2018

Time: 10:15-12:15

Room: Retiro A

Type: Oral Presentation

Gastrointestinal colonization by vanA glycopeptide resistant *Enterococcus* species harbouring multiple virulence genes in western Nepal

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Background: Gastrointestinal colonization by vancomycin resistant *Enterococcus* (VRE) has regularly been reported worldwide. Fecal carriage rate and virulence properties of such colonisers have not been established so far in context to Nepal. This study was conducted to address these prevailing issues.

Methods & Materials: Rectal swabs were screened for multi drug resistant (MDR) *Enterococcus* species. MICs of vancomycin and teicoplanin were determined by E- test. VRE isolates were further investigated for various pathogenic markers. Pulsed field gel electrophoresis (PFGE) was used to investigate the genetic relatedness between VRE strains. *Drosophila melanogaster* insect model was used to determine the colonisation capability and virulence of VRE.

Results: Of the 270 subjects studied, 142 (52.59%) yielded *Enterococci* spp. Forty seven (33.1%) out of 142 *Enterococci* were MDR. 31 (72.1%) of 43 hospitalizes individuals were colonised with MDR *Enterococci*, as compared to only 16 (16.2%) of 99 community individuals ($\chi^2= 42.35$; $p < 0.001$). We found that 18.6% (8/43) of the hospitalised patients and 1.01% (1/99) community subjects was colonised with VRE, ($\chi^2=15.63$; $p < 0.001$), faecal colony counts ranging between 10^2 to 10^4 CFU/gm. Seven VRE isolates were identified as *E faecium* and two as *E faecalis*. All the isolates belonged to vanA genotype. *In vitro* virulence determinants such as biofilm production, extracellular enzymatic and haemolytic activities were absent, despite all the strains possessing multiple virulence genes like *esp*, *asa1*, *gelE*, *ace*, *hyl*, *cylA*, *cpd* and *ebpA* and being capable of producing slime. PFGE analysis revealed two different traits of which, majority (6/9) had the same clonal origin. None of the VRE isolates were capable of gut colonization or causing death in *Drosophila* during the 10 days study period as assessed by fly feeding experiment. Mean VRE concentrations in the gut of flies were 24×10^4 CFU/ml after 36 hours of feeding, which decreased gradually and became undetectable at the end of 168 hours without any visible adverse effect.

Conclusion: Colonization by MDR *Enterococcus* and VRE encoding multiple virulence genes in the studied population is alarming. Further work, involving suitable experimental model is warranted to elucidate the molecular pathobiology of VRE in the gut, in order to understand the commensal-pathogen continuum.

Final Abstract Number: 29.006

Session: Oral Presentations: Bacterial Infections and Antimicrobial Resistance

Date: Saturday, March 3, 2018

Time: 10:15-12:15

Room: Retiro A

Type: Oral Presentation

Utility of neutrophil-lymphocyte ratio, platelet-lymphocyte ratio and mean platelet volume as predictive and prognostic markers in patients with liver abscess in a tertiary care center in India

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Background: Liver abscess is an extremely rare condition and it requires prompt diagnosis and also close follow up of the inflammatory parameters or else it can lead to sepsis and even cost the life of the patient. Currently CRP is used as diagnostic and prognostic marker of bacterial infections, it is expensive and adds cost burden to the patients from poor socio-economic conditions. The objective of our study is evaluating the indicative potential of NLR, PLR and MPV to be used as predictive and prognostic markers in patients with liver abscess, which will be a cost effective inflammatory marker and also aid in better patient care in developing countries like India

Methods & Materials: We have conducted the present study by screening 2,08,486 patients who have got admitted during the period January 2013- June 2017 as in patients in AIMS, Kochi. The data collected were analyzed for Neutrophil-Lymphocyte Ratio, Platelet-Lymphocyte Ratio and Mean Platelet Volume. Inclusion criteria was patients of all age group with liver abscess USG/CT proven. Exclusion criteria: All cases other than liver abscess. The data was collected and analyzed on windows excel

Results: Male preponderance was seen 66 cases and female were only 15, mean age was 54 years. Eight Mortality were reported among the study population. The incidence of liver abscess was highest in coastal areas. NLR and PLR were highly significant with p- value 0 and 0.001 respectively and comparable to CRP with a p-value 0 but MPV with p-value 0.65 was not statistically significant to be used as diagnostic marker

Conclusion: From our study, we conclude that NLR, PLR are better cost-effective predictor and prognostic markers of liver diseases compared to CRP. These ratios can be used at the primary health care level as it can be derived from a simple peripheral smear. This will aid in early identification and management of liver abscess even in rural areas of developing country like India in the most cost effective way.

Final Abstract Number: 29.007

Session: Oral Presentations: Bacterial Infections and Antimicrobial Resistance

Date: Saturday, March 3, 2018

Time: 10:15-12:15

Room: Retiro A

Type: Electronic/Moderated Poster Presentation

Pharmacodynamic evaluation of vancomycin by Monte Carlo simulation against *Staphylococcus* spp isolated in a hospital teaching

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Background: Vancomycin is the first-choice drug for the treatment of Gram-positive infections. The pharmacokinetic (PK) and pharmacodynamic (PD) indexes of this antimicrobial are the main determinants of its in vivo efficacy. The PK/PD parameter to vancomycin is the 24-h area under the curve to minimum inhibitory concentration ratio (AUC₂₄/MIC_{≥400}), which can be associated with improvement of treatment outcomes. The aim of this study was to evaluate the therapeutic success probability of different dosing regimens of vancomycin by Monte Carlo simulation (MCS) and compare its coverage to vancomycin MIC against staphylococci isolates from a Brazilian teaching hospital over six years (2011 to 2016).

Methods & Materials: In total, 1112 clinical samples were enrolled, 578 *Staphylococcus aureus* and 426 *Staphylococcus epidermidis*. The vancomycin MICs were obtained by automated Phoenix BD™. The AUC₂₄/MIC index of vancomycin was evaluated by MCS in the following dosing regimens: 1g every 12 h (q12h), 1g q8h, 1g q6h and 1.5g q6h. The probability of target attainment (PTA) ≥ 0.9 and AUC / MIC ≥ 400 were considered adequate.

Results: During the six years of the study, no change was observed in MIC₅₀ and MIC₉₀ of vancomycin for *Staphylococcus aureus* (MIC = 1µg/mL). In the same period we identified that MIC₅₀ = 1µg/mL for *S. epidermidis* in 2011 increased to 2µg/mL from 2014, while MIC₉₀=2µg/mL was predominant. The PK/PD analysis of the different dosing regimens showed that vancomycin 1g q12h achieved adequate PTA only for MIC=0.5 µg/mL. Vancomycin 1g q8h and 1g q6h reached the MIC target ≤ 1µg/mL, while 1.5g q6h covered MIC up to 2 µg/mL. No dosing regimen proposed in this study achieved adequate PTA for MIC > 2 µg/mL.

Conclusion: The results showed that vancomycin achieved pharmacodynamic coverage for MIC = 1 µg/mL in high daily doses (≥ 3 g); for MIC=2 µg/mL to achieve the same therapeutic target, 6 g/day was required. Considering that high daily doses of vancomycin increase the risk of toxicity, we suggest the individual and monitored use of this antimicrobial to optimize PK/PD parameters, or when possible, the use of other antimicrobial agent with activity against these microorganisms.

Final Abstract Number: 29.008

Session: Oral Presentations: Bacterial Infections and Antimicrobial Resistance

Date: Saturday, March 3, 2018

Time: 10:15-12:15

Room: Retiro A

Type: Electronic/Moderated Poster Presentation

Pangenome analysis of *Enterococcus faecium* to get insight into the virulence potential and novel vaccine candidates

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Background: *Enterococcus faecium* is leading cause of nosocomial bacteremia, surgical wound infection and UTIs. *E. faecium* has rapidly accumulated antibiotic resistance genes. The therapeutic challenge given by *E. faecium* necessitates exploring genomics of the bacterium. We have explored pan-genome of *E. faecium* strains, followed by reverse vaccinology approaches to identify potential vaccine targets against it.

Methods & Materials: A comprehensive analysis was performed on all completely sequenced genomes (15) of *E. faecium* available on NCBI. Pan- and core genome were estimated based on BLAST similarities between the genomes following 50/50 cut off. The virulence factors were estimated by employing VFDB. CARD was used to explore presence of antibiotic resistance genes in core genome. For prediction of potential vaccine candidates, core genome was subjected to sequential steps in order to find proteins which are at surface [psortB], and are essential [DEG], virulent [VFDB] and non host homologs. Those proteins which were simultaneously essential, virulent, non-host homologs, exposed with ≤ 1 trans-membrane helices prioritized as vaccine candidates. The prioritized proteins were subjected to epitope mapping steps. Vaxijen was used to check antigenicity of epitopes. Blast2GO was employed for studying biological, molecular behavior of prioritized proteins.

Results: Pangenome of *E. faecium* strains consists of 5,473 CDS, of which 1509 represent core and 3,964 constitute dispensable genome. *E. faecium* carried a number of virulent genes (235) as part of its core genome which assists the bacteria in pathogenesis (e.g., cagA, OmpB). Core genome was found out to contain antibiotic resistance genes including trimethoprim/fluoroquinolone/aminoglycoside resistance gene, beta-lactam resistance gene. The essential genes [904] are involved in significant biological processes. The results of essentiality, non host homologs, virulence, and sub-cellular localization were added up and eight core proteins have been prioritized as potential vaccine targets including glutamate dehydrogenase, glycosyl transferase family 51, periplasmic solute binding protein, phosphomethylpyrimidine kinase, GAF protein, extracellular solute binding protein family 3, alpha L arabinofuranosidase and glycosyl transferase. Epitope mapping of target proteins revealed presence of surface exposed 9-mer T-cell epitopes which exhibits high antigenicity scores.

Conclusion: Pangenomics and reverse vaccinology approaches directed us to find eight vaccine targets against *E. faecium* which can generate significant immune response.

Final Abstract Number: 29.009

Session: Oral Presentations: Bacterial Infections and Antimicrobial Resistance

Date: Saturday, March 3, 2018

Time: 10:15-12:15

Room: Retiro A

Type: Oral Presentation

First study on genetic characterisation of clinically isolated NDM-7 producing *Klebsiella pneumoniae* and *Escherichia coli* from different tertiary care hospitals, Pakistan

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Background: New Delhi MBL (NDM) is a carbapenamase conferring resistance to all β -lactam antibiotics and other classes of antibiotics. These have mainly been described in *Enterobacteriaceae* particularly in *K. pneumoniae* and *E. coli* as compare the non-fermenters. NDM is endemic to the Indian subcontinent but has spread worldwide since its first description in 2008. Now there are many NDM types have been identified (NDM-1-NDM-18). The rapid global dissemination of NDM producing bacteria and the presence on mobile genetic elements in a broad range of species have established NDM as a major public health threat.

Methods & Materials: A total of 302 clinical isolates of carbapenem resistant Gram-negative bacteria were collected from different source of specimens (blood, urine and pus) from different tertiary care hospitals Pakistan. Isolates were identified and confirmed by Vitek 2 system and MALDI-TOF. Molecular identification of *bla*_{NDM-7} was done by sequencing followed PCR amplification. MIC of *bla*_{NDM-7} producing bacteria was of performed using Vitek 2 System by GN XN05 cards. Multi-locus sequence typing (MLST) of *bla*_{NDM-7} producing bacteria was performed by amplifying the house keeping genes. Plasmid analysis was performed by SI digestion Pulse Field Gel Electrophoresis and in Gel DNA DNA hybridization.

Results: Out of 300 clinical isolates, 4 *E. coli* and 4 *K. pneumoniae* were identified and confirmed for *bla*_{NDM-7} by two amino acids substitution at position 130 (ASP –Asn) and 154 (Met-Leu). These isolates were recovered from urine and blood samples. MIC of the *bla*_{NDM-7} producing bacteria showed 100% resistance to all the β -lactam antibiotics including the carbapenem and moderate resistance to other class of antibiotics. MLST analysis revealed that *E. coli* isolates belongs to the sequence type (ST) of 405 and 648 however *K. pneumoniae* belongs to the ST of 11 and 147. These isolates contained different number and size of plasmids and most of them contained *bla*_{NDM} on ~50kb and ~280kb of plasmids.

Conclusion: This study first identified NDM variant in *E. coli* and *K. pneumoniae* of different sequence types. NDM-7 producing bacteria have high level of antibiotics resistance and carried *bla*_{NDM} on different size of plasmids.

Final Abstract Number: 29.010

Session: Oral Presentations: Bacterial Infections and Antimicrobial Resistance

Date: Saturday, March 3, 2018

Time: 10:15-12:15

Room: Retiro A

Type: Oral Presentation

Appropriateness of molecular testing for Clostridium Difficile: An evaluation of provider ordering
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Background: Molecular testing has been embraced as a sensitive and specific test for C difficile. However, there are problems with specificity for C. difficile infection versus colonization. Overtesting and inappropriate testing are increasing concerns among healthcare centers who use these methods.

Methods & Materials: We reviewed all of our C. difficile testing orders for a 3 month period: April through June 2017 to investigate appropriateness and characteristics associated with positive test results. This time period corresponds to the end of the academic year for medical trainees as well as the end of viral respiratory season in the United States. Variables of interest for each order included: ordering provider, patient age, patient location, patient laxative receipt within 24 hours of the order, documented presence of diarrhea, and pcr test result.

Results: During the 3 month interval, 849 C. difficile pcr tests were ordered; roughly 1 of every 14 admitted patients received a C difficile test. Medical trainees (residents and fellows) as well as Nurse Practitioners (NPs) ordered the majority of tests. These 2 groups were also the most likely to order C difficile tests on patients actively receiving laxatives (27% and 23% of tests respectively) (p=0.0003). Physicians, either attending or trainee, had a higher proportion of positive test results (18% positive for both groups) compared to NPs (11%) or other nurses (3%) (p=0.0464). There was no difference in age between patients testing positive versus negative for C. difficile by pcr (p=0.2853).

Conclusion: The volume of C. difficile molecular testing at our institution and the prevalence of C difficile testing on patients receiving laxatives, suggests overttesting, particularly among trainees and nurse practitioners who provide the bulk of patient care. Education and decision support to target these groups may limit overdiagnosis and excess treatment of patients colonized with C. difficile at our center.

Final Abstract Number: 29.011

Session: Oral Presentations: Bacterial Infections and Antimicrobial Resistance

Date: Saturday, March 3, 2018

Time: 10:15-12:15

Room: Retiro A

Type: Oral Presentation

Isolation of *Escherichia coli* O157:H7 in table eggs from selected farms in Ibadan: Efficacy of *Lactobacillus rhamnosus* GG probiotic for its control

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Background: *Escherichia coli* O157:H7 is an important food borne pathogen causing severe diarrhoea and hemolytic uremic syndrome. There is limited information on the control of pathogenic *Escherichia coli* (*E. coli*) from table eggs using probiotics. This study was designed to determine the occurrence of *Escherichia coli* O157:H7 in table eggs from poultry farms in Ibadan, Southwestern Nigeria and to assess the antibiotic sensitivity profile. The efficacy of *Lactobacillus rhamnosus* GG probiotic for inhibition of this pathogen was also evaluated.

Methods & Materials: Three hundred and sixty (n=360) table eggs were sampled from twelve farms in Ibadan. Isolation of *Escherichia coli* O157:H7 was done using selective pre-enrichment on Tryptone soy broth and Sorbitol MacConkey Agar as selective medium. Morphological and biochemical tests were done using standard procedures. Serological identification of the organism was performed using *Escherichia coli* O157 antisera. Total aerobic bacteria and coliform counts were done on Nutrient agar and MacConkey agar, respectively. Antibiotics susceptibility test was done using the agar disc diffusion method. Inhibitory activity of *Lactobacillus rhamnosus* GG probiotic against the isolates was assessed using Agar Well Diffusion Method at 10⁸, 10⁴ and 10² concentrations. Data were analysed using descriptive statistics and ANOVA at $\alpha_{0.05}$.

Results: The prevalence of *Escherichia coli* O157:H7 was 7 (9.8%) (entirely from egg shell). The Total aerobic bacteria count (Mean Log CFU) was 1.43 ± 1.65 and 4.95 ± 0.24 for egg contents and shell, respectively, and the Total coliform count was 1.36 ± 1.46 and 4.84 ± 0.33 for egg contents and shell, respectively. All isolates were resistant to Ampicillin, Ceftazidime, Cefuroxime and Amoxicillin. In all 100% of the isolates were multidrug resistant. The isolates were mostly susceptible to Ciprofloxacin (87.5%) and Ofloxacin (87.5%). *Lactobacillus rhamnosus* GG has inhibitory effect on 42.8%, 28.6% and 28.6% of the isolates at 10⁸, 10⁴ and 10² concentrations, respectively.

Conclusion: The presence of multidrug resistant *Escherichia coli* O157:H7 in table eggs in Ibadan was established. *Lactobacillus rhamnosus* GG can be used for the control of *Escherichia coli* O157:H7. Improvement in hygiene by poultry farmers and control of the use of antibiotics in poultry is strongly recommended.

Final Abstract Number: 40.001

Session: Oral Presentations: HIV / Tuberculosis

Date: Saturday, March 3, 2018

Time: 15:15-16:45

Room: Retiro A

Type: Electronic/Moderated Poster Presentation

Prevalence of tuberculosis infection among South African adolescents

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Background: We aimed to measure changes in adolescent prevalence of latent tuberculosis (TB) infection (LTBI) over a 10-year period (2005-2015), in which TB disease incidence fell 34% from 1,038 – 682 per 100,000 per annum, in order to evaluate impact of effective TB control efforts on transmission to children.

Methods & Materials: We compared baseline data from a TB cohort study (2005-2007) and a TB vaccine trial (2014-2015), which enrolled adolescents from the same 8 high schools near Cape Town, South Africa. LTBI was defined by positive QuantiFERON®-TB Gold In-Tube (QFT) test. Data were analysed by two-sample test of equality of proportions for survey data and logistic regression for survey data.

Results: We analysed data from 6,848 adolescents with median age of 15.5 years (range 12.3 - 19.1). 4,880 (71%) adolescents were tested between 2005-2007 and 1,968 (29%) between 2014-2015. Prevalence of LTBI was 43.8% (95% Confidence Interval (CI) 28.4-59.1) vs 48.5% (CI: 41.1-55.8); and annual risk of Mycobacterium tuberculosis infection (ARTI) was 3.6% (CI: 2.1-5.5) vs 4.2% (CI: 3.4-5.2), in the period 2005-2007 vs 2014-2015, respectively. Marked heterogeneity in LTBI prevalence was observed at school level, ranging from 12-65%. LTBI prevalence increased on average by 13% between age 12-18 years in lower socio-economic quintile schools, in which average LTBI was 54% in 2005-2007 and 53% in 2014-2015, consistent with ongoing, but stable risk of TB transmission. By contrast, LTBI prevalence did not increase with age in highest socio-economic quintile schools, in which average LTBI prevalence increased from 20-38% over the same period, consistent with increased risk of transmission prior to school entry.

Conclusion: Adolescent LTBI prevalence remained high over a decade, suggesting TB transmission to children was not yet impacted by effective TB control efforts that had reduced regional TB disease notification rate by more than one-third. Trends in school LTBI prevalence should be interpreted in the context of socio-economic and other TB risk factors that affect risk of transmission prior to school entry.

Final Abstract Number: 40.002

Session: Oral Presentations: HIV / Tuberculosis

Date: Saturday, March 3, 2018

Time: 15:15-16:45

Room: Retiro A

Type: Oral Presentation

Tuberculosis prevalence survey reveals the high proportion of asymptomatic disease, and points to high-burden households as a site for potential intervention in peri-urban slums of Callao, Peru

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Background: To improve the reach of tuberculosis elimination, we must understand the population that does not seek medical contact. Prevalence surveys are widely used to measure undiagnosed TB disease, but rarely characterize the clinical and social risk factors and barriers to care that obstruct diagnosis, notification, and treatment.

Methods & Materials: A cross-sectional prevalence survey of pulmonary TB disease was undertaken with sputum culture on Middlebrook 7H11 thin-layer agar in a cohort of 1668 households known to have been affected by TB in the past 10 years. Symptoms, co-morbidities, and health-seeking behaviour were assessed for all household members, and treatment records from community health posts were used to identify all courses of antitubercular therapy prescribed to household members.

Results: Sputum was obtained from 6380 residents over 8 years old (1744 former patients; 4636 other residents). 101 participants were taking antitubercular therapy and no longer sputum-culture-positive. 51 culture-positive cases of prevalent TB disease were detected, of whom only 13 met the national clinical criteria for sputum testing (>2 weeks of productive or bloody cough). 11 had been tested for TB, 10 diagnosed, and 4 had been initiated on treatment at the time of the survey.

Multiple treatment episodes within the household (whether due to repeated infection, re-initiation of uncompleted therapy, or change of treatment scheme) were associated with increased odds of prevalent disease in the survey. Participants who had undergone two or more treatment episodes had 8.6 times the odds of prevalent TB of those with none (95%CI:3.9-18.7;P<0.001). Members of households with more than two treatment episodes had 3.2 times the odds of TB of those without—2.9 after adjustment for age, sex, poverty, HIV status, and drug and alcohol misuse (95%CI:1.6-5.3;P<0.001).

Conclusion: Accelerating currently recommended case management strategies could achieve a four-fold increase in treatment coverage for this population, but 75% of potentially infectious cases would still remain undetected. New strategies are needed to identify and engage populations at risk of undetected, minimally symptomatic disease. Meanwhile, follow-up of households affected by TB to provide preventative therapy for latent TB and active surveillance for new illness episodes will aid control and elimination of TB.

Final Abstract Number: 40.003

Session: Oral Presentations: HIV / Tuberculosis

Date: Saturday, March 3, 2018

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Room: Retiro A

Type: Oral Presentation

Vertical transmission of HIV infection and associated determinants in the era of option B+ use in Mbeya Region, Tanzania-2016

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Background: Mother-to-child transmission (MTCT) accounts for over 90% of new HIV infections among children. Without treatment, there is likelihood of 20% to 45% of infected mothers transmitting their infection to their children. Tanzania Ministry of Health, started implementing Option B+ (Tenofovir/Lamivudine/Efavirenz (TLE) combined) as one of the strategies to eliminate mother to child HIV transmission (eMTCT). We determined the rate of vertical transmission and associated determinants in the era of TLE use in Prevention of Mother to Child Transmission (PMTCT).

Methods & Materials: Nested-Case Control study design was carried out to determine rate of vertical transmission and determinants of MTCT among pregnant/breastfeeding women on TLE from October 2013 to December 2015. Data was collected using a structured questionnaire and record review. Bivariate and multivariate analysis were done. Odds ratio (OR) was used as a measure of association and all variables with $p < 0.05$ at multivariate level was considered independently associated with the outcome.

Results: The median age of 292 (247pregnant and 45breastfeeding) mothers enrolled in the study was 30 years (range 18-47 years).Sixty percent (177) were married while 86.3% (252) had primary education. The HIV vertical transmission rate during TLE use was found to be 10.6%, (95%CI 7.3%-14.7%).

Significant determinants for vertical transmission of HIV during TLE use were: Home delivery Adjusted Odds Ratio (AOR) =28.5, 95% Confidence Interval (CI) (1.61-506.43), short duration (<6months) on TLE AOR=219.0, 95% CI (11.03-4346.62) and practice of mixed feeding AOR=69.7 95% CI (2.68-1815.16).

Conclusion: The rate of MTCT of HIV infection is unacceptably high in Mbeya region in this era of TLE use compared to the recommended rate. Mixed feeding during the first six months of child's life, Home delivery and short duration of being on TLE were significant determinants for vertical transmission of HIV. PMTCT programming should be tailored to promote facility delivery, early diagnosis and initiation to TLE and adherence to exclusive breastfeeding in the first six months of life of an exposed child

Final Abstract Number: 40.004

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Date: Saturday, March 3, 2018

Time: 15:15-16:45

Room: Retiro A

Type: Oral Presentation

Two birds one stone?-Effectiveness of community engagement and integrated TB/HIV interventions for hard to reach migrant population, Thailand's experiences

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Background: As part of Thailand National TB/HIV response, World Vision Foundation of Thailand (WVFT) has awarded the sub recipient of Global Fund round 13 within 2015-2016. It targeted for migrants population from neighboring countries like Myanmar, Cambodia, Lao and Vietnam . The program was set up in six borders between Thailand- Myanmar and urban areas (Tak, Bangkok, Pathumthani, Kanchanaburi, Phuket and Ranong) which are high TB/HIV burden in Thailand. Target population was set at 100,139 and WVFT launched RRTTR (Reach-Recruit-Test-Treat and Retain) strategy to obtain community engagement to fight against TB/HIV at the same time approach.

Methods & Materials: WVFT launched to engage the community engagement for systematic community mapping, screening and selection of migrant health volunteers. Those volunteers were received by intensive training of trainer (ToT)integrated TB/HIV training categorized by three modules like roles and responsibilities of migrant health volunteers, TB/HIV counseling & management and public communication skills by native health personnel.

Results: After two years, WVFT classified 504 migrant community clusters and reached 220 clusters. 650 migrant health volunteers were recruited for intensified TB/HIV case finding and health talks around their clusters. In TB component, 61,320 migrant community people were screened by verbal Intensified TB case finding (ICF)screening and 61% (61320/100139) achieved against the project target. 3, 681 migrants people were notified as presumptive TB cases and 100 % tested for TB diagnosis. Among them, 341 and 196 presumptive TB cases were identified as all TB cases and New smear positive TB patients respectively and 100 %(196/196) of New Smear positive TB patients and 98 %(333/341) of all TB patients were enrolled for TB treatment. In HIV sector, 26,768 migrant people received HIV service package and 6,526 people were tested. HIV incidence rate was about 2% (124/6526) among migrants and 44 %(54/124) are accessed to Antiretroviral therapy (ART)

Conclusion: This evidence showed that integrated same time TB/HIV interventions, role of community engagement and participation of civil society organization (CSO) are crucial part of ending TB /HIV in hard to reach population. It is also cost effective and able to overcome language barriers, legal status and other socio cultural and structural barriers.

Final Abstract Number: 40.005

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Date: Saturday, March 3, 2018

Time: 15:15-16:45

Room: Retiro A

Type: Oral Presentation

Time to change our diagnostics to win the battle against TB in Pakistan

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Background: Pakistan ranked as 4th in the world for tuberculosis burden⁵. In Pakistan, the incidence of TB is 231/100,000 with prevailing prevalence and mortality of 310/100,000 and 39/100,000 respectively. Sputum smear microscopy is a routine test done in all the patients suspecting to have pulmonary tuberculosis. Diagnosis becomes challenging when patient has smear result as negative for Acid Fast Bacilli (AFB). Present study was done to assess the importance of Xpert MTB/RIF assay for the diagnosis of tuberculosis in patients negative for AFB on sputum smear.

Methods & Materials: An observational study done at Federal General Hospital (FGH), Islamabad from June 2015- 30th June 2016. After taking informed consent, two sputum samples of each patient were sent to TB reference laboratory, one processed for smear microscopy and second for Gene Xpert (MTB/RIF). Data was obtained and analyzed by SPSS 14.

Results: There were total 201 cases. Mean age of 36 years (\pm SD 2.8). Most of the patients were in 13-33 years age group, young adult group. Out of 201, 72 (36%) samples were positive and 129 (64%) negative using Xpert[®] MTB/RIF assay whereas 52 (26%) were positive and 149 (74%) were negative for AFB using microscopy. Only 2 (3%) were resistant to rifampicin on Xpert and both resistant cases were females. Sensitivity and specificity of microscopy was 71% and 99% respectively where as positive predictive value (PPV) and negative predictive values (NPP) were 98% and 86% respectively resulting in accuracy of microscopy to be 46% only.

Conclusion: Gene Xpert MTB/RIF assay is much more sensitive and specific than sputum microscopy. At the same time information given about rifampicin resistance and availability of the result in almost 2 to 3 hours with fully automated process makes it very much useful in the diagnosis of tuberculosis. Sputum culture was not performed among study participants as it is a gold standard diagnostic for TB diagnosis so accurate sensitivity and specificity of Xpert MTB/RIF assay could not be established. It is recommended that any person with cough for two weeks or more with unexplained chronic fever and/or weight loss should be assessed for TB

Final Abstract Number: 40.006

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Time: 15:15-16:45

Room: Retiro A

Type: Electronic/Moderated Poster Presentation

Immune biomarkers associated with active pulmonary Tuberculosis

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Background: Tuberculosis (TB) is a dreadful scourge for humanity since centuries. It has been declared as a major global health concern by World Health Organization. According to most recent survey undertaken in 2014, an estimated 9.6 million (equivalent to 133 cases per 100,000 population) new TB cases occurred, in which 5.4 million among men, 3.2 million among women and 1.0 million among children globally. The numbers of deaths due to TB were also calculated approximately 1.5 million, of which 0.89 million were men, 0.48 million were women and 0.14 million were children. Despite the public health importance of this disease, the profile of immune activation during the pathogenesis of the disease is still under investigation.

Methods & Materials: Here, we examined the mRNA profile of peripheral blood mononuclear cells (PBMCs) obtained from uninfected (n=25) and *M.tb* infected (n=31) individuals during the early stage of the disease living in Pakistan using gene arrays for 70 immune markers involved in Th₁ & Th₂ differentiation.

Results: Our results identify only 18 transcribed genes which were significantly (p value less than 0.05) altered by *M.tb* infection. Most of the genes are involved in Th₁ differentiation (upregulated; STAT1, IRF1, IL-27, and TLR4 and downregulated; CXCR3, STAT4, TBX21, CD80, CD28, and IL2RA), and Th₂ differentiation (downregulated; CCL5, PTGDR2, NFATC1, IL-24, IL-7, MAPK8, TGFB3, and TYK2).

Conclusion: In a nutshell, our results suggest that the local immune response in the *M.tuberculosis* infected host is neither dominated by TH₁, nor by TH₂ signature cytokines. However, we observed an over expression of new biomarker i.e. IL-27, which accompanied with other makers of gene expression data, is speculated to be involved in negative modulation of the host immune responses and contributing to the TB pathogenesis. Secondly, immune function of studied TB patients was further characterized by poor macrophages & lymphocyte trafficking and perturbed T-cell hemostasis in our study.

Final Abstract Number: 40.007

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Date: Saturday, March 3, 2018

Time: 15:15-16:45

Room: Retiro A

Type: Oral Presentation

Surgical Management of Abdominal Tuberculosis: Five years experience of a tertiary care centre

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Background: Abdominal Tuberculosis (AT) remains the common extrapulmonary presentation of tuberculosis. Most of these cases of AT present in surgical emergency with intestinal obstruction, intestinal perforation and/or peritonitis. Surgical procedures vary with the status of the patient and no standard surgical management procedures have been outlined till now.

Methods & Materials: We conducted a retrospective cohort study on all patients who presented to us in surgical emergency in Services Hospital, Lahore from 2012-2017. All patients who underwent exploratory laparotomy were included in the study. Out of 96 cases presented, 64 cases were included in the study based on clinical suspicion and histopathology where available.

Results: Of the total cases reviewed, 20 (31%) were males and 44 (69%) were females. The mean age of our patients was 24 ± 9.7 . 38.1% patients presented with constitutional signs and symptoms of peritonitis, 15.9% patients presented with intestinal obstruction, while 3.20% patients presented with right iliac fossa pain. Rest of the patients either had concomitant pulmonary tuberculosis (PT) or had had PT earlier in life. Consultants operated upon 44 patients while 20 cases were handled by the postgraduate residents. Operative findings were stricture-perforation complex in 73.4% of patients, ileal perforation with hyperplastic gut in 23.4% of patients while 3.12% patients had stricture with hyperplastic gut. Segmental resection and ileostomy was done in 71% of patients while 19% of patients underwent primary anastomosis. No difference was found in the post-operative complications between the patients who underwent ileostomy or primary anastomosis ($p > 0.05$). Uneventful recovery was seen in 52.8% of patients while wound infection was seen in 31.2% of patients, while 5.0% of patients developed anti-tuberculosis therapy-related complications. Five out of sixty-four patients expired during hospital stay.

Conclusion: Surgical management of AT remains a challenging task. Randomized-controlled trials are needed to determine the differences in short and long-term outcomes in patients undergoing explorations for AT in emergency department comparing primary anastomosis and ileostomy. Such studies will help develop surgical management guidelines of ileal perforations and gut strictures.

Final Abstract Number: 40.008

Session: Oral Presentations: HIV / Tuberculosis

Date: Saturday, March 3, 2018

Time: 15:15-16:45

Room: Retiro A

Type: Oral Presentation

Evolution of virulent genotypes and an emerging threat of multidrug resistant tuberculosis in Bamako, Mali

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Background: Bamako, Mali, has a well-structured hierarchy for tuberculosis (TB) case management. However, in recent years Bamako has been faced with an emerging threat from multidrug resistant TB (MDR-TB). Here we present insights into the genomic epidemiology of TB and the evolutionary mechanisms driving the emergence of MDR-TB in Bamako.

Methods & Materials: Isolates recovered from tuberculosis patients from local reference centers and the University Teaching Hospital at Point G, in Bamako, Mali between 2006 and 2012 (n=208), were tested for antimicrobial susceptibility at the MRC Unit The Gambia. A subset of 76 isolates were analysed using whole genome sequencing. A time dated phylogenetic tree was reconstructed using BEAST. Lineage and resistance conferring mutations were inferred using PhyResSe.

Results: Patients included 21 females and 55 males aged between 3 to 78 years, among whom 12(16%) were infected by MDR-TB. Most patients 61(80%) were new cases and among 15 retreatment cases 9(60%) were MDR-TB. The phylogeny was reconstructed from 8508 variant core genome sites. The dominant lineage was the Euro-American super lineage, lineage 4. Within lineage 4, the Cameroon genotype was the most prevalent genotype (n = 20, 26%) followed by the Ghana genotype (n=16, 21%). Cameroon genotype isolates diverged from a common recent ancestor ~161 years ago to form three clusters, one of which emerged ~22 years ago and is likely to be involved in on-going transmission. Seven Ghana genotype isolates were MDR-TB representing over half all MDR-TB in this dataset (7/12). Ghana genotype isolates were more likely to cause MDR-TB than other genotypes after controlling for treatment status (OR=5.6, p-value=0.043). The MDR-TB Ghana genotype isolates formed a clade that diverged approximately 30 years ago, in which the *katGSer315Thr* mutation was conserved. Other Euro-American genotypes included the six LAM, two H37Rv-like and one Uganda. Four patients were infected with closely related Beijing strains and five patients were infected with non-MDR *Mycobacterium africanum*2.

Conclusion: The Cameroon and Ghana genotypes are endemic to West Africa. Their association with on-going spread and MDR-TB in Bamako respectively is a major concern. The rise of Beijing genotype in Bamako is worrying given its high transmissibility and virulence.

Final Abstract Number: 45.001

Session: Oral Presentations: Zoonoses & One Health

Date: Saturday, March 3, 2018

Time: 17:00-18:00

Room: Retiro A

Type: Oral Presentation

Camel Toxoplasmosis: Seroprevalence and zoonotic aspects in Cholistan desert area of Bahawalpur, Pakistan

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Background: Toxoplasmosis is parasitic zoonosis and is demonstrated in domestic livestock including camels. Cholistan desert of Pakistan is hub and native place for camels. For desert nomads camel is a source of milk, meat, transportation and recreation, thus, playing pivotal role in socioeconomics of the community. In view of camel-human interaction, present study was accomplished for seroprevalence and zoonotic potential of camel toxoplasmosis in Cholistan desert of Bahawalpur, Pakistan.

Methods & Materials: Serum samples from 226 camels and 226 humans (n=113 camel keepers; n=113 humans with no contact history to camels) were collected and analyzed for anti-toxoplasma-antibodies. Data about each camel and human were entered in a "data capture form". The serum samples collected from camels and humans were processed for anti-toxoplasma antibodies using Latex Agglutination Test at dilutions 1:16, 1:64, 1:128 and 1:256. Finally percentage prevalence was calculated and analyzed statistically by Chi square test.

Results: Of the camels tested, 9.73% were seropositive for anti-toxoplasma antibodies at titers of 1:16 or higher. As to gender, 11.1% female camels and 8.69% male camels were positive for anti-toxoplasma antibodies. The highest prevalence (12%) was observed in camels of 11 year or above age group followed in order by 6-10 year (9.8%) and 1-5 year (4.4%). The prevalence of toxoplasmosis was high in the 3rd trimester of pregnancy (18.1%) while in the 1st and 2nd trimesters it was 10.5% and 13.3%, respectively. Overall, 12% humans were seropositive for anti-toxoplasma antibodies. The highest seroprevalence of toxoplasmosis was observed in camel keepers (15.92%) than people with no contact history to camels (7.96%). As to gender, 11.97% women and 11.76% men were seropositive for anti-toxoplasma antibodies. Age related prevalence of anti-toxoplasma antibodies was 15.25% in persons between 31-40 years or above age followed in order by 12.8% in 21-30 years, 9.61% in 15-20 years and 5.88% in ≤15 year old age groups.

Conclusion: It was concluded that toxoplasmosis is prevalent among camels in Cholistan desert area of Bahawalpur, Pakistan and there is high risk of transmission of toxoplasmosis to humans having contact with these camels.

Final Abstract Number: 45.001

Session: Oral Presentations: Zoonoses & One Health

Date: Saturday, March 3, 2018

Time: 17:00-18:00

Room: Retiro A

Type: Oral Presentation

Identifying Behavioral Risk Intervention Points to Prevent Zoonotic Spillover at Animal Markets, Farms, and Abattoirs in Egypt

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Background: Human-animal interfaces pose opportunities for pathogen spillover from animal hosts into humans through contact with animal blood, secretions, or other means. Reducing spillover is a concern in Egypt, where diseases like brucellosis and Middle East Respiratory Syndrome have potential to spread from animal to human. Identification of behavioral risk intervention points at human-animal interfaces in Egypt may inform interventions to reduce this risk.

Methods & Materials: Cross-sectional surveys were conducted at 5 abattoirs, 2 animal markets, and 1 camel farm in Egypt from October 2016 to May 2017. Participants completed a standardized questionnaire. Beliefs about animal to human disease risks and behavioral practices were assessed to generate prevalence ratios (PRs) and 95% confidence intervals (CIs) modeling unsafe behavioral practices using belief about animal to human disease risks as an independent variable. PRs were adjusted for potential confounders (age, gender, education, and site type).

Results: Overall, 700 individuals completed the questionnaire (75% from abattoirs, 22% from markets, and 3% from the farm). Of them, 492 (70%) did not believe there are risks associated with slaughtering or butchering animals while having an open wound, and only 194 (28%) were worried about diseases in live animals. Those who believe there are risks associated were significantly less likely to have not washed, rinsed, or bandaged their most recent wound from animal bites or scratches or from butchering or slaughtering animals (adjusted PR=0.69, 95% CI=0.52-0.91). Similarly, those who believe there are risks associated were significantly less likely to not use personal protective equipment (PPE) at work (adjusted PR=0.75, 95% CI=0.66-0.86). Among 378 abattoir workers using PPE, only 7 (2%) use a mask and 16 (4%) use gloves.

Conclusion: A belief that animals do not pose disease risks to humans was prevalent, highlighting a knowledge gap that could be addressed through educational intervention. A sizable portion of those interviewed engage in behavioral practices that may increase their risk of a zoonosis, such as not washing wounds from animals. A multi-faceted intervention that increases knowledge about zoonotic disease risk and provides material resources like PPE and training may reduce spillover risk at human-animal interfaces in Egypt.

Final Abstract Number: 45.002

Session: Oral Presentations: Zoonoses & One Health

Date: Saturday, March 3, 2018

Time: 17:00-18:00

Room: Retiro A

Type: Oral Presentation

Avian Influenza Surveillance: Reassortant Clade 2.3.4.4 Avian Influenza H5N8 virus in Northern Eurasia (2016-2017)

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Background: Recent outbreaks of an avian-origin H5N8, H6N1, H7N9, H10N8 influenza viruses raise concern of the emergence of novel reassortant viruses in Eurasia and the potential threat to the human population.

Wild aquatic birds migrate to and congregate in Asian wetlands and lakes for breeding and molting. Major wild aquatic bird migration routes overlap in Asian part of Russia, connecting this broad geographic area to the wintering grounds of Eurasia and Africa. The unique ecosystem of these territories has been implicated and plays a crucial role in the geographical dispersal of the virus as it was shown by HPAI H5N1 spreading in 2005–2010 and in 2014-2015.

Methods & Materials: During AIV surveillance in wild bird population in Asian part of Russia in 2016-2017 more than 1100 avian samples were collected and screened according to the standard protocols. All samples were collected from the various sites located at the studied territory, such as Novosibirsk region, Tuva region, Russian Far East.

Results: In total, more than 60 LPAI viruses and 15 HPAI H5N8 were isolated. The LPAI viruses were further subtyped as H1N1, H3N8, H4N6, H5N3, H8N4, H11N9. In summer and autumn of 2016, several outbreaks were reported at Uvs-Nuur Lake on the border of Russia and Mongolia and in Novosibirsk region and then spread to the west to European countries. In winter 2017 the virus re-emerged to Central Russia and caused poultry outbreaks. All isolated viruses, which caused outbreaks, belong to novel highly pathogenic avian influenza viruses of subtype H5N8, clade 2.3.4.4. The H5N8 viruses were found to be reassortant with other avian influenza viruses in waterfowl and shorebirds of Northern Eurasia.

Conclusion: We conducted the pathogenic potential assessment of the viruses with molecular-biological analysis and animal models. In this study we have shown circulation of different Avian Influenza viruses in Russia in 2016-2017. The report contains more detailed comparative virological, molecular, pathogenic characteristics of viruses with emphases at HPAI H5N8. This study demonstrates the need for ongoing surveillance to detect new variants of influenza viruses and facilitate prevention of outbreaks.

This work was supported by Russian Science Foundation (grant #17-44-07001).

Final Abstract Number: 45.003

Session: Oral Presentations: Zoonoses & One Health

Date: Saturday, March 3, 2018

Time: 17:00-18:00

Room: Retiro A

Type: Oral Presentation

Prevalence of Brucella Antibodies in goats and the practices of farmers regarding Brucellosis in Wukari, Taraba State Nigeria

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Background: Brucellosis is a bacterial zoonosis with devastating public health significance. It causes serious economic losses in livestock production manifesting as abortion, infertility and low milk yield. This study aimed to determine the prevalence of *Brucella* antibodies in goats and the practices of farmers regarding Brucellosis in Wukari L.G.A Taraba State.

Methods & Materials: Using convenience sampling, a cross-sectional approach was employed to sample 386 goats by jugular venipuncture in three Political Wards; Puje, Avyi and Hospital. Rose Bengal Plate Test (RBPT) was used to screen the sera harvested by centrifugation. A total of 176 structured questionnaires were administered to goat owners to know their practices as regard Brucellosis. Data analysis was done using Pearson's Chi-square and values of $P < 0.05$ was considered significant.

Results: The RBPT revealed a seroprevalence of 15%, 6.6% and 7.6% in Puje, Avyi and Hospital wards respectively. Age-specific seroprevalence yielded 2.8%, 8%, 18.7%, and 1% for <20 months, 22-35 months, 36-45 months and $\geq 46-55$ months age categories respectively with a statistically significant association ($P < 0.05$). Male goats had 9.5% seroprevalence while female had 9.8%. Red Sokoto, Kano Brown, Sahel and West Africa Dwarf Goat had 12%, 12.8%, 11.6%, 5.4% and 7.4% seropositivity respectively. Only 10.5% and 11.6% of the goats sourced from the market and Inherited were positive for *Brucella* antibodies respectively. Fifty-one of the respondents had experienced abortion in their herds while one hundred and twenty-five had not; 6 (11.8%) and 13 (10.4%) of these were positive for *Brucella* antibodies respectively. Only 11.6% and 10.5% were positive for *Brucella* antibodies from the herds that had the history of retained placenta and herds that had not respectively.

Conclusion: There is an evidence of Brucellosis (9.6%) in Wukari L.G.A, Taraba State and the practices of goat owners, as regards the disease is poor. There is a need to enlighten the public on the zoonotic potentials of Brucellosis.

Final Abstract Number: 45.004

Session: Oral Presentations: Zoonoses & One Health

Date: Saturday, March 3, 2018

Time: 17:00-18:00

Room: Retiro A

Type: Oral Presentation

Naturally acquired human infections with the simian malaria parasite, *Plasmodium cynomolgi*, in Sarawak, Malaysian Borneo

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Background: Human infections with *Plasmodium knowlesi*, a malaria parasite of long-tailed and pig-tailed macaques, were thought to be extremely rare until a large focus of human infections were reported in the Kapit division of Sarawak, Malaysian Borneo in 2004. Human infections have since been reported throughout Southeast Asia and *P. knowlesi* is regarded as the fifth *Plasmodium* species causing human malaria. These zoonotic infections were only identified following the use of newly-developed PCR primers for *P. knowlesi* (*Pk*) since *Pk* is morphologically identical to *P. malariae* (*Pm*). Macaques in Sarawak also harbour *P. cynomolgi* (*Pcy*) *P. inui* (*Pin*) *P. coatneyi* (*Pct*) and *P. fieldi* (*Pfld*). Under experimental conditions *Pcy* and *Pin* can infect humans, and there has been one previous case of a naturally-acquired human infection with *Pcy* in Peninsular Malaysia. The aims of the study were to determine whether human infections with *Pcy* and *Pin* occur in Sarawak, Malaysian Borneo.

Methods & Materials: Blood samples were obtained from 332 malaria patients, diagnosed by microscopy as follows: 291 *Pk*, 13 *P. vivax* (*Pv*), 21 *P. falciparum* (*Pf*), 3 *P. ovale* (*Po*), 1 *Pm* and 3 mixed species infections. DNA extracted from these samples was screened with nested PCR assays using primers specific for *Pk*, *Pf*, *Pv*, *Pm*, *Po*, *Pcy* and *Pin*.

Results: The nested PCR assay results indicated 273 *Pk*, 22 *Pv*, 19 *Pf*, 1 *Pm*, 5 *Pcy+Pk*, 2 *Pf+Pv*, 1 *Pf+Po* and 1 *Pv+Po* infection. The five patients with *Pcy+Pk* infections had parasitaemia of 34560, 35738, 15120, 1760 and 560 parasites/uL blood. For two of these patients, early trophozoite-infected erythrocytes with stippling, characteristic of *Pcy*, were observed. However, these constituted only 1.5% and 4.7% of the total parasites in the blood. The very low proportion of *Pcy* parasites in these two cases is the most likely reason that these were undetected by routine microscopy.

Conclusion: In conclusion, this is the first report of naturally-acquired human infections with *Pcy* in Malaysian Borneo. Molecular detection methods are necessary to investigate whether these newly emergent zoonotic infections occur elsewhere in Southeast Asia.

Final Abstract Number: 45.005

Session: Oral Presentations: Zoonoses & One Health

Date: Saturday, March 3, 2018

Time: 17:00-18:00

Room: Retiro A

Type: Oral Presentation

DNA based detection of brucella zoonosis as a blood transfusion hazard in metropolitan population of Lahore and Okara, Punjab, Pakistan

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Background: Brucellosis is a severe zoonotic disease, due to its increasing prevalence in Punjab, Pakistan. A study computing *Brucella* zoonosis in blood donors was conducted, at Okara and Lahore districts, Punjab, Pakistan.

Methods & Materials: This is the first report of human brucellosis spread through blood transfusion from Pakistan by the combined use of serological and DNA based methods, to detect the *Brucella* infection of two hundred blood transfusion samples collected from Okara and Lahore, reflected as *Brucella* endemic areas. Fifty negative control blood samples from healthy individuals collected from "Blood transfusion center, Islamabad", were also included in the study. All samples were then subjected to *Coxiella burnetii* specific qRT-PCR analysis to determine the co-infection with brucella.

Results: This study concludes that 89 out of 200 human Blood Transfusion samples were positive with RBPT (Rose Bengal plate agglutination test), with seroprevalence of 44.5% (95% Confidence Interval [CI]: 37.61 – 51.4). The qRT-PCR (quantitative real-time polymerase chain reaction) analysis showed, 41 out of 200 samples were found positive to *Brucella* genus, with 20.5% seroprevalence (95% Confidence Interval [CI]: 14.9 – 26.09) for all *Brucella* genus positive samples found positive to *Brucella abortus*. Four samples were tested positive with qRT-PCR with prevalence of 2% (95% Confidence Interval [CI]: 0.06 – 3.94). All control samples tested negative with RBPT and qRT-PCR.

Conclusion: This data indicates a high rate of *Brucella* bacteremia, proposing a high risk of transfusion transmitted brucellosis. Blood donation screening for brucellosis may be considered in *Brucella*-endemic areas of Pakistan.

Final Abstract Number: 51.001

Session: Oral Presentations: Tropical Infectious Diseases

Date: Sunday, March 4, 2018

Time: 10:15-12:15

Room: Retiro A

Type: Oral Presentation

Dermatitis linearis caused by *Paederus colombinus* in Colombia: A review and case series

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Background: Dermatitis linearis caused by *Paederus* spp is a distinct type of contact dermatitis, characterized by the presence of erythematous and vesicular lesions on exposed areas of the body, which usually follow a linear pattern of distribution. It is caused by toxins contained in the endolymph of *Paederus* beetles, which belong to the class Insecta, order Coleoptera (beetles), family Staphylinidae (rove beetles), subfamily Paederinae, tribe Paederini, subtribe Paederina.

Methods & Materials: We present a series of five selected cases that reflect the clinical and epidemiological spectrum of this clinical entity from a recent outbreak in two departments of Colombia. The aim of the study is also to report the occurrence of the first outbreak ever reported in Colombia. A thorough physical examination was performed obtaining a detailed description of the cutaneous lesions and looking for signs and symptoms of systemic affection. *Paederus* beetles recovered from patient's dwellings were submitted for entomological identification.

Results: Affected patient ages ranged from 32 to 50 years old, with an average of 42 years old and a female predominance. Lesions presented as eczema with latent burn sensation (60%); as erythematous maculopapular lesions (20%) and papular and erythematous lesions (20%). In all cases, lesions were accompanied by burning / stinging sensation (100%) with pruritus (20%). Afterwards the lesions became vesicular and finally squamous (100%) around the fifteenth day of evolution. In Latin America, reports of dermatitis linearis outbreaks are scarce. The present study reports the occurrence of the first confirmed cases in the Atlantic Coast of Colombia, along with a detailed clinical, entomological and epidemiological description of dermatitis caused by *Paederus colombinus*.

Conclusion: This *Paederus* spp. dermatitis report represent the first ever described in Colombia, emphasizing on the correct approach for a successful diagnostic based on its differentiation from other common skin conditions such as herpes zoster and simplex, bullous impetigo, pustular psoriasis, phytophotodermatitis, Snedder-Wilkinson disease, mycotic infections and other allergic reactions.

Final Abstract Number: 51.002

Session: Oral Presentations: Tropical Infectious Diseases

Date: Sunday, March 4, 2018

Time: 10:15-12:15

Room: Retiro A

Type: Oral Presentation

Evidences of the low implication of mosquitoes in the transmission of *Mycobacterium ulcerans*, the causative agent of Buruli ulcer

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Background: Buruli ulcer (BU) continues to be a serious public health threat in wet tropical regions and more specifically in the coastal west and central Africa. The mode of transmission of its etiological agent, *Mycobacterium ulcerans* (*MU*), remains poorly understood. In Australia, *MU* has been identified in several environmental samples including both the larval and adult mosquitoes. However, there is no clear information linking mosquitoes to BU transmission in Africa, the continent with the highest endemicity of this disease. In this study, mosquito species collected in endemic villages in Benin were screened for the presence of *MU*. In addition, the ability of mosquitoes larvae to pick-up *MU* from their environment and remain colonized through the larval developmental stages to the adult stage was investigated.

Methods & Materials: Seven thousand two hundred and eighteen (7,218) adults and larvae mosquitoes were sampled from endemic and nonendemic villages and screened for *MU* DNA targets (IS2404, IS2606, and KR-B) using quantitative real time PCR.

Results: *MU* was not detected in any of the field collected samples. Additional studies of artificially infected larvae of *Anopheles kishumu* with *MU* strains revealed that mosquitoes larvae are able to ingest and host *MU* during L1, L2, L3, and L4 developmental stages. However, we noticed an absence of these bacteria at both pupae and adult stages, certainly revealing the low ability of infected or colonized mosquitoes to vertically transmit *MU* to their offspring.

Conclusion: The overall findings highlight the low implication of mosquitoes as biological vectors in the transmission cycle of *MU* from the risk environments to humans.

Final Abstract Number: 51.003

Session: Oral Presentations: Tropical Infectious Diseases

Date: Sunday, March 4, 2018

Time: 10:15-12:15

Room: Retiro A

Type: Oral Presentation

Outbreak investigation of "Brain Eating Amoeba" (Primary Amoebic Meningoencephalitis) caused by *Naegleria fowleri*—Karachi, Pakistan, 2012–2014 (with 2015 updated)

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Background: *Naegleria fowleri* is an amoeba that causes a rare and a life-threatening infection of the brain with CFR 97-100% (primary amoebic meningoencephalitis (PAM)). Swimming in warm fresh water, and deep rinsing of the nose with infected water are the associated risk factors. In early September 2014, the media reported many PAM deaths in Karachi. The Department of Health deputed Field Epidemiology & Laboratory Training Program fellows to investigate the outbreak and provide recommendations for control.

Methods & Materials: PAM cases were identified (diagnosed by CSF and PCR) in Karachi through review of records. Three patients and families of the deceased patients were interviewed and geographical coordinates of last places of residence were recorded. Water supply routes, supply methods and water sources were investigated.

Results: Twenty three PAM cases (3 females) were found in Karachi. Case fatality rate was 100%. Age range was 4-67 years (mean: 30). All patients were diagnosed from May to October. Fifteen of 23 (65.2%) patients lived in the 2/6 districts of Karachi in a geographical cluster with one water filtration plant (total 4 pumping plants in Karachi). Fourteen (60.8%) were using municipal water and 11 (47.11%) regularly used water for rinsing the nasal passages during ablution. No chlorination records were found for the years 2012 -2014 for the said pump.

Conclusion: This was the largest outbreak of *Naegleria fowleri* being reported in Pakistan. A poorly chlorinated water supply and warm temperatures may have caused this outbreak. After the start of the outbreak investigation and media coverage, the government initiated corrective measures including increased chlorination of water and an awareness campaign. In 2015 (July) only 02 out of 09 new cases arose from the previously effected districts.

Final Abstract Number: 51.004

Session: Oral Presentations: Tropical Infectious Diseases

Date: Sunday, March 4, 2018

Time: 10:15-12:15

Room: Retiro A

Type: Oral Presentation

Plasmodium vivax Erythrocyte Binding Protein gene copy number, but not Duffy Binding Protein, is significantly higher in Malagasy isolates than in Cambodian ones

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Background: Among the five species of *Plasmodium* that infect humans, *Plasmodium vivax* is the most widespread, with billions of people at risk in nearly 100 different endemic countries in South America, Africa and Asia. *P. vivax* being responsible for millions of cases, a blood stage vaccine would considerably alleviate the burden inflicted by this parasite. Invasion mechanisms of *P. vivax* are still unclear and the prevailing paradigm that makes the interaction between *Plasmodium vivax* Duffy binding protein (PvDBP) and Duffy antigen receptor for chemokines (DARC) essential for *P. vivax* invasion is questioned since this parasite has been observed in individuals lacking the Duffy antigen. The pathways by which the parasite is able to enter the Duffy negative reticulocytes are unknown but two possible mechanisms have been suggested in the literature: the amplification of the gene coding for PvDBP as well as the involvement of alternate proteins, in particular a newly described Erythrocyte Binding Protein, PvEBP, which is able to bind Duffy negative red blood cells, while PvDBP cannot.

Methods & Materials: In this context, to further study these two hypothesis, we analyzed the genomic polymorphisms (copy number variation and sequence polymorphism) in the second exon of PvDBP and PvEBP in isolates from two different locations: Cambodia where the vast majority of people are Duffy positive and Madagascar, where an admixture of Duffy positive and Duffy negative individuals coexists.

Results: Our molecular epidemiology approach demonstrates that rather the PvDBP gene, it is the PvEBP gene that seems to be involved in Duffy negative invasion. We first observed that PvEBP is far more conserved than PvDBP, then, that its copy number variation is significantly higher in isolates from Madagascar compared to Cambodia, whereas we observed no significant difference for the copy number variation of PvDBP.

Conclusion: Since PvEBP shows evidence of weak binding to Duffy negative reticulocytes and assuming that gene amplification leads to increased amount of protein and therefore a better binding to Duffy negative reticulocytes, the higher gene expansion in areas where *P. vivax* encounters Duffy positive but also negative individuals further strengthen the possible role of PvEBP in the invasion of Duffy negative individuals.

Final Abstract Number: 51.005

Session: Oral Presentations: Tropical Infectious Diseases

Date: Sunday, March 4, 2018

Time: 10:15-12:15

Room: Retiro A

Type: Oral Presentation

Frequent and complex relapses confound assessment of chloroquine resistance in Cambodian *Plasmodium vivax*

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Background: *Plasmodium vivax* resistance to chloroquine has been observed in several endemic countries. In Cambodia, up to 17% clinical treatment failure following 3-days standard chloroquine treatment was reported in vivax malaria patients in 2009. The loss of chloroquine efficacy was solely described in northeast area of Cambodia while chloroquine seemed to remain fully effective in other provinces. This led to the withdrawn of chloroquine and its replacement by dihydroartemisinin-piperaquine in 2012. To rigorously assess the extent of *P. vivax* chloroquine-resistance in Cambodia, we conducted a comprehensive therapeutic efficacy study with extensive genotyping of the parasites.

Methods & Materials: The study was conducted in Rattanakiri, in northeastern Cambodia in 2014. 40 enrolled patients were treated with chloroquine (30mg/kg) for three days and followed for two months. Reinfection was controlled for half of the patients by relocating them to a no-transmission area. The 2-months follow-up consisted in frequent clinical examination and capillary blood collection for microscopic, molecular parasite detection and drug concentration measure. The entire genomes of the initial and recurrent parasites were sequenced and complemented by genotyping of more than 100 SNPs for each PCR-positive blood samples collected during follow-up.

Results: Recurrences occurred in 24/40 (60%) patients within the follow-up. No difference was observed between relocated and non-relocated patients. Recurrent parasites were always detected when chloroquine concentration in blood was below therapeutic level. Genotyping revealed that all *P. vivax* clones, within a given infection, responded similarly to CQ. In addition, whole genome sequencing unambiguously showed that most relapsing parasites were different from those in the initial infections.

Conclusion: Recurrences within two months are frequent among Cambodian vivax malaria patients and originate from relapsing parasites from the liver. Pharmacological and genetic analyses revealed no evidence of CQ resistance and suggest that CQ is fully effective against *P. vivax* episodes in Rattanakiri Cambodia. Our results suggest that CQ resistance might be over-diagnosed and confounded with relapses from liver parasites. Our clinical and analytical framework has the potential to differentiate between relapse and resistance and should be implemented in vivax malaria endemic areas with suspected drug resistance.

Final Abstract Number: 51.006

Session: Oral Presentations: Tropical Infectious Diseases

Date: Sunday, March 4, 2018

Time: 10:15-12:15

Room: Retiro A

Type: Oral Presentation

Novel vectors of the zoonotic malaria parasite, *Plasmodium knowlesi*, in two districts of Sarawak, Malaysian Borneo

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Background: The zoonotic malaria parasite, *Plasmodium knowlesi* (*P. knowlesi*), is the most common cause of human malaria in Sarawak, Malaysian Borneo. It accounted for over 80% of hospitalised malaria cases from 2014-2016. Previously identified vectors of the parasite in nature in Malaysia and Vietnam all belong to the *Anopheles* Leucosphyrus Group. Only one study on vectors of *P. knowlesi* has been conducted in Sarawak that incriminated *Anopheles latens* (*An. latens*) as the vector in the Kapit District. This project was therefore undertaken to identify malaria vectors in other districts of Sarawak.

Methods & Materials: Human landing catches were conducted in forested sites of the Betong and Lawas Districts. The salivary glands of anophelines were removed, DNA was extracted and screened with nested PCR assays for *Plasmodium* and species of *Plasmodium*. The sequences of the small sub-unit ribosomal RNA (SSUrRNA) genes of *Plasmodium* spp. and the internal transcribed spacer 2 (ITS2) region and mitochondrial cytochrome c oxidase subunit 1 (CO1) gene of the mosquitoes were derived from the *Plasmodium*-positive samples.

Results: Collectively, 237 anophelines and 2,128 culicines were caught. *An. letifer* (44.8%, n=172) and *An. balabacensis* (47.7%, n=65) were found to be the predominant anophelines in Betong and Lawas districts, respectively. By PCR, 26 anophelines were found to be infected with *P. knowlesi* and other simian *Plasmodium* species (*P. coatneyi*, *P. cynomolgi*, *P. fieldi* and *P. inui*) while phylogenetic analysis of the SSUrRNA genes confirmed the presence of those malaria parasites in 3 *An. barbirostris*, 6 *An. balabacensis*, 6 *An. latens* and 6 *An. letifer*. Phylogenies inferred from the ITS2 and CO1 sequences of *An. balabacensis* and *An. barbirostris* indicate that the former is genetically indistinguishable from *An. balabacensis* in Borneo while the latter is a sibling species of the Barbirostris Subgroup. Preliminary phylogenetic analysis of the CO1 gene of *An. letifer* suggests that they are distinct, but closely related to the *An. letifer* from Singapore.

Conclusion: New vectors of *P. knowlesi* were identified in Betong (*An. latens* and *An. letifer*) and Lawas (*An. barbirostris* and *An. balabacensis*), including 2 species (*An. barbirostris* and *An. letifer*) which are not from the *Anopheles* Leucosphyrus Group.

Final Abstract Number: 51.008

Session: Oral Presentations: Tropical Infectious Diseases

Date: Sunday, March 4, 2018

Time: 10:15-12:15

Room: Retiro A

Type: Oral Presentation

Leishmaniasis occurrence is significantly higher among internally displaced people of Colombia: An analysis from 2007 to 2014

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Background: Leishmaniasis is considered a Neglected Tropical Disease (NTDs) and one of the most frequently reported tegumentary parasitic diseases among refugees and internally displaced populations (IDPs) in Africa and Asia, nevertheless there is lack of studies about it in Latin America, even in Colombia, the country with the highest number of IDPs in the world.

Methods & Materials: This ecological study assessed incidence and differences, of leishmaniasis between general population and IDPs in Colombia and its departments (32) during 2007–2014. Epidemiological data was collected from the National Surveillance System (SIVIGILA-SISPRO), retrieving the codes for tegumentary (CL and MCL) and visceral leishmaniasis (VL) in both populations. We estimated leishmaniasis incidence rates on both populations (cases/100,000 pop), using reference population of the IDPs (official record of the Secretary of Social Welfare) and the general population (from the national statistics institute, DANE). Incidence rates ratios were calculated comparing both populations.

Results: In general population, 82,012 cases of leishmaniasis occurred (98.43% CL, 1.32% MCL and 0.24% VL) (179.13 cases/100,000 pop, 95%CI 178.0–180.0) while 2,434 among IDPs (98.02% CL, 1.97% MCL and 0.37% VL) (797.2 cases/100,000 pop, 95%CI 765.0–829.0). Leishmaniasis was 4.5 times higher among IDPs than in general population ($p < 0.05$) (reaching up to 7 times higher in 2013 and during that year 132.7 times higher in Caldas department). IDPs leishmaniasis cases occurred in 75.6% in males and 24.4% in females. By age groups, 69.2% were <40 y-old (4.4% <10 y-old). All cases of VL corresponded <20 y-old.

Conclusion: This study evidenced a significantly higher leishmaniasis incidence among IDPs, being higher in male and below 40 y-old, when compared with general population in the same territories, which would be expectable given the socioenvironmental conditions in which these subjects have lived. The presence of VL corresponding to pediatric internally displaced persons should be alerted. This has relevant implications for screening, diagnosis and management among IDPs, especially in still highly endemic areas. More studies are required to improve the understanding of tropical diseases among vulnerable populations, as well to provide better medical interventions and for the development of public policies in countries, such as Colombia, with IDPs.

Final Abstract Number: 51.009

Session: Oral Presentations: Tropical Infectious Diseases

Date: Sunday, March 4, 2018

Time: 10:15-12:15

Room: Retiro A

Type: Oral Presentation

Onchocerca volvulus/Loa loa co-infection in rural communities of southeast Nigeria-Implication for ivermectin therapy

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Background: Ivermectin therapy for onchocerciasis poses a great danger to health in areas that are co-endemic with *Loa loa*. Individuals with high microfilarial loads of *Loa loa* are at increased risk of neurologic serious adverse (SAE) events following ivermectin treatment against onchocerciasis. RAPLOA (Rapid Assessment Procedure for loiasis), is a very useful tool to identify areas at potential risk of *Loa loa* post ivermectin treatment encephalopathy. Several rural communities in Ebonyi state are endemic for onchocerciasis with suspected cases of loiasis. Ivermectin distribution is going on.

Methods & Materials: The survey was carried out from 29th April to 16th May, 2015 using the standard procedure as outlined in the Guidelines for the Rapid Assessment of *Loa loa*. Fifty-seven villages in 13 local government areas of Ebonyi state, southeast Nigeria were covered. The Rapid Assessment Procedure for loiasis was based on the restricted definition of the eye worm; the past experience of eye worm, confirmed by a photograph of *Loa loa* adult worm in the white part of the eye and with the duration of the most recent episode being between 1 to 7 days. The questionnaires were administered in the English language, pidgin English, and the local dialect and where necessary, interpreters from the community assisted in the interview process according to the RAPLOA guidelines.

Results: Out of the 57 villages surveyed, 11 exceeded the 40% prevalence. They are as follows: Ohofia Agba, Ishielu – 55%, Okpoto, Ishielu - 45%, Agodo, Ohaukwu - 42.5%, Omocha Emezam Amoffia, Ohaukwu - 47.5%, Ndierukwu, Izzi - 51.3%, Ndiokpoto, Izzi - 45%, Ndiaja Ndiagu Okpoitumo, Abakaliki - 43.8%, Afikpo, Ivo - 43.8%, Ezeigwu Itim, Afikpo North - 50%, Okpo Ezi, Afikpo South - 51.3%, Unwana, Afikpo North- 41.3% respectively. These endemic villages are distributed in 7 out of the 13 local government areas of Ebonyi state. They are; Ishielu, Ohaukwu, Izzi, Abakaliki, Ivo, Afikpo North, and Afikpo South

Conclusion: Sensitization/mobilization was found to be poor in some places. Adequate mobilization is critical to the success of a survey of this nature and must be seen to have been achieved before embarking on the survey.

Final Abstract Number: SADI 01.002

Session: Inmunocomprometidos / Immunocompromised Hosts

Date: Thursday, March 1, 2018

Time: 09:00-10:30

Room: Libertador A

Type: Oral Presentation

Prognostic factors for 7-day and 30-day mortality during gram-negative bacteremia episodes in cancer and hematopoietic stem cell transplant patients

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Background: Gram-negative bacteremia (GNB) in cancer and hematopoietic stem cell transplant (HSCT) patients is a major cause of infection-related mortality. We performed a study to identify factors associated with 7-day and 30-day mortality during GNB episodes in cancer and HSCT patients.

Methods & Materials: Prospective multicenter study. Episodes of GNB in adult cancer and HSCT patients were included in 10 centers of Argentina, from May 2014 to November 2016. To identify factors associated with 7-day and 30-day mortality, variables with $p < 0.05$ in univariate analysis and clinically relevant variables were included in a logistic regression model for multivariate analysis.

Results: 460 episodes of GNB were included. From these, 295 (64.13%) had haematological malignancies, 80 (17.39%) solid tumors and 85 (18.47%) HSCT. 7-day and 30-day mortality was 18.04% and 25.2%, respectively. In the univariate analysis, the factors associated with mortality were: treatment with corticosteroids, combined antibiotic treatment, skin and soft tissue source, respiratory source, breakthrough bacteremia, multidrug-resistant GNB, hypotension, intensive care requirement, shock, multiorgan failure, Pitt score > 4 , Charlson score > 4 and APACHE II score > 24 . In multivariate analysis, factors independently associated with 7-day mortality were: multidrug-resistant GNB (OR, 3.01, 95% CI, 1.17-7.73, $p = 0.022$), respiratory source (OR, 2.86, 95% CI, 1.00-8.19, $p = 0.049$), shock (OR, 5.09, 95% CI, 1.69-15.34, $p = 0.004$), multiorgan failure (OR, 4.91, 95% CI, 1.84-13.07, $p = 0.001$) and APACHE II score > 24 (OR, 5.56, 95% CI, 1.45-21.34, $p = 0.012$). Independent factors for 30-day mortality were: multidrug-resistant GNB (OR, 2.67, 95% CI, 1.21-5.87, $p = 0.014$), respiratory source (OR, 2.96, 95% CI, 1.10-7.97, $p = 0.031$), shock (OR, 6.68, 95% CI, 2.34-19.04, $p = 0.0001$) and multiorgan failure (OR, 5.67, 95% CI, 2.20-14.65, $p = <0.0001$).

Conclusion: The identification of certain prognostic factors would allow the stratification of patients at high risk for mortality during GNB episodes. The appropriate medical intervention of a multidisciplinary team on these factors could improve the outcome of these patients. Since multidrug-resistant GNB are one of the independent prognostic factors, it is essential to identify the patients at risk and treat them appropriately.

Final Abstract Number: SADI 01.003

Session: Inmunocomprometidos / Immunocompromised Hosts

Date: Thursday, March 1, 2018

Time: 09:00-10:30

Room: Libertador A

Type: Oral Presentation

Bacteremia in solid organ transplant recipients: Incidence, etiology, risk factors and evolution. A multicenter study

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Background: Solid-organ transplantation (SOT) has become the preferred approach to treat end-stage organ disease. While preventive strategies have reduced the risk for classical opportunistic infections, bacterial -particularly bloodstream infections (BSI)- remain the most frequent short-term complications in SOT recipients and potentially life threatening. Our objective was to analyze the epidemiology, microbiological characteristics and risk factors associated with morbidity and mortality of BSI in SOT during the first 90 days after transplantation.

Methods & Materials: Prospective, observational, multicenter study. Through a single data collection record, all BSI in SOT during the first 90 days post-transplantation were enrolled between May 2016 and September 2017.

Results: We documented 104 episodes of BSI in: kidney (67%), liver (13%), heart (8%) and other (12%) transplant recipients. Thymoglobulin plus corticoids was the most common induction immunosuppression (43%) in kidney transplant, while tacrolimus, steroids and micofenolic acid was for maintenance (68.5%). 34% of the patients were colonized by multi-drug resistant organisms (MDRO) 12 months prior to BSI, 29% had a previous infection by these MDRO, and 71% received antibiotics 90 days prior to transplantation. Of the 104 BSIs, 92.3% were of nosocomial acquisition and 20 patients (19.2%) had more than one BSI. Secondary bacteremias accounted for 85% of the episodes, being urinary (56.7%) and surgical site infection (12.5%) the most frequent foci. Gram-negative bacilli (GNB) caused 83% of the BSI, with *Klebsiella pneumoniae* registered as the most common agent (33%). 60% of the specimens were MDRO, being extended spectrum b-lactamase (ESBL) the most frequent mechanisms (59.7%), followed by carbapenemase production (15%). There was no significant difference in clinical symptoms, signs and severity (measured by Pitt and APACHE II scores) between patients infected by MDRO and non-MDRO. An adequate empiric antibiotic therapy was registered in 80% of non-MDRO BSI, and 73% in MDRO BSI (p=0.67) There was no difference in 30-day overall mortality between both groups (24% vs 21%, p=0.68)

Conclusion: It is essential to know the epidemiology of BSI and the mechanisms of resistance of the MOs in order to improve prophylaxis and empirical therapies, to finally reduce the impact of these infections in mortality.

Final Abstract Number: SADI 01.004

Session: Inmunocomprometidos / Immunocompromised Hosts

Date: Thursday, March 1, 2018

Time: 09:00-10:30

Room: Libertador A

Type: Oral Presentation

Impact of implementing universal prophylaxis with ciprofloxacin in patients undergoing autologous hematopoietic stem cell transplantation

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Background: Patients with autologous hematopoietic stem cell transplantation (HSCT) due to solid tumor, malignant and non-malignant hematological diseases may benefit from the use of systemic antibiotic prophylaxis. The aim of this study was to measure the effect of using ciprofloxacin as universal prophylaxis in patients with HSCT, admitted to an acute hospital.

Methods & Materials: The study has an uncontrolled before and after quasi-experimental design, with a retrospective analysis. Pre-intervention period: 40 patients under standard care (acyclovir plus fluconazole) for autologous HSCT and post-intervention period: 168 patients under standard care plus prophylaxis with ciprofloxacin 500 mg once daily PO or 20-30mg/kg IV bid. Comparison: suspected episodes of infection, acute diarrhea, confirmed infections (bacteremias, infections due to multiresistant gram-negative bacilli, infections due to *Clostridium difficile*), hospital length of stay and mortality due to infection. Statistical analysis was made with tests chosen upon the nature and distribution of the study variables. A significant p value was established at 0.05. Database and calculations: Excel for Office 365

Results: Patients who received ciprofloxacin presented:

Statistically significant reduction: a) suspected episodes of infection (97.5% vs 77% - OR 0.01- IC95%: 0.001- 0.08 - p<0.0001).

Non statistically significant reduction: a) confirmed infections (45% vs 36.4% - OR 0.66 - IC 95%: 0.32- 1.38 - p: 0.28); b) bacteremias (37.5% vs 25%-OR 0.77-IC95%:0.36-1.62-p:0.49); c) acute diarrhea (50% vs 38.7%- OR 0.63-IC95%: 0.31-1.26- p: 0.19); d) length of stay (average 22.9 vs 20.3 - p: 0.99)

Non -statistically significant increase in: a) infections due to multiresistant gram negative bacilli (n=0 vs 3 - O: 2.18-IC95%: 0.11- 43.2- p: 0.61) b) infections due to *Clostridium difficile* (n=0 vs 1 -OR: 0.95- IC95%: 0.04-24.3 - p: 0.97)

No episodes of mortality due to infection in either period.

Conclusion: We conclude that prophylaxis in patients undergoing autologous HSCT reduces episodes of suspected infection. Study designs with better statistical power should be used to compare confirmed infectious episodes and further prevention, or infections related to antibiotic use.

Final Abstract Number: SADI 01.005

Session: Inmunocomprometidos / Immunocompromised Hosts

Date: Thursday, March 1, 2018

Time: 09:00-10:30

Room: Libertador A

Type: Oral Presentation

Cytomegalovirus reactivation. Risk factors after allogeneic hematopoietic cell transplantation

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Background: Cytomegalovirus (CMV) is cause of increased morbidity and mortality after transplantation of hematopoietic cells. The pathogenesis of CMV disease or infection is complex with multiple interactions with the immune system, mainly in acute and chronic graft-versus-host disease (GVHD). The aim of this study is to analyze the risk factors for the reactivation of CMV in patients undergoing allogeneic hematopoietic cell transplantation (HCT).

Methods & Materials: Prospective descriptive study of the risk factors for the reactivation of CMV in the described population. Univariate and multivariate analysis of the predisposing factors were performed: donor graft, treatment with corticosteroids, use of antithymoglobulin, serologic status, conditioning regimen and the presence of GVHD.

Results: During the period between August 2014 until January 2017, 71 patients were evaluated. 42.25% (n:30) had reactivation of CMV. Average reactivation was 58 days pos- transplant. Both (recipient and the donor) had positive CMV IgG in 78.9%. In the univariate analysis, the reactivation of CMV was associated with haploidentical transplantation (p: <0.01), with the use of corticosteroids (p: <0.01) and GVHD (p: <0.01). In the multivariate analysis, the haploidentical transplant maintained its statistical significance in comparison with the related allogeneic transplant (p: 0.0012, OR:7.07; IC95%:2.4-20.6) as well as the use of corticosteroids (p: 0.0014, OR:9.25; IC95%:2.6-32.4). 100% of patients receiving corticosteroid treatment had grade II / III GVHD. The serologicac status, myeloablative conditioning regimen and the use of ATG showed no statistically significant association.

Conclusion: In patients undergoing allogeneic transplantation, were found as risk factor to reactivation, those who received haploidentical transplantation and treatment with corticosteroids. Another risk factor that showed greater reactivation was the presence of GVHD.

Final Abstract Number: SADI 01.006

Session: Inmunocomprometidos / Immunocompromised Hosts

Date: Thursday, March 1, 2018

Time: 09:00-10:30

Room: Libertador A

Type: Electronic/Moderated Poster Presentation

The impact of time to antibiotic administration and outcome in febrile neutropenia. An unresolved issue?

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Background: Time to antibiotic administration (TTA) is well recognized as determinant of mortality in patients with sepsis. Few studies that have investigated the impact of the TTA on the mortality of patients with febrile neutropenia (FN) are available. The aim of the study was to determine relationship between TTA and negative clinical outcomes (intensive care unit [ICU] admission, in-hospital mortality) in adult cancer patients with FN treated with chemotherapy.

Methods & Materials: A prospective study was conducted to show for all consecutive events of FN from June 2014 to June 2017. Demographic, microbiologic and clinical data were recorded. TTA was defined as the time between the onset of fever and antibiotic administration. Results are presented as median for numerical variables and percentage for categorical ones. To compare proportions chi² test was used. A value of $p < 0.05$ was considered significant.

Results: One hundred nine events of FN in 67 patients (32 men and 35 women) were evaluated.

Hematological malignancies account for most cases of cancer (72.5%). One or more comorbidity factor was present in 52.3%. In 70.6% of cases the absolute neutrophils count were $< 100 \text{ cell/ mm}^3$.

Bloodstream infections were responsible for 23,8%. Overall 22.7% cases with hematologic malignancies required ICU admission compared with 6.6% solid tumor ($p = 0.06$).

The TTA in survival group was 133.37 minutes versus 222.27 in mortality group. During the study there were 11 deaths (10.1% of all cases) of which 82% ($p = 0.06$) required ICU admission.

While univariate analysis age, bloodstream infections, ICU admission and TTA were significantly correlated with mortality, the hematological malignancies and bloodstream positive were related with ICU admission. On multivariate analysis no variables significantly correlated with mortality or ICU admission.

Conclusion: This preliminary study did not show association between delay in TTA and hospital mortality or ICU admission. However, the early administration of the empirical antibiotic therapy continues to be an important risk factor in the prognosis of the FN patients.

Final Abstract Number: SADI 03.002

Session: Microbiología y Antibióticos / Microbiology and Antibiotics

Date: Thursday, March 1, 2018

Time: 09:00-10:30

Room: Libertador C

Type: Oral Presentation

Transmission dynamics of antibiotic resistance genes in human and environmental microbiomes in Lima, Peru

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Background: The increased use of antibiotics in recent decades has led to the emergence of multidrug-resistant bacteria that compromise our ability to treat infectious disease. Due to the high likelihood of contact and genetic exchange with pathogens during disease progression, the gut microbiota is one of the main reservoirs of antibiotic resistance genes (ARGs) available to pathogens. The spread of resistant organisms and ARGs occurs not only between humans through direct contact, but can also be disseminated into human-associated environments, with important consequences for the emergence of resistant organisms and their movement into the clinic.

Methods & Materials: We obtained fecal samples humans and domestic animals from eight households in a periurban slum with high population density and high prevalence of respiratory and gastrointestinal infections in Lima, Peru, as well as sewage samples from a nearby treatment plant that serves this population. 16S rDNA, functional metagenomic selections, and shotgun metagenomic sequencing were used to characterize these microbial communities, measure ARG abundance, and identify potential ARG transmission pathways within the study community.

Results: We identified ~1500 resistance determinants, many of which are evolutionarily distant to known ARGs. We found extensive sharing of ARGs between adults, infants, and domestic animals within households. High sequence similarity and synteny with mobile genetic elements suggest direct transmission of ARGs among family members or acquisition from a common environmental source. Microbial communities from treated sewage effluent were significantly different from influent and fecal samples and represent a novel pool of ARGs with high potential for re-introduction into human populations. Resistomes were generally constrained by the phylogenetic diversity of their underlying microbiota, although we also found evidence for ARG recombination across species and environments.

Conclusion: The immense diversity of resistance genes in the gut microbiota and human-associated environments are likely to contribute to the future emergence of antibiotic resistance in pathogens and emphasizes the need to apply genomic and ecological tools for the characterization of microbial communities in resource-poor settings, where inhabitants remain the most vulnerable to infection and development of multidrug resistance.

See: Pehrsson*, Tsukayama*, Dantas. 2016. *Nature* 533, 212–216. doi:10.1038/nature17672

Final Abstract Number: SADI 03.003

Session: Microbiología y Antibióticos / Microbiology and Antibiotics

Date: Thursday, March 1, 2018

Time: 09:00-10:30

Room: Libertador C

Type: Oral Presentation

In vitro activity of zinc chelators combined with antifungals against Mucormycetes

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Background: Mucormycetes are resistant to most antifungals and new treatment approaches are needed. Different combination therapies for mucormycoses were reported, with variable results. Zinc deprivation by hosts during infection represents an important antifungal mechanism. Thus, combination of chelators with antifungals may be a plausible chemotherapeutic alternative. This strategy has been tested against other fungal pathogens, with promising results.

In this work we study *in vitro* interactions between amphotericin B, posaconazole and the zinc chelators Clioquinol (5-chloro-7-iodo-quinolin-8-ol), N,N,N',N'-tetrakis(2-pyridylmethyl)ethane-1,2-diamine (TPEN) and 1,10-Phenanthroline against six Mucormycetes species.

Methods & Materials: Twenty-seven Mucormycetes isolates were studied: 2 *Rhizopus oryzae*, 18 *Rhizopus microsporus*, 1 *Mucor* spp, 1 *Lichteimia cornymbifera*, 4 *Syncephalastrum racemosum* and 1 *Cunninghamella* sp.

MIC values (no visible growth) for amphotericin B, posaconazole and the chelators Phenanthroline, Clioquinol and TPEN were obtained using the CLSI M38-A2 broth microdilution method.

All drugs were purchased at Sigma in the form of standard powders, dissolved in 100% dimethylsulphoxide to make stock solutions and stored at -70°C until required. The dilution ranges were 0.007 to 4 mg/L for amphotericin, 0.015 to 8 mg/L for posaconazole and 0.03 to 16 mg/L for the chelators. The interactions between the antifungals and the chelators were studied by determining the fractional inhibitory concentration index (FICI) using a checkerboard method. The data was interpreted as synergy (FICI≤0.5), antagonism (FICI>4) or no interaction (FICI >0.5–4).

Results: Amphotericin and posaconazole MICs ranged between 0.25-4 and 0.5-2 mg/L, respectively. Chelators MICs ranged between 0.25 and >16 mg/L. The FICI results were strain dependent. TPEN and posaconazole were synergistic against *Cunninghamella* sp. Clioquinol demonstrated synergy with both antifungals against 41% of *R. microsporus* isolates. Phenanthroline and TPEN with either posaconazole and amphotericin demonstrated no interaction for most isolates (80%).

Conclusion: Clioquinol proved to be the most effective zinc chelator against the isolates in our Mucormycetes collection. Combination of posaconazole with this drug showed promising results for further *in vivo* studies in a model such as *Galleria mellonella*.

Final Abstract Number: SADI 03.004

Session: Microbiología y Antibióticos / Microbiology and Antibiotics

Date: Thursday, March 1, 2018

Time: 09:00-10:30

Room: Libertador C

Type: Oral Presentation

Stress survival and antimicrobial characterization of *S. Enteritidis* from different hosts in Chile

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Background: *Salmonella* is a Gram negative bacteria that colonizes the intestinal tract of humans and animals. Infections with *S. Enteritidis* are of great concern to the public health, being one of the main causes of foodborne diseases in Chile and the world. Wild birds are of increasing importance to public health, because of their association with highly transmissible zoonotic pathogens, and their ability to disseminate them. In this work, the *S. Enteritidis* strains isolated from different hosts were characterized to enlighten the human-animal interface of this bacteria in Chile. Phenotypic assays were done to determine the pathogenic potential of the isolates of *Salmonella* of different hosts.

Methods & Materials: In this work we determined the oxidative stress survival (H_2O_2 15mM and $NaNO_2$ 10mM), acidic pH (pH3), starvation (D10 and D20) and antimicrobial susceptibility of 90 *S. Enteritidis* strains, isolated from poultry, shore birds and humans from different regions of the country, comparing between each strain and among hosts. The statistical analysis were done with Infostat software.

Results: The results show that there is statistical differences among the studied strains in all stress survival assays. When analyzed by host, significant differences ($p < 0.05$) were found in starvation assays (D10 and D20). No differences were found in the oxidative stress and acidic pH assays when grouped by host. When analyzing antimicrobial susceptibility, most of the strains have resistance to at least one antimicrobial. The strains isolated from shore birds had a high resistance to tetracycline (73,3%), human strains had a higher resistance to sulfisoxazol (40%) and in poultry the highest resistance was for nalidixic acid (43,3%). We detected multiresistance in the 36,7% of the strains, most of which came from shore birds (42,4%). Finally, grouped by host, there are no differences ($p > 0.05$) in the presentation of the resistance.

Conclusion: Shore birds can be reservoirs of *Salmonella* strains with potential risk to public and animal health, and could partially explain the progressive rise in the incidence of these serotype-associated outbreaks.

There is a high resistance rate of AM commonly use in Chile, which justifies monitoring these hosts as bio-indicators of AM resistance spread in the environment.

Final Abstract Number: SADI 03.005

Session: Microbiología y Antibióticos / Microbiology and Antibiotics

Date: Thursday, March 1, 2018

Time: 09:00-10:30

Room: Libertador C

Type: Oral Presentation

Community-acquired uncomplicated urinary tract infections (UTI): current etiology and antimicrobial susceptibility in Argentina. A prospective, observational, multicentre study

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Background: UTI are a frequent problem in primary care and represent one of the main reasons for the prescription of antibiotics. Latest IDSA guidelines recommend local prospective studies and unbiased resistance surveillance of uropathogens in order to improve antimicrobial prescription and prevention of resistance. This study aims to analyze the etiology and antimicrobial susceptibility of uropathogens causing uncomplicated UTI from clinical practice to laboratory data in order to avoid bias in resistant patterns.

Methods & Materials: Methods: prospective, multicenter (14 hospitals), observational study (08/16/16 to 08/31/17). Inclusion criteria: non-pregnant woman older than 15 years with urinary symptoms and positive urine culture. Microbiological procedures were performed according to the CLSI standards.

Results: Out of 487 patients recruited, 467 fulfilled the inclusion criteria. Median age 37.6 years, 339 (72%) of episodes were cystitis. Isolates: *E. coli* 82%, *Proteus spp.* 4%, *Klebsiella spp.* 3%. Global antibiotic resistance: ampicillin-sulbactam 22%, trimethoprim /sulfamethoxazole 26.7%, 1st generation cephalosporins 9.9%, quinolones 9%, nitrofurantoin 6.6%. Analyzing in particular *E. coli* resistance: 22.4% for ampicillin-sulbactam, 28% for trimethoprim/sulfamethoxazole, 1st generation cephalosporins 8.7%, for ciprofloxacin, 9.6% and for nitrofurantoin 0.6%. There were no differences in resistance when comparing the group of patients over 50 years of age (397) versus those under 50 (97). We also observed that previous antibiotic use in patients younger than 50 years old (52), was associated with a significant increase in the resistance rates, ampicillin-sulbactam 24%(NS), trimethoprim /sulfamethoxazole 41.3%(p= 0.020; OR: 2.07), 1st generation cephalosporins 21.7%(p= 0.001; OR 3.56) quinolones 34.1%, p < 0.001; OR 10.77), nitrofurantoin 8% (NS).

Conclusion: In our country, resistance levels have increased. Ampicillin-sulbactam and trimethoprim/sulfamethoxazole resistance exceed 20%, which should discourage their use as empirical antibiotic treatment. The previous use of antibiotics was associated with increase of resistance levels. This kind of research allows the improvement of local treatment guidelines.

Final Abstract Number: SADI 03.006

Session: Microbiología y Antibióticos / Microbiology and Antibiotics

Date: Thursday, March 1, 2018

Time: 09:00-10:30

Room: Libertador C

Type: Oral Presentation

Caspofungin and Anidulafungin behave as a fungistatic agent against *Candida auris*

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Background: *Candida auris* is an emerging multiresistant nosocomial pathogen responsible for outbreaks around the world. It is associated with therapeutic failure and high mortality rates. Echinocandins are the empiric treatment choice for *C. auris* infections. However, clinical reports show that some patients respond poorly to this therapy.

The aim of this study was to determine the *in vitro* activity of Caspofungin and Anidulafungin against *C. auris* by time-kill curves method.

Methods & Materials: Twenty *C. auris* strains were studied. They were isolated from patients with proven invasive fungal infection. Susceptibility testing were performed following the Clinical and Laboratory Standards Institute (CLSI) M27-A3 and S4 documents. Time-killing experiments were conducted for 10 of the 20 isolates (in duplicate on 2 separate days) using RPMI-1640 buffered with MOPS. Caspofungin and anidulafungin tested concentration were 0.12, 0.25, 0.50, 1.00 and 8.00 µg/ml. The inoculum was adjusted to 1x10⁵ CFU/ml using Neubauer chamber. A 0.05 ml aliquot of each dilution was taken at different time points (0, 2, 4, 6, 8, 10, 24 and 48 h). These aliquots were serially diluted in sterile water, spread onto Sabouraud plates and incubated at 35°C to determine the numbers of CFU per milliliter. The killing kinetics and the fungicidal activity were analyzed by fitting the mean data at each time point to an exponential equation: $N_t = N_0 \times e^{-kt}$ (N_t viable yeasts at time t ; N_0 starting inoculum; K killing rate; t incubation time).

Results: Anidulafungin and caspofungin geometric means were 1.68 µg/ml (range: 0.5-8.0 µg/ml) and 2.55 µg/ml (range 0.25-8.0 µg/mL), respectively. None of the drugs were able to reach fungicidal activity (no 99.9% inhibition). The mean time to reach 50% growth reduction were 5.30 ± 2.81 h and 1.74 ± 0.45 h for using the MIC values of each strain for anidulafungin and caspofungin, respectively.

Conclusion: The tested echinocandins showed no *in vitro* fungicidal activity against *C. auris* at concentrations reached in serum despite strain's MICs. Caspofungin exhibited the highest time-kill rate

Final Abstract Number: SADI 04.002

Session: Infecciones en Pediatría / Pediatric infections

Date: Thursday, March 1, 2018

Time: 09:00-10:30

Room: Retiro A

Type: Oral Presentation

Intra-abdominal infections in children: A retrospective study

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Background: Intra-abdominal infections are treated with antibiotic empirically. Each institution chose the antibiotics based on several factors, specially on epidemiological data. In Argentina there is limited information about the best treatment option.

Methods & Materials: An analytical-retrospective study was performed at the Pediatric Pedro Elizalde Hospital in Argentina from August 2014 to December 2015. Peritoneal fluid secondary to appendicitis was cultured in order to determine microorganism and sensitivity pattern. We analyzed the risk factors, empirical treatment, days of treatment and evolution, in order to determine if inadequate treatment is associated with complications.

Results: In this period were performed 442 abdominal surgeries (142 generalized peritonitis, 45 localized peritonitis, 224 appendicitis, 18 appendicular plastrons). 158 (36%) were cultivated (study population); patient mean age was 86 months. Predominant microorganism was *E. coli* [112 (70%)], followed by *P. aeruginosa* [21 (13%)]; 33 samples were negative. The initial empirical treatment used in all patients was ampicillin-sulbactam (AMS). The mean days of intravenous treatment was 5.

E. coli were resistance to some group of drugs in 79%, resistance to ampicillin and AMS was 66 and 43% respectively. 70 patients (45%) received inadequate treatment according to resistance pattern.

Complication was seen in 29/158 patients (18.3%), generalized peritonitis raised to 23 episodes (80%). 10/29 (34%) of complicated patients received inadequate treatment. Only 5 *E. coli* (5/22) were resistant to AMS (23%). 5 patients required longer hospital stay and different treatment (ceftriaxone-metronidazole) due to poor outcome. There were 24 readmissions (mean 5.72 days), mostly due to intra-abdominal collections (18 patients).

129 patients did not show complications in spite of 47% of them had no concordance with the antibiotic treatment and the *E. coli* sensitivity.

Conclusion: We found high antibiotic resistance in the predominant microorganism (*E. coli*), but it was not associated with poor outcome (OR 0.5/0.30-0.86). We observed an association of complications with the diagnosis of generalized peritonitis (OR 4.01/1.5-10.5). These results suggest that the torpid evolution is not related with the antibiotic treatment instead to the extension of the infection and the difficulty in achieving a correct drainage.

Final Abstract Number: SADI 04.003

Session: Infecciones en Pediatría / Pediatric infections

Date: Thursday, March 1, 2018

Time: 09:00-10:30

Room: Retiro A

Type: Oral Presentation

Molecular etiological profile of atypical bacterial pathogens, viruses and coinfections among infants and children with community acquired pneumonia admitted to a national hospital in Lima, Peru
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Background: In the world, in recent years we have identified several types of viruses that cause pneumonia in children in different age groups and increased detection rates of atypical disease-causing bacteria

We aimed to study the incidence and clinical characteristic of community-acquired pneumonia (CAP) due to respiratory viruses and atypical pathogens in children adding PCR to routine conventional laboratory tests.

Methods & Materials: Consecutive children patients diagnosed of CAP from January 2009 to December 2010 were included. Nasopharyngeal swabs were processed for study of respiratory viruses and atypical pathogens. PCR conventional was used for detection of atypical pathogens and for respiratory viruses used detection of nucleic acids by two independent multiplex RT-PCR assays. According to the aetiology, patients were categorized in 4 groups: (1) atypical pathogens detected, (2) virus detected, (3) mixes, virus and atypical pathogens and (4) unknown aetiology.

Results: Atypical pathogens were detected in 40% (58/146); viral etiologies in 36% (52/146) and coinfections in 19% (27/146). The most common etiological agent was *M. pneumoniae* (n=47), followed by *C. pneumoniae* (n=11). The most frequent respiratory viruses detected were: respiratory syncytial virus A (n= 35), influenza virus C (n= 21) and parainfluenza virus (n= 10). Viral-bacterial and bacterium-bacterium coinfections were found in 27 cases. In our study population, atypical bacteria (40%) were detected as frequently as respiratory viruses (36%). The presence of *M. pneumoniae* and *C. pneumoniae* should not be underestimated as they can be commonly isolated in Peruvian children with CAP.

Conclusion: Our study revealed that both atypical bacteria and respiratory viruses are among the most frequent agents detected in children with CAP from Lima, Peru. The incorporation of highly sensitive and specific molecular techniques, such as RT-PCR, should be considered in order to achieve an accurate etiological diagnosis and therapeutic management, avoiding the empirical use of antibiotic therapy, particularly in children with pneumonia of viral etiology. In addition, an increase in macrolide resistance has been observed worldwide among CAP patients infected with *S. pneumoniae* and *M. pneumoniae*. This highlights the importance of a precise etiological diagnosis during the management of CAP in children.

Final Abstract Number: SADI 04.004

Session: Infecciones en Pediatría / Pediatric infections

Date: Thursday, March 1, 2018

Time: 09:00-10:30

Room: Retiro A

Type: Oral Presentation

Community vs hospital acquired *Staphylococcus aureus* bacteremia in patients admitted in a children hospital in Buenos Aires, Argentina: Clinical and antibiotic resistance

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Background: Community-associated (CA) methicillin-resistant *Staphylococcus aureus* (SA) isolations predominate in children in Argentina. Antibiotic resistance, molecular and clinical characteristics differ between CA-SA and hospital-associated (HA) *Staphylococcus aureus* infections.

This study was performed to identify differences in clinical features and antibiotic resistance between CA-SA bacteremia (SAB) and HA-SA bacteremia (HA-SAB) in children

Methods & Materials: Surveillance observational retrospective study. We randomized a sample of patients admitted in a third level children hospital in Buenos Aires, Argentina with SAB between 2014 and 2016. SAB were classified in HA or CA. Demographic, clinical characteristics and resistance patterns between groups were compared. Chi² or rank sum test was used depending on the variable. P<0.05 was considered significant.

Results: n: 160. HA-SAB: 80, CA-SAB: 80. Fifty (62%) of HA-SAB were male, and 58 (72%) of CA. Median age in months were HA-SAB: 36 (IQR 7-72) vs CA-SAB: 84 (IQR 34-144), p <0.01. Bacteremia was classified as: primary bacteremia in 13 (16%) in HA-SAB vs 3 (4%) in CA-SAB, p <0.05; secondary 29(36%) vs 77 (96%), p <0.01. Thirty-eight (47%) of HA-SAB was catheter-related bacteremia. Length of bacteremia >5 days in HA-SAB in 12 (15%) vs CA-SAB 17 (23%), p= 0.6. Intensive care admission was recorded in 30 (37%) HA-SAB vs 19 (25%) CA-SAB, p= 0.4. Length of parenteral antibiotic was HA-SAB 14 days (IQR 10-16) vs CA-SAB 17 (10-25), p= 0.3. Methicillin resistance was identified in HA-SAB in 35 (43%) vs CA-Sab 55 (69%), p<0.01; Clindamycin resistance 17 (22%) vs 5 (6%), p<0.05. Any antibiotic resistance was recorded in HA-SAB 43 (54%) vs CA-SAB 60 (75%).

Conclusion: Clinical characteristics differ between CA-SAB and HA-SAB. Although methicillin resistant SAB predominated in CA infections, other antibiotic resistance was more frequent in HA-SAB. Continuous surveillance is crucial in institutions to identify epidemiology of SAB.

Final Abstract Number: SADI 04.005

Session: Infecciones en Pediatría / Pediatric infections

Date: Thursday, March 1, 2018

Time: 09:00-10:30

Room: Retiro A

Type: Electronic/Moderated Poster Presentation

Invasive disease caused by *H. influenzae* non- b serotypes in children

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Background: *Haemophilus influenzae* (six serotypes, a-f and non typable) causes upper and lower respiratory infections and invasive disease. Invasive disease due to non-b *Haemophilus influenzae* is an emerging disease after the introduction of universal vaccination strategy for serotype b in infants and toddlers (1998) in Argentina. Although the first strain was isolated at the hospital in 1994 during the prevaccinal period. Aim: to describe the frequency for invasive disease.

Methods & Materials: We prospectively studied 113 strains non-b *H. influenzae* invasive disease isolated from 109 children aged 1 month-10 years (1997-2015) at the Microbiology Department, Sor Maria Ludovica Children Hospital, La Plata, Argentina. Blood (Bact/Alert, Organon Teknika Corp), CSF, and samples from other normally sterile sites were cultured. Isolation was made by standard methods, and identification with DIFCO™ capsular specific serum (Detroit, Michigan, USA).

Results: None to 13 strains were isolated per year. Frequency according to type of sample was: blood culture 76.1% (n=86), pleural effusion 12.4% (n=14); CSF 10.6% (n=12), peritoneal fluid 0.9% (n=1). The distribution by serotypes was: non typable 77.8% (n=88); a, 9.7% (n=11); c, 0.9% (n=1); d, 1.8% (n=2); e, 3.5% (n=4); and f, 6.2% (n=7). Twenty three strains (20.3%) were beta-lactamase positive. Clinical manifestations were: bacteremic pneumonia, 51.2% (n=57), pneumonia and empyema, 11.9% (n=13); meningitis, 11.0% (n=12), bacteremia, 11.9% (n=13); sepsis, 12.8% (n=14); peritonitis, 0.9 (n=1). Children < 2 years of age accounted for 92.7% cases (n=101).

Conclusion: With the success of *H. influenzae* b conjugate vaccine to prevent invasive disease (n=104 for the studied period, 59 for years 1997-1998) we observed an increase for other serotypes although the number is reduced compared with the past impact of serotype b (>20 cases/year).

Final Abstract Number: SADI 04.006

Session: Infecciones en Pediatría / Pediatric infections

Date: Thursday, March 1, 2018

Time: 09:00-10:30

Room: Retiro A

Type: Electronic/Moderated Poster Presentation

Clostridium difficile infection in the pediatric population of a general hospital in Argentina

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Background: Clostridium difficile diarrhea (Cd) is one of the most frequent health care associated infections and is linked to use of antibiotics. Although it is more frequent in adults, its incidence in children is increasing worldwide. The objective of this work is to describe the epidemiology of diarrhea caused by CDI in pediatric patients in a general hospital in Buenos Aires city.

Methods & Materials: We analyzed all patients with CDI diarrhea under 18 years of age treated in the Hospital Italiano de Buenos Aires between January 2015 and October 2017. The CDC/NHSN definitions were used, Community onset (CO): onset in the community \leq 3 days after admission to a healthcare facility. Community-Onset Healthcare Facility-Associated (CO-HCFA): onset in the community \leq 3 days after admission and less than 4 weeks after the last discharge; Healthcare Facility-Onset (HO): onset $>$ 3 days after admission, Indeterminate onset (IO): onset $>$ 4 weeks of admission and $<$ 12 weeks, Recurrent (R) an episode $<$ 8 weeks after onset of a previous episode.

Results: During this period, 39 positive samples were obtained for CDI of 37 patients all with diarrhea. CO: 26%, CO-HCFA: 26%, HO: 41%, IO: 5% and R 2%, The median age was 4.25 years, of the outpatients was 3.1 years.

56% were male, 79.5% had underlying diseases, 56% had immunosuppression (Bone Marrow transplantation 13%, Oncohematologic 36%). The 70% of CO patient don't have risk factors only 16% required hospitalization. The 74% had received antibiotic treatment (Atb) within the last month. The 84.6% presented watery diarrhea, 7.7% prolonged, 12.8% with bloody diarrhea and 2.6% with pancolitis.

The patient with pancolitis died, although given her bone marrow transplantation and a zygomycetes infection it was difficult to establish the cause of death. In a single sample, the Hypertoxigenic strain 027/NAP1 was isolated.

The rate CDI with hospital acquisition was 0.3/1000 patient/days in 2015, 0.15 in 2016 and 0.54 in 2017, with an outbreak in October.

Conclusion: There is limited data on Clostridium difficile infection in pediatric patient, performing this review we observed that the rates are similar to those in adults.

Final Abstract Number: SADI 07.002

Session: Vacunas / Vaccines

Date: Thursday, March 1, 2018

Time: 11:00-12:30

Room: Libertador A

Type: Oral Presentation

Rotavirus massive vaccination in Argentina: better than we expected

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Background: Although Latin America has seen a rapid and successful introduction of rotavirus vaccines since 2006, Argentina only incorporated monovalent vaccine into its National Immunization Program in 2015. No specific surveillance strategy has yet been designed to accurately measure the impact of this recent introduction on the diarrheal disease burden in our country. Thus, we assessed post-vaccine introduction data (all-cause acute diarrhea and rotavirus laboratory confirmed cases, and genotype distribution), compared to pre-vaccination period in children under 5 years of age in Argentina.

Methods & Materials: We conducted an observational, cross-sectional ecologic analysis of all-cause acute diarrhea and rotavirus laboratory confirmed cases reported to clinical and laboratory-based modules of the Argentine Surveillance Health System. Endemic channel and global and seasonal incidence rates of pre- (2011-2014, mean) and post-vaccination (2016) periods were assessed. For comparison purposes, rate ratios (RR) and 95% confidence intervals (CI) were calculated. Rotavirus laboratory confirmed cases data was compared using chi-square test and considering p-value <0.05 significant. Also, conventional binary genotypification on rotavirus-positive samples was performed.

Results: In post-vaccination period, a global decrease of 20.8% (RR: 0.792, 95% CI: 0.789-0.795) in the rate of all-cause acute diarrhea cases in children under 5 years of age was found. Seasonal analyses showed that the highest rate reduction (42.5%) was observed in the epidemiological weeks 16-36 season (RR: 0.575, 95% CI: 0.571-0.579), mainly due to declination in the under 1 year of age group (55.9%; RR: 0.441, 95% CI: 0.434- 0.448). Also, the endemic channel showed that declination was more significant in the autumn/winter season. Rotavirus laboratory confirmed cases showed 61.7% of reduction (p<0.05) and weekly distribution analyses indicated a significant flattening of the expected seasonal peak. G2P[4] was the most prevalent circulating genotype (57.2%).

Conclusion: These results highlight the shifting of diarrheal disease burden and lead to the supposition that the entire rotavirus circulation dynamic is changing in our country. This study represents the first assessment of this high-impact event since rotavirus massive vaccination strategy was implemented and we come to the conclusion that its introduction represented a very successful public health intervention in Argentina.

Final Abstract Number: SADI 07.003

Session: Vacunas / Vaccines

Date: Thursday, March 1, 2018

Time: 11:00-12:30

Room: Libertador A

Type: Electronic/Moderated Poster Presentation

An economic evaluation of Varicella vaccination in Argentina

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Background: In 2015, Argentina introduced universal varicella vaccination (UVV) as a one-dose programme offered at 15 months of age. The objective of this analysis was to evaluate the health and economic implications of scheduling options for a transition to two dose UVV, considering both monovalent varicella vaccines (V) and quadrivalent measles-mumps-rubella-varicella vaccines (MMRV) in Argentina.

Methods & Materials: A dynamic transmission model of varicella disease was adapted using data from a recently conducted local study on varicella healthcare resource utilization and complications, and previously published Argentinian seroprevalence data. Strategies considered varied between long (> 4 years) and short (≤6 months) intervals between doses and use of V/MMRV formulations (age/coverage rate): Long V/V (V 15 months/90%, V 6 years/85%), Long V/MMRV (V 15 months/90%, MMRV 6 years/85%), Short V/MMRV (V 15 months/90%, MMRV 18 months/85%), Short MMRV/MMRV (MMRV 12 months/90%, MMRV 18 months/85%). MMRV vaccines were assumed in the base case to be 33% more costly than the component prices, and a grid search strategy was used to identify the price at which it would be more cost-effective to use MMRV instead of V. Costs were calculated in 2017 United States Dollars (USD), with costs and benefits discounted at 3%. ; Payer and societal perspectives were considered over 100 years.

Results: In the absence of UVV, the model predicts over 600,000 varicella cases, 80 deaths, and 68.8 million USD expenditure for treatment annually. The most effective strategy in reducing total varicella cases and deaths is the short V/MMRV, followed by Short MMRV/MMRV; although all strategies are cost saving compared to no vaccination, the least costly strategy is Long V/V, followed by Long V/MMRV and Short V/MMRV. From both the societal and payer perspectives, the most cost-effective strategy is Long V/V, followed by Short V/MMRV and Short MMRV/MMRV.

Conclusion: 2 dose UVV is a cost-effective intervention in Argentina, and short intervals between doses will lead to the best health outcomes. The most cost-effective choices of schedule and product (V, MMRV) will be determined by the eventual price of the quadrivalent vaccine compared to the component vaccines.

Final Abstract Number: SADI 07.004

Session: Vacunas / Vaccines

Date: Thursday, March 1, 2018

Time: 11:00-12:30

Room: Libertador A

Type: Electronic/Moderated Poster Presentation

Measles and Rubella immune status among healthcare workers at a teaching hospital in Guatemala
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Background: In the last years worldwide outbreaks of measles have occurred. Healthcare workers (HCW) are a high-risk group of acquiring and transmitting infectious diseases to patients and staff. It is important to identify and immunize susceptible HCW to prevent and control hospital infections.

The aim of the study was to determine the immunization status to measles and rubella in HCW of a tertiary care hospital, in a developing country with mandatory single dose MMR vaccination since 2002.

Methods & Materials: A cross-sectional study of 89 randomly selected HCW from the emergency room of the Pediatrics, Obstetrics and Surgery departments was performed. Closed question survey information of immunization and disease history was obtained. Antibodies were detected at the National Laboratory with an enzyme-linked immunosorbent assay for measles and rubella (MR).

Results: Overall rates of serological positivity to MR were 85.39% (76/89) and 97.75% (87/89), respectively. No differences were observed between healthcare groups, sex, age or length of employment in the hospital. Although the difference was not statistically significant, the rate of seroprevalence of antibodies was lowest for measles. The reported history of at least one MMR vaccination dose was 82.03%.

Despite neither report of vaccination history of MMR nor disease, 17.1% (13/76) HCW showed immunity to measles and 8.04% (7/87) to rubella. HCW with negative results were given an MMR vaccine.

Conclusion: Immunity levels were suboptimal although 82.89% had been previously vaccinated against measles. This highlights the importance of following the two-dose measles vaccination program. Immunity levels in 31.46% HCW with neither vaccination nor disease history were found, which could represent a possible sub clinical and undetected disease. This could've possibly lead to a delay in isolation and confirmation of the suspected subject which could've resulted on a measles outbreak. These data confirms that screening and vaccination of susceptible healthcare worker is essential to keep Latin America as a measles and rubella free region according to the 2016 declaration of the Pan American Health Organization (PAHO).

Final Abstract Number: SADI 07.005

Session: Vacunas / Vaccines

Date: Thursday, March 1, 2018

Time: 11:00-12:30

Room: Libertador A

Type: Electronic/Moderated Poster Presentation

Surveillance and molecular characterization of human adenovirus in children up to 5 years old with acute gastroenteritis in the era of rotavirus vaccine, Brazil, 2015

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Background: Following the establishment of rotavirus (RVA) vaccination in Brazil in 2006, a significant decrease was observed in under-5-years diarrhea-related mortality and hospital admissions in the country. In this context, other enteric viruses could emerge; including enteric Adenovirus types 40 and 41 (AdV 40/41). The aim of this study was to determine the frequency of AdV in children <5 years with acute gastroenteritis in Brazil, and conduct the molecular characterization.

Methods & Materials: A total of 456 fecal samples were obtained in 2015, and first screened for RVA and norovirus (NoV). A total of 250 RVA and NoV negative samples were tested further for the presence of AdV by PCR. Positive AdV samples were sequenced to genotype characterization.

Results: AdV was detected in 29 cases (11.6%); median age of 11.3 months. AdV infection was observed throughout the year, with an increased incidence occurring from February to April. AdV F 41 was the most frequent genotype (51.7%, 15/29), followed by AdV F 40 (10.3%, 3/29), AdV C 1 (10.3%, 3/29) and AdV C 2 (10.3%, 3/29). Together, AdV F 41 and 40 were responsible for more than half (62%) of the AdV positive cases obtained here. Other genotypes, including AdV C 5 (6.9%, 2/29), AdV A 12 (3.5%, 1/29), AdV A 31 (3.5%, 1/29) and AdV D 56 (3.5%, 1/29), were also detected. The nucleotide analysis showed that the Brazilian AdV samples clustered together with strains from distinct continents, indicating that AdV strains circulating in Brazil were closely related to those strains circulating worldwide.

Conclusion: Although AdV species F was the most frequent detected, the role of non-enteric AdV species A and C cannot be ignored in diarrheal children. AdV D 56 was described for the first time in a fecal sample from patients with acute gastroenteritis, although a clear association between genotype and acute diarrhea could not be established. The results presented *suggest an increase in the AdV detection rate after RVA vaccine introduction*. AdV screening should be considered as differential diagnosis in Public Health Laboratories, and continuous studies are essential to verify the impact of others enteric viruses in the community after RVA vaccination.

Final Abstract Number: SADI 07.006

Session: Vacunas / Vaccines

Date: Thursday, March 1, 2018

Time: 11:00-12:30

Room: Libertador A

Type: Electronic/Moderated Poster Presentation

A cost-effectiveness analysis of vaccinating older adults with the 23-valent pneumococcal polysaccharide vaccine (PPV23) compared to no vaccination, the 13-valent pneumococcal conjugate vaccine (PCV13), or PCV13 followed by PPV23 in Colombia

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Background: The objective of this study was to assess the cost-effectiveness of PPV23, when compared with no vaccination, PCV13 and the sequential use of PCV13 and PPV23 in adults 60 years and older in Colombia.

Methods & Materials: A state-transition Markov model was developed. Five health states were considered: no pneumococcal disease, invasive pneumococcal disease (IPD), nonbacteremic pneumococcal pneumonia (NBPP), postmeningitis sequelae (PMS), and death. A cohort of 60-year-olds in Colombia was followed up to 100 years of age or until death. Vaccine efficacy against IPD was obtained from a meta-analysis and a clinical trial. Vaccine efficacy against NBPP was obtained from a population-based cohort study and a clinical trial. Costs were obtained from the Pan American Health Organization, Colombian official list prices and published literature. Costs and outcomes were discounted at 5.0% per year, the analysis took the perspective of the third payer and costs were expressed in Colombia Pesos and inflated to 2016 rates where necessary. Incremental cost-effectiveness ratio (ICER) per quality-adjusted life year (QALY) gained was the main outcome. The World Health Organization definition of less than 3 times of per capita Gross Domestic Product in Colombia (i.e. COP 68,933,306 per QALY gained) was used as the threshold of cost-effectiveness. Sensitivity analyses were conducted to test the robustness of the result.

Results: A cohort of 3,324,291 immunocompetent individuals was followed. In the base case analysis, compared to no vaccination, vaccinating with PPV23 was associated with a reduction of cost by COP 28.5 billion and an increase in QALYs by 2,844. Compared to vaccinating with PCV13, vaccinating with PPV23 was associated with a reduction of cost by COP 97.7 billion and an increase in QALYs by 755. The sequential strategy was estimated to have incremental cost of COP 138.2 billion and incremental QALYs gained of 393 compared to PPV23, however it was deemed not cost-effective at an ICER of COP 351,514,729.

Conclusion: In conclusion, our study suggests that vaccination with PPV23 is the optimal strategy for prevention of pneumococcal disease in Colombia in adults 60 years and older.

Final Abstract Number: SADI 11.002

Session: Infecciones en Pacientes Críticos / Infections in Critical Patients

Date: Thursday, March 1, 2018

Time: 11:00-12:30

Room: Retiro BC

Type: Oral Presentation

Post-sternotomy mediastinitis (PSM): facing a difficult-to-treat serious infection (1998-2016)

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Background: PSM is uncommon but one of the most feared complication of cardiac surgery, with high mortality and cost of treatment.

Our objective is to describe the clinical characteristics, microbiology, medical and surgical management and the results of PSM in a single cardiovascular reference center.

Methods & Materials: Retrospective analysis of consecutive episodes of PSM registered in the institutional database. Categorical variables were compared using Chi-square or Fischer exact tests; continuous variables with Student's t was used as applicable. IBM® SPSS Statistics program version 21 was used.

Results: From November/1998 to December/2016, 182 (1.78%) PSM episodes in 10.233 cardiothoracic surgeries performed (57% CABG, 18% valve replacement and 22% CABG + valve replacement; 72% programmed) were included. Mean age: 65 yo (SD + 11,96). Male: 131 (72%). BMI: 28.83 (SD+4.91). Comorbidities: DBT 43%, previous MI 33%, smokers 50%, CHF 19%, previous cardiac surgery 8.8%, bilateral internal thoracic artery grafting 29%. Clinical picture: fever 70%, pain 46.7%, erythema 33.5%, sternal click 13%, purulent discharge 69.2 %, wound dehiscence 16%, sepsis 30%. Most frequent combined clinical signs/symptoms were: fever + purulent discharge (11%). Most PSM turned up during the 2nd week after surgery (median time: 11 d). Diagnostic methods: subxiphoid aspiration was positive in 121/134 (90.3%); blood cultures 107/161 (66.45%). Microbiology: GPC 122 (60.7%); S. aureus 41.7%, CNS 13.9%, Enterococcus spp 3.8%, SVG 1.3%), GNB 78 (42.9%); K. pneumonia 23%, P. aeruginosa 21%, E. coli 18%), polimicrobial 33 (18.1%), Candida spp 7 (1.3%), negative cultures 1.1%. Surgical treatment: 159/180 (88%) pts underwent open debridement; in 157 surgical treatment was completed with primary sternal closure in the early 72 hs from the diagnosis of PSM. Complications: infective endocarditis 1.6%, sternal osteomyelitis 23%, in-hospital mortality: 17%. Outcome: cure and improvement 145 (80.6%); relapse 2/180 (1.1%) requiring second debridement.

Conclusion: PSM is an unusual but very complex and frequently subtle disease that requires a high index of suspicion to be identified. It demands combined medical and surgical approach in order to decrease the mortality. Wound (subxiphoid) aspiration is an extremely easy way to perform rapid diagnosis, yielding high microbiology performance. Immediate debridement, drainage and primary sternal closure could be an interesting approach.

Final Abstract Number: SADI 11.003

Session: Infecciones en Pacientes Críticos / Infections in Critical Patients

Date: Thursday, March 1, 2018

Time: 11:00-12:30

Room: Retiro BC

Type: Oral Presentation

Extended-spectrum β -lactamases (ESBL) TEM and SHV in intensive care unit patients with Health-care associated infections, silenced genes?

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Background: The extended-spectrum β -lactamases (ESBL) Ambler's class A are capable of hydrolyze broad spectrum penicillin and cephalosporins, and mostly are codified by plasmidial genes. Health-care associated infections (HAI) are a group of entities with a high frequency worldwide, specially in critical adult patients and children in Intensive Care Units (ICU). The frequency of ESBL in this kind of patients is unknown nowadays in ICU in Cartagena de Indias D.T., Bolívar Colombia.

Methods & Materials: The goal of this project was to describe the epidemiology of ESBLs type TEM and SHV in the city of Cartagena de Indias D.T state of Bolívar in Colombia. Clinical samples (blood, urine, LRT secretion, surgical site secretion) were collected from adult patients under HAIs diagnosis (Ventilator Associated Pneumonia, Bloodstream Infection, Urinary Tract Infection, Surgical Site Infection).

Phenotypic identification, susceptibility test and antibiotic profile was performed with an automatized method according the current CLSI standards, following of genotypic identification with molecular biology methods as PCR and sequencing to confirm the presence of TEM and SHV genes in susceptible and resistant bacteria.

Results: The presence of ESBLs type TEM and SHV was frequent in the samples collected, finding that the presence of TEM/SHV at the same time was found in 43.3% of the samples and TEM ESBL was the most frequent, these findings were observed in susceptible and resistant bacteria. *K pneumoniae* was the most frequent bacteria (33.3%) follow by *P. aeruginosa* (28,9%) with TEM and SHV genes in susceptible and resistant samples at the same time.

Conclusion: The presence of ESBL type TEM and SHV in susceptible and resistant bacteria in Health-care associated infections (HAI) in Intensive Care Units (ICU) patients has an importance in antibiotic therapy and prognosis of this kind of patients worldwide. Silenced genes in susceptible strains has been described in this kind of isolates, in Cartagena, Colombia this kind of findings are new, and could be part of the reason of the negative outcome on these patients.

Final Abstract Number: SADI 11.004

Session: Infecciones en Pacientes Críticos / Infections in Critical Patients

Date: Thursday, March 1, 2018

Time: 11:00-12:30

Room: Retiro BC

Type: Oral Presentation

Epidemiology of KPC producing *Klebsiella pneumoniae* infection in an intensive care unit

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Background: During the last decade the reports of KPC producing *Klebsiella pneumoniae* (kpn-KPC) have increased all over the world. It has emerged as a public health problem with a high rate dissemination. The mortality rate ranges from 18 to 60% being higher in patients with bacteriemia. The inadequate empirical treatment and presence of pan resistance worsen the clinical outcome. Our objective was to describe the episodes of bacteriemia due to kpn-KPC and evaluate the outcome and relationship with colonization.

Methods & Materials: We conducted a retrospective observational study. Data were extracted from medical records of patients hospitalized in the ICU with bacteriemia due to kpn-KPC of a general hospital from January 2016 to June 2017. Susceptibility in vitro was tested for colistin, gentamicin, amikacin, tigecycline, and fosfomycin according with CLSI. Colonization was defined as the positive rectal swab. Surveillance was carried out once a week. The samples were processed in chromogenic agar (CHROMagar).

Results: 14 episodes were included in the study. 10 in 2016 and 4 in 2017. 7 men and 7 women. The mean age was 56 years. The most frequent comorbidities were renal insufficiency (50%) and diabetes (50%), the causes of ICU admission was shock (57%), post abdominal surgery 14,2%), acute respiratory failure (21,42%) and patients with neurological impairment (7,14%). 64% of the strains were resistant to aminoglycosides, 78% to colistin and 21% were resistant to all the tested antibiotics. The most frequent empiric treatment was the carbapenem-colistin association, in 92% of the cases a change was needed to carbapenem-aminoglycosides or combinations with tigecycline or double carbapenem. The attributable mortality was 48,8%. In 94% of the cases the rectal swab was positive whereas 18,1% of the patients with positive swab developed infection.

Conclusion: KPC-kpn infection develops in severely ill patients resulting in high morbidity and mortality rates in spite of appropriate treatment. Colonization may predict the development of infection, highlighting the importance of active surveillance and fulfillment of prevention measures.

Final Abstract Number: SADI 11.005

Session: Infecciones en Pacientes Críticos / Infections in Critical Patients

Date: Thursday, March 1, 2018

Time: 11:00-12:30

Room: Retiro BC

Type: Oral Presentation

The era of multidrug-resistant microorganisms: Impact on febrile neutropenic patients

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Background: Antimicrobial treatment for febrile neutropenic (FN) patients has become a challenge due to the growing emergence of multidrug-resistant microorganisms (MDR-MO). The characteristics of these infections vary depending on the geographical areas and the level of local resistance.

The objective of this study was to analyze the characteristics of the FN population due to oncological diseases and the incidence of MDR-MO.

Methods & Materials: Retrospective, observational and descriptive study from June 2015 to August 2017 in FN adults hospitalized at a public hospital of tertiary complexity in Buenos Aires city, Argentina. Demographic, clinical and microbiological characteristics were analyzed.

We included the following MDR-MO: extended spectrum beta-lactamase (ESBL) and carbapenemase-producing *Enterobacteriaceae* (CPE), *Acinetobacter baumannii*, vancomycin resistant *Enterococcus* (VRE) and *Stenotrophomonas maltophilia*.

Results: Thirty-two patients were included; 56% were women, the median age was 53 years old (range 18-75) and the average of time of hospitalization was 42 days. Sixteen percent of the patients had solid neoplasms and 84% haematological diseases. Of these, 56% were acute leukemias. Colonization by CPE or VRE was observed in a 59% of the patients.

There were 148 infectious episodes (IE) in 81 episodes of FN. Microbiological documentation was observed in 41% of the IE. Of them, MDR-MO were responsible for 25% of the episodes. The most frequent MDR-MO were: carbapenemase-producing *Klebsiella pneumoniae* 47%, ESBL producing *Enterobacteriaceae* 26%, *Acinetobacter baumannii* 16%, VRE 5% and *Stenotrophomonas maltophilia* 5%. MDR-MO were isolated from the following foci: bacteremia 47%; urinary infections 26%; pneumonia 11% and other 16%. Patients with MDR-MO had acute leukemia in a 67%. The median time of hospitalization was 61 days and 80% had colonization CPKP or VRE. Inadequate treatment for MDR-MO was observed in 63% of the cases and 12% for susceptible microorganisms ($p < 0.01$). The overall mortality was 45%: 53% for MDR-MO and 27% for susceptible microorganisms ($p = ns$).

Conclusion: MDR-MO infections were frequent in the studied population with predominance of bacteremia due to enterobacteria, especially CPE and ESBL-producing *Enterobacteriaceae*. According to these results MDR-MO should be taken into account for the empiric antimicrobial treatment in febrile neutropenic patients.

Final Abstract Number: SADI 11.006

Session: Infecciones en Pacientes Críticos / Infections in Critical Patients

Date: Thursday, March 1, 2018

Time: 11:00-12:30

Room: Retiro BC

Type: Electronic/Moderated Poster Presentation

Living with the tenant: Associated factors in *Clostridium difficile* infection with toxin and/or positive antigen in hospitalized elder patients

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Background: In the last decades, *Clostridium difficile* (CDI) infection has become the causal agent of diarrhea with a great impact in morbi-mortality.

Describe the associate factors of CDI in hospitalized patients with diarrhea samples and positive toxin or antigen tests, treatment outcomes, severity and mortality factors.

Methods & Materials: Retrospective cases between september 2016 and september 2017. Inpatients with CDI toxin/ positive antigen in feces samples.

C.DIFF QUICK CHECH COMPLETE immunocromatographic rapid test was used for diagnosis and toxigenic culture (C-tcd).

Possible associated factors to CDI: sex, age, comorbidities, previous antibiotics (p-ATB) and the admission, proton pump inhibitors (PPI), histamine inhibitors (HI), days in hospital, severity markers (SM), leukocyte (BC) ≥ 15000 cell/mm³, albumin ≤ 3 g/dl and creatinine 1.4mg/dl, CDI treatment and high mortality.

The constant variables were described with media and standard deviation (SD) or media range time interval (IIQ) according to distribution. The categorical variables were expressed in total n and percentages.

Results: In a total of 32 hospitalized patients with CDI the mean range age was 74 years-old (IIQ 67-80), men 15 (55,6 %), comorbidities: diabetes mellitus 7 (26 %), solid organs tumor 8 (29,6 %), autoimmune disease 8 (29,6 %), chronic kidney failure 6 (22 %), days in hospital 9 (IIQ 3-21), PPI 25 (92,6 %), HI 4 (14,8 %). Positive ICT-Tcd 14 (51,8 %), C-tcd 18 (66,7 %), pathological abdominal ultrasound scan 7 (25,9 %).

The p-ATB 18 (66,7 %): Carbapenemes 12 (44,4 %), Piperaciline/tazobactam 10 (37 %), Quinolones 6 (22,2 %), Amoxiciline/clavulanic 13 (48.1 %), Cefalosporines 5 (18,5 %).

The SM CDI: BC 9730 (IIQ 7900-13240), hypoalbuminaemia 14 (58,3 %), acute renal failure 5 (18,5 %).

Treatment was metronidazol-vo 17 (63 %), metronidazol-EV 7 (25,6 %).

Mortality at discharge: 8 (29,6 %).

Conclusion: CDI's current evidence in elder hospitalized population is limited.

We were able to describe DCI associated factors, the importance of toxigenic culture in negative toxin samples in its first CDI lecture.

We recommend to bear in mind the CDI in a diarrhea episode, identify a method of diagnosis and an optimization of infection control measures.

Final Abstract Number: SADI 12.002

Session: Infecciones Endémicas y Regionales / Regional and Endemic Infections

Date: Thursday, March 1, 2018

Time: 11:00-12:30

Room: La Pampa

Type: Oral Presentation

Living with dogs and cats: Is it a risk factor for skin and soft tissues infections caused by community-acquired methicillin-resistant *Staphylococcus aureus*?

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Background: Colonization by community-acquired methicillin-resistant *Staphylococcus aureus* (CA-MRSA) is a risk factor for infections related to this bacteria. It is unknown the role of dogs and/or cats (D/C) in the transmission of this pathogen. This study was aimed to evaluate the relationship between the coexistence and close contact with D/C and CA-MRSA skin and soft tissues infections (CA-MRSA SSTI).

Methods & Materials: Case-control study (G₁-SSTI with CA-MRSA isolation and G₂-SSTI without CA-MRSA isolation), of SSTI episodes treated in two hospitals in Argentina, from October 2014 to October 2017. The samples were taken by percutaneous aspirate, and bacterial identification was performed with automatized methods (MALDI-TOFTM BDTM and PHOENIXTM BDTM). Methicillin resistance was confirmed by Kirby Bauer's method with cefoxitin discs. Data about the coexistence with D/C and classic risk factors for CA-MRSA SSTI (CRF) was collected. Recurrent SSTI (rSSTI) was defined by the presence of ≥ 2 episodes in the last 6 months; and close contact with D/C as they remained inside the house most hours of the day. The Mann-Whitney-Wilcoxon and Chi² tests were used, and for the multivariate model, logistic regression was used. The statistical analysis was performed with Epi-InfoTM 7.2.1.0.

Results: 166 episodes were included (G₁ 54.4% -G₂ 45.8%). Mean age was 39.0 years (IQR 27), and 65.1% were men. In univariate analysis, age in years (32.5 vs. 43.0 p<0.001), presence of ≥ 1 CRF (86.7% vs. 73.7%, p=0.03), rSSTI (42.2% vs. 22.4%, p=0.007), living with D/C (74.4% vs. 60.5%, p=0.05, OR1.9, CI_{95%} 1.1-3.7) and close contact with D/C (42.2% vs. 28.9%, p=0.007, OR1.8, CI_{95%} 0.99-3.43) were significant. In the multivariate model, close contact with D/C showed 1.3 times more chances of CA-MRSA SSTI (OR2.32, CI_{95%} 1.12-4.78, p=0.23). On the other hand, younger age (OR0.96, CI_{95%} 0.94-0.98, p<0.001) and the rSSTI (OR2.9, CI_{95%} 1.37-6.14, p=0.005) proved an increased risk of isolation CA-MRSA in the lesions.

Conclusion: Close contact with D/C, age and rSSTI were independently associated with CA-MRSA SSTI. In this scenario, it would be useful to evaluate the correlation of these findings with the animal carrying of CA-MRSA.

Final Abstract Number: SADI 12.003

Session: Infecciones Endémicas y Regionales / Regional and Endemic Infections

Date: Thursday, March 1, 2018

Time: 11:00-12:30

Room: La Pampa

Type: Oral Presentation

IL-10, IFN- γ and IL-1 β polymorphisms influence the development of OT in a Colombian population
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Background: Toxoplasmosis is caused by infection with the protozoan parasite *Toxoplasma gondii* which has the capacity to infect all warm-blooded animals worldwide. It is estimated that 30-70% of the human population is infected with this parasite, and essentially the entire human population is at risk of infection. A limited number of people develop symptoms, suggesting that host susceptibility and strain disparity can play a role in the variability of clinical symptoms. Toxoplasmosis is a major cause of visual defects in the Colombian population, however, the association between genetic polymorphisms in cytokine genes and susceptibility to ocular toxoplasmosis has not been studied in this population.

Methods & Materials: This work evaluates the associations between polymorphisms in genes coding for cytokines TNF- α (rs1799964, rs1800629, rs1799724, rs1800630, rs361525); IL-1 β (rs16944, rs1143634, rs1143627), IL-1 α (rs1800587); IFN- γ (rs2430561); IL-10 (rs1800896, rs1800871), and the presence of ocular toxoplasmosis (OT) in a sample of Colombian population (61 patients with OT and 116 healthy controls). Genotyping was performed with the "ddNTP primer extension" technique. Functional effect predictions of SNPs were done using FuncPred.

Results: Genotype distribution of all polymorphisms did not deviate significantly from the Hardy-Weinberg equilibrium. Significant higher frequencies in IL-1 β , IFN- γ and IL-10 polymorphisms were observed in the OT group. A polymorphism in the IL-10 gene-promoter (-1082G/A) was significantly more prevalent in OT patients than in controls ($P=1.93e-08$; OR=5.27e+03; 95%CI= 3.18-8.739; pBONF=3.48e-07). In contrast, the haplotype "AG" of the IL-10 gene promoter polymorphism (rs1800896, rs1800871) was present with lower frequency in OT patients [$P=7e-04$, OR (95%CI) 0.10 (0.03-0.35)]. The polymorphism (+ 874 A/T) of IFN- γ was associated with OT ($P= 3.37e-05$; OR=4.2; 95%CI= 2.478-7.12; pBONF= 6.07e-04). The haplotype "GAG" of the IL-1 β gene promoter polymorphisms (rs1143634, rs1143627, rs16944), appeared to be significantly associated with OT ($P=0.0494$).

Conclusion: The IL-10, IFN- γ and IL-1 β polymorphisms influence development of OT in the Colombian population. Our study provides evidence that common genetic variants in Th1 (IL-1, IFN- γ , TNF- α) and Th2 (IL10) genes are associated with risk to develop OT in patients from Colombia.

Final Abstract Number: SADI 12.004

Session: Infecciones Endémicas y Regionales / Regional and Endemic Infections

Date: Thursday, March 1, 2018

Time: 11:00-12:30

Room: La Pampa

Type: Oral Presentation

Low prevalence after the first Zika virus epidemic wave in Southeastern Brazil

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Background: Zika virus (ZIKV) emerged in Brazil in 2014. One year later its teratogenic effect was noticed in Northeastern Brazil and elsewhere. With the aim to determine the seroprevalence of ZIKV antibodies among parturient women, the incidence of ZIKV infection among the newborns, the risk of transmission from an infected mother to the newborn, the incidence of congenital anomalies among the infected babies, and the dynamics of viral excretion in breastmilk and urine, a cohort study was set up at Hospital Ana Costa (HAC), a private institution, located in Santos, Southeastern Brazil.

Methods & Materials: Women who came to HAC for delivery were invited to participate. The ones who agreed to participate signed the Informed Consent Form. The study was approved by the USP Medical School Ethics Review Board. A blood sample was collected for the woman serology. After delivery, samples of colostrum and breastmilk were obtained, as well as a sample of cordblood and urine of the newborn for PCR. EIA for ZIKV antibodies was carried out. Positive samples were confirmed by flow cytometry neutralization test (FRNT).

Results: From June 2016 to February 2017 a total of 740 parturient women and their 753 newborns were enrolled in the study. ZIKV seroprevalence among the women was 7.2% (53/740). No infected newborns nor any ZIKV-related congenital anomalies were observed. Seroprevalence was higher among women living in two of the Santos metropolitan region cities, as compared to the others. Seroprevalence was not related to the mothers' age, to the duration of pregnancy, to the referral of ZIKV-like symptoms during pregnancy, nor to the referral of family members or neighbors with ZIKV-like symptoms during pregnancy. The only variable significantly associated with seroprevalence was a previous history of dengue.

Conclusion: ZIKV seroprevalence among parturient women in Santos metropolitan region after the first epidemic wave was low, and no mother to baby transmission was observed. The region is endemic for dengue. Since its emergence in 1997 eight large outbreaks were reported. 2017 is being characterized as a low transmission year for dengue and ZIKV in Brazil. New ZIKV outbreaks should be expected in the future. Grant FAPESP no.2016/16069-8

Final Abstract Number: SADI 12.005

Session: Infecciones Endémicas y Regionales / Regional and Endemic Infections

Date: Thursday, March 1, 2018

Time: 11:00-12:30

Room: La Pampa

Type: Oral Presentation

2016 dengue outbreak in Buenos Aires: A case series

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Background: In 2016, the Metropolitan Area of Buenos Aires suffered the largest dengue outbreak ever recalled with 12495 cases assisted in the city. The main circulating serotype was DEN-1 and affected a population predominantly non-immune.

Methods & Materials: Description of clinical and biochemical characteristics of suspected dengue cases (as defined by argentinian guidelines), in adults attended on a specialized hospital between the 11th and the 18th epidemiological week of 2016, when the outbreak was officially announced.

Results: 1728 adults with an acute febrile illness were assisted; 1468 fulfilled the inclusion criteria. 57 cases had recently travelled to areas with active circulation of dengue and 124 had risk factors for severe dengue. The median age was 34 (range 18-80) and 50% were women. The symptoms most frequently associated were headache (87%), myalgia or arthralgia (83%), nausea or vomiting (55%), diarrhea (24%), abdominal pain (29%), rash or pruritus (36%). 7.5% presented with bleeding, mainly epistaxis (28%), gingival hemorrhage (29%) and metrorrhagia (22%).

Blood tests were performed in 1300 patients. Before the fifth day of symptoms (n=924), 66% of patients presented with laboratory findings suggestive of dengue: hematocrit > 47 (11%), leucopenia (44%) and thrombocytopenia (41%).

During the overall follow-up period (median of 2 consults, range 1-10), 82% showed laboratory findings suggestive of dengue, mainly thrombocytopenia (64%), leucopenia (54%) and relative lymphocytosis (32%).

222 patients required IV fluids and 49 of them were hospitalized.

Conclusion: In these series, there was a high frequency of gastrointestinal symptoms, supposing a challenge for the differential diagnosis. The course of the illness was benign in most cases.

A normal CBC before the fifth day of symptoms should not exclude the diagnosis of dengue. In the context of an outbreak, a close follow up is essential for the diagnosis and the early detection of alarm signs, in order to prevent the progression to severe dengue.

Final Abstract Number: SADI 12.006

Session: Infecciones Endémicas y Regionales / Regional and Endemic Infections

Date: Thursday, March 1, 2018

Time: 11:00-12:30

Room: La Pampa

Type: Oral Presentation

2007-2017: 10 years of *Rickettsia parkeri* rickettsiosis in Argentina

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Background: *Rickettsia parkeri* spotted fever (RpSF) is a tick-borne disease, emergent in Argentina. The first cases were related to transmission through the tick *Amblyomma triste*, but a role was soon after described for *A.tigrinum*, a relevant fact since this supposed an expansion of the endemic area, given its wide distribution in our country. The aim of this study was to describe clinical and epidemiological characteristics of the disease in our country.

Methods & Materials: A retrospective analysis through revision of medical records (n: 20) of a series of cases of patients with diagnosis of RpSF. A case was considered probable in the presence of clinical and epidemiological clues associated to seroconversion to *Rickettsia spp.*, and confirmed when Rp was identified by means of a positive PCR in a tissue biopsy.

Results: 60% were women (n:12/20). Average age was 48 years (Range: 15-73). Geographical distribution by provinces: 40% Buenos Aires, 25% San Luis, 10% San Juan, 10% Córdoba, 5% La Rioja, 5% Entre Ríos, 5% La Pampa. Environment where contact with the vector took place: 45% peri-urban, 25% rural, 30% wild areas. Activity performed at contact with the vector: 30% occupational, 20% recreational, 50% household. 35% of patients had confirmed contact with dogs. Clinical characteristics: see table 1. Eschar distribution: 30% scalp and neck, 30% trunk, 20% lower limbs, 5% hands, upper limbs, mammary glands and disseminated (each). 80% were treated with doxycycline, 20% received no antimicrobial treatment. All cases resolved without sequelae.

Table 1.

Fever	95%
Headache	75%
Myalgias	75%
Regional lymphadenopathies	30%
Rash	85%
Maculo-papular	76%
Maculo-vesicular	18%
Purpuric	6%
Inoculation eschar	95%

Conclusion: Described for the first time as a human pathogen in USA in 2004, Rp was shortly after reported in Argentina. RpSF represents a major challenge for the health system, with increasing number of reports throughout the country. Urbanization in the rural-urban interfase and lack of ectoparasite control in dogs could favour its dissemination

Final Abstract Number: SADI 19.002

Session: Infectologia General / General Infectious

Date: Thursday, March 1, 2018

Time: 15:30-17:30

Room: Retiro A

Type: Oral Presentation

Infective Endocarditis in a general Hospital in Argentina

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Background: Infective endocarditis (IE) is a complex disease that has received considerable attention by clinicians and scientists in the last century but remains to have a high morbidity and mortality. The clinical outcome is variable, depending on the involved microorganism, the presence of structural valve disease, prosthetic valves or intravascular devices and the varied clinical manifestations.

Our objective was to describe the clinical features, microbiology and outcome of the patients with IE that were hospitalized in a General Hospital.

Methods & Materials: We conducted a retrospective cohort analysis of 26 patients with IE during the period of January 2014 to September 2017. The date was recorded in the index cards designed for EIRA 3. We analyzed variables related to age, medical history, echocardiogram, treatment and attributable mortality. The Duke criteria were used to define definite IE and possible IE.

Results: During the study period we registered 26 IE, 24 definite and 2 possible. The mean age was 73.5 years. 69% without structural valve disease, 11.5% with prosthetic valve, 7.6% in native valve with underlying valvular disease and 11% with intracardiac devices. 38% of the patients had procedures associated with health care. The involved microorganisms were: *Staphylococcus aureus* 42.3% (11.5% MRSA, 30.8% MSSA), 11.5% *Staphylococcus epidermidis*, 7.7% *Enterococcus faecalis*, 15.2% *Streptococcus spp*, 11.4% Gram negative bacilli, 7.6 % Gram positive bacilli, 3.8% without microbiological finding. The 34% involved aortic valve, 30.8% mitral valve, 19.2% tricuspid valve, 11.5% aortic and mitral valves combined, 3.8 % involved intracardiac devices. Transthoracic echocardiography detected the presence of intracardiac vegetations in 38% of the cases whereas transesophageal echocardiography detected 61% of the vegetations. 50% received appropriate empirical antibiotic treatment, 38% required surgery. 53.8% had favorable evolution and were discharged. The attributable mortality was 50%.

Conclusion: Despite advances in medical and surgical treatment, IE remains to carry a considerable risk of death. In our analysis *Staphylococcus aureus* was the most common microorganism associated with IE followed by *Streptococcus spp* and *Staphylococcus epidermidis*. Transesophageal echocardiography was very useful in the diagnosis approach to patients with suspected IE.

Final Abstract Number: SADI 19.003

Session: Infectologia General / General Infectious

Date: Thursday, March 1, 2018

Time: 15:30-17:30

Room: Retiro A

Type: Oral Presentation

Infective Endocarditis in Argentina: what have we learn in the last 25 years?

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Background: The epidemiology of Endocarditis (IE) is changing due to a number of factors, including aging, health-related comorbidities and medical procedures.

The aim of this study is to assess the main clinical, epidemiologic and etiologic changes of IE in the last 25 years in Argentina.

Methods & Materials: Comparative analysis of three cross-sectional, observational registries which enrolled consecutive patients with IE: 2 multicentric studies (EIRA-1 [1992-1994] and EIRA-2 [2001-2002]) and 1 single third level cardiology referral center (CRC [2002-2017]). Categorical variables were compared using Chi-square test; continuous variables with Student's t test or Mann-Whitney U test was used as applicable. A value of $p < 0.05$ was considered significant.

Results: A total of 1065 IE episodes were included; definite IE (modified Duke Criteria) $>70\%$ in the three periods considered. There were no differences regarding sex; patients were older in each period ($p < 0.001$). Device associated IE was more frequent in the last decade: pacemaker IE 5.4% vs 23% ($p < 0.0001$); PVIE 8.5% vs 19.2% vs 47.5% ($p < 0.0001$). IVDA ($p < 0.0001$) and congenital heart diseases ($p = 0.001$) significantly decrease as predisposing factors and pts without known predisposing heart diseases has increased (45% vs 33.8% vs 47.8%; $p < 0.0001$). Etiology changes were observed: VGS (30.8% vs 26.8% vs 15.94%; $p < 0.001$) and *S. aureus* IE (26% vs 30% vs 16.27%; $p = 0.014$) decreased significantly, being more frequent the infection by CNS (1.7% vs 8% vs 18,3%; $p < 0.0001$). Surgical treatment was more frequently implemented in the last decade (28.2% vs 24.3% vs 41.86%; $p < 0.00001$). Mortality remained stable in the three periods, with a tendency to decrease in the last period (23.5% vs 24.3% vs 17.2%; $p = 0.06$).

Conclusion: In Argentina, IE affects older people, particularly with intracardiac device (PM and PV). This is remarkable when comparing the multicenter studies with CRC. *Staphylococcus* spp predominates, with CNS being more frequent than *S. aureus*. Mortality showed a tendency to decrease probably related to the fact that surgery is more frequently implemented in CRC. These findings show a change in the profile of IE in Argentina and highlights the importance of managing this complex disease in centers with extensive experience in the care of patients with IE.

Final Abstract Number: SADI 19.004

Session: Infectologia General / General Infectious

Date: Thursday, March 1, 2018

Time: 15:30-17:30

Room: Retiro A

Type: Oral Presentation

Characterization of influenza A(H3N2) strains circulating in Argentina during the 2017 season
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Background: Influenza A viruses are an important cause of severe infectious diseases in humans and are characterized by their fast evolution rate. The continuous antigenic drift of these virus significantly contributes to the emergence of new strains and the reduced effectiveness of the vaccine. In 2017, influenza A(H3N2) (FLUA/H3) was the predominant circulating virus detected, followed by both influenza B virus lineages in very low proportion. This year, the FLUA/H3 vaccine component in Argentina was A/Hong Kong/4801/2014 and belonged to clade 3C.2a. Recent publications have shown evidence for suboptimal vaccine effectiveness against laboratory-confirmed FLUA/H3 infection due to the circulation of variants capable of causing disease even in vaccinated patients. Here, we report the diversity of FLUA/H3 viruses circulating in Argentina and try to estimate their temporality across the 2017 season.

Methods & Materials: The Argentine National Influenza Center (NIC) routinely receives influenza positive respiratory specimens collected from pediatric and adult inpatients and outpatients coming from all the country for isolation and further characterization. Between January and October, the NIC received a total of 2,663 influenza positive samples and 1,952 viruses were characterized as FLUA/H3. A set of 44 viruses collected between EW 13-30 was selected for sequencing the HA1 of the HA (986 bp). Sequences were analyzed using BioEdit and MEGA 6 programs.

Results: Sequencing analysis shown the detection of one clade 3C.2a related to the vaccine virus and one subclade 3C.2a1 related to a new FLUA/H3 virus that emerged in the last Northern Hemisphere season called A/Bolzano/7/2016. The dominant virus subcluster was 3C.2a/T31K/R142K (54.5%) related with the vaccine H3 component followed by 3C.2a1/N171K/T135K (18.2%), and 3C.2a1/N171K/N121K / K92R/H311Q (13,6%), both related with the new virus Bolzano. In the early season (EW13-19), 70% of the circulating viruses were related to recently emerged viruses, however, in the middle and latter season (EW 20-30) the 69.7 % of the viruses were related to vaccine H3 component.

Conclusion: The genetic analysis of the Argentinean FLUA/H3 viruses demonstrated a co-circulation of viruses from vaccine clade 3C.2a and Bolzano subclade 3C.2a1 and a temporal distribution of these variants through the season.

Final Abstract Number: SADI 19.005

Session: Infectologia General / General Infectious

Date: Thursday, March 1, 2018

Time: 15:30-17:30

Room: Retiro A

Type: Oral Presentation

Infective Endocarditis: how many ultrasonography studies are necessary to reach the diagnosis? A real world scenario (2008-2017)

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Background: The central role of echocardiography in the diagnosis, prognosis, and management of infective endocarditis (IE) has been clearly established. Both echocardiography and blood cultures are the major criteria to reach the diagnosis of IE. Although 2D transthoracic echocardiography (TTE) and transesophageal echocardiography (TEE) have complementary roles, TEE has more sensitivity and specificity especially in the presence of intracardiac device. Sometimes, however, in spite of a high clinical suspicion, the first study that is carried out does not contribute with elements that confirm this suspicion and many expert and guidelines suggest to repeat the study in a relatively short time.

To analyze the role of repeated echoes in the diagnosis of definite IE.

Methods & Materials: Retrospective, observational study of consecutive cases of Definite IE according to modified Duke Criteria, in adults patients admitted in a single cardiovascular referral center.

Results: From January/2008 to June/2017, 148 definite EI (43 native valve, 72 prosthetic valve, 33 pacemaker-associated IE) were included. All pts underwent TTE and TEE. The first echoe was made a median of 2 d since the hospitalization day (range= 0-13 d; SD +/- 2) and showed images suggesting IE in 106/148 pts (71.6%). A 2nd echoe was performed in 18 pts in a median time of 7 days and showed images not seen in the previous echoe in 11/18 pts (61%).

Considering only "valvular IE" (n=115) the first echo was "positive" for IE in 76.5% and 86% in the 2nd echoe: native valve IE 81.4% vs 83.7%; PVIE 73.6% vs 87.5% (early PVIE - n: 32 - 75% vs 90%) respectively.

Conclusion: Ultrasonography is unequivocally the mainstay of diagnostic imaging in IE. Repeat the study in the case of a high clinical suspicion could notably increase the possibility of achieving the diagnosis of IE, especially when intracardiac device (e.g: prosthetic valves) are probably involved.

Final Abstract Number: SADI 19.006

Session: Infectologia General / General Infectious

Date: Thursday, March 1, 2018

Time: 15:30-17:30

Room: Retiro A

Type: Oral Presentation

Invasive disease due to B-hemolytic Streptococcus. Epidemiology and mortality

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Background: B-hemolytic streptococci(EBH) are responsible for diseases such as necrotizing fasciitis, toxic shock syndrome(SSTE) and post-infectious complications. EBHGA can present fulminant manifestations, as well as subtypes of EBHGC and EBHGG, which express homologous proteins.

Objective: To characterize invasive disease due to EBH(EI) in adults, incidence, risk factors, presentation, subtypes, sensitivity and mortality in a period of 5.5 years in a Private Hospital

Methods & Materials: Clinical, observational, descriptive and analytical study, transversal design.

Retrospective review of positive EBH cultures during the period 01/01/2012-30/06/2017.

Inpatients and outpatients older than 18 years were included. EIE was defined for the isolation of EBHGA, B, C, G and F in sterile place(blood, CSF, joint fluid, pleural, ascitic and collection)

Blood cultures were performed in BACT/ALERT, cultured on sheep blood agar and latex particle agglutination typing. Sensitivity:disc diffusion and CIM using test strips(Etest)

Data analysis:EPI Info7, $P2\alpha < 0.05$ statistically significant.

Results: 141 patients:male 51.7%, median age 72 years, 92.2% of cases in hospitalized patients .Total Mortality was 21.3%(30/141), 83.3% of the deceased(25/30) had comorbidities, with Age >65 years being a statistically significant variable with an impact on mortality, both in the bivariate and multivariate analysis.

The absence of clinical focus showed a statistically significant higher mortality with high RR(2.84). The 81.25%(13/16) of bacteremia without focus occurred in >65 years old, with a mortality of 75%(6/8). The SBHGB was responsible for 50%(8/16). The SBHGB was the most frequent agent(39.72%), with a mortality of 19.6%(11/56).

The incidence in >65 years was 60.7% with a mortality of 90.9%(10/11). The clinical foci:deep abscess(29/141) and meningitis (6/141) had an impact on mortality, a statistically significant result in the multivariate analysis for meningeal focus and SSTE(30/141) $p < 0.001$ RR:6.39

Sensitivity to penicillin 100%, to clindamycin 80.5% of the strains tested.

Conclusion: The EIE continues to be a prevalent disease, with a great impact on the elderly population and a high rate of lethality in the presence of risk factors. Greater mortality is highlighted in the absence of clinical focus and with SBHGB compared to other publications. The SSTE was caused equally by SBHGA and B.

Final Abstract Number: SADI 19.007

Session: Infectologia General / General Infectious

Date: Thursday, March 1, 2018

Time: 15:30-17:30

Room: Retiro A

Type: Oral Presentation

Analysis of 10 years of surveillance of infections associated with hip and knee prostheses

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Background: Surgical site infections are the third reported cause of healthcare-associated infections (HAIs), representing 14% to 16% of them.

Prosthetic joint infection (PJI) are one of the most frequent complications that lead to an increase in morbidity and mortality.

In the first world countries, surveillance systems report an approximate infection rate for total hip arthroplasties (THAs) and total knee arthroplasties (TKAs), from 0.5 to 1% and 0,5 to 2% respectively. Due to the lack of knowledge of local epidemiology, we propose to describe the rates associated with these procedures, the most frequent microbiological isolations and their resistance patterns.

Methods & Materials: A retrospective study, from 2006 to 2016, of the PJI episodes of THAs and TKAs was carried out through the review of the events reported by all the institutions in Argentina that voluntarily joined the National Surveillance System (VIHDA) for HAI and selected such procedures.

Results: They were surveyed 11114 THAs and 4262 TKAs, presenting 410 and 157 PJIs respectively, which constituted a global rate for the period described of 3.68% for THAs and 3.69% for TKAs.

The mean age for THAs and AR were 65.5 and 71 years, respectively.

Female sex predominated for both procedures with 62.7% (hips) and 61.8% (knees).

The main etiologies for THAs infections were *Staphylococcus aureus* (n=153, 43% MRSA), *Pseudomonas aeruginosa* (n=69, 22% resistant to ciprofloxacin), *Escherichia coli* (n=62, 42% resistant to ciprofloxacin), and coagulase-negative *Staphylococcus* (n=52, 54% methicillin-resistant). In TKAs infections, the most commonly found microorganisms were: *Staphylococcus aureus* (n=41, 20% MRSA), coagulase-negative *Staphylococcus* (n=38, 32% methicillin-resistant), *Enterococcus* sp. (n=9; 0% resistant to vancomycin) and *Pseudomonas aeruginosa* (n=8; 50% resistant to ciprofloxacin). 32% of THAs infections and 18% of TKAs infections were polymicrobial.

Conclusion: The infection rates in both procedures were similar, being relatively low.

The mean age was lower for THAs and the female sex predominated in both surgeries.

In TKAs, gram-positive cocci (77%) predominated over gram-negative bacilli (23%).

The THAs perceives the similar percentages of Gram-positive cocci isolates (48%) and Gram-negative bacilli (52%), with 2/3 of the Enterobacteriae.

A high rate of isolations of resistant microorganisms was observed.

Final Abstract Number: SADI 19.008

Session: Infectologia General / General Infectious

Date: Thursday, March 1, 2018

Time: 15:30-17:30

Room: Retiro A

Type: Oral Presentation

Measles outbreak in the context of post-elimination phase in individuals with prior evidence of immunity. Secondary immune response or re-infections?

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Background: Several outbreaks of imported and imported-related cases were recorded in Argentina after measles elimination.

Secondary vaccine failure (measles in vaccinated individuals with confirmed seroconversion) can occur. Confirmation of measles in vaccinated individuals and negative IgM suggests a secondary immune response.

Re-infection is a confirmed case in a person with high-avidity IgG. The best method for confirmation is RT-PCR.

Methods & Materials: Descriptive study of an imported measles outbreak.

Results: In April 2017 a suspected measles case was notified in a traveler who returned from Australia and Indonesia, subsequently confirmed by IgM and RNA detection. Two secondary cases were detected. None could recall evidence of measles immunity. High-avidity IgG was detected in samples from all the cases. D8 genotypes was confirmed, revealing a single transmission chain. Outbreak investigation and control actions encompassed 9 argentine provinces and 11 countries.

	Age	#Serum sample (days after rash)	IgM	IgG (mIU/mL)	IgG Avidity (%)	RT-PCR NPS* (CT [¶] value)	RT-PCR Urine (CT Value)	Genotype
Case1	25	Serum 1 (1)	Positive	1548	High (87%)	Positive (27)	Positive (25)	D8
		Serum 2 (14)	Positive	5519	High (81%)			
Case2	30	Serum 1 (4)	Positive	25867	High (93%)	Positive (32)	Positive (36)	D8
Case3	36	Serum 1 (2)	Negative	3226	High (78%)	Positive (34)	Positive (39)	D8
		Serum 2 (48)	Negative	26575	High (98%)			

*NPS nasopharyngeal swab

¶ CT value: RT-PCR average cycle threshold

Conclusion: This travel-related limited measles outbreak in individuals with prior immunity reflects the high protection in the population of Argentina, unlike what happens in other regional countries where the outbreak magnitude is higher due to the presence of non-immune population and heterogeneous vaccine coverage.

Generally, secondary immune response cases present with low viral load and have limited transmission. However, case #1 had high viral load and infected the other cases. The absence of circulating virus and the periodic boosting that may have provided additional protection from infection may alter the paradigm of lifelong immunity.

The diagnosis of measles in the context of elimination is a challenge. Supplementary tests are needed besides specific IgM determination, only possible to perform in highly-specialized laboratories

Final Abstract Number: SADI 19.009

Session: Infectologia General / General Infectious

Date: Thursday, March 1, 2018

Time: 15:30-17:30

Room: Retiro A

Type: Oral Presentation

Frequency and coinfection between genotypes of human papillomavirus in a population of asymptomatic women in northern Peru

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Background: Cancer of the uterine cervix is the third most common gynecologic cancer worldwide, with the human papilloma virus (HPV) present in 99% of patients. HPV is a group of more than 150 related viruses; however, just a few of the HPV genotypes can cause cervical cancer. The HPV 16 and 18, are present in about 70% of all cases highlighting the importance of genotype identification in women infected with the virus. In Peru, the PCR detection of the HPV virus is not considered as a screen test for the national surveillance and most cases of cervical cancer are detected on advanced stages.

To assess the frequency of the HPV genotypes and risk factors for cervical cancer in asymptomatic sexually-active women studied from March 2016 to September 2017 in Cajamarca, Peru.

Methods & Materials: A total of 398 pap smears were assessed via PCR for the presence of HPV. Positive samples were sent for commercial sequencing and genotype characterization. A standardized questionnaire was performed to evaluate risk factors for cervical cancer in our population.

Results: The HPV was detected in 29.9% of samples (119/398) and coinfection with more than one genotype was observed in 13 cases. A high-risk for cervical cancer genotype was detected in 61.3% (73/119) of the positive samples. The most common genotypes isolates were HPV 31 (17.6%), HPV16 (10.1%), HPV70 (7.6%), and HPV6 (6.7%). The number of sexual partners ($p=0.015$) and not using condoms ($p=0.04$) were both associated with the presence of high-risk genotypes.

Conclusion: In our study population, the high-risk genotypes HPV 31 and 16 were the most prevalent in Cajamarca. Further investigations should be conducted to describe the frequency of HPV genotypes in Peru.

Final Abstract Number: SADI 20.002

Session: VIH y Hepatitis Virales / HIV and Viral Hepatitis

Date: Thursday, March 1, 2018

Time: 15:30-17:30

Room: Retiro BC

Type: Oral Presentation

Factors related to pre-exposure prophylaxis prescription by argentine physicians

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Background: Pre-exposure prophylaxis (PrEP) is an effective measure to prevent HIV transmission. If the adherence is high, transmission rates are reduced by more than 90%. In Argentina, FTC-TDF is not yet approved for PrEP by the local regulatory agency. PrEP awareness, PrEP adoption, and factors associated with adoption among argentine physicians has not been studied to date.

Methods & Materials: Cross-sectional online survey conducted in August 2017 among argentine physicians. Information items assessed: PrEP awareness, PEP and PrEP adoption (ever prescribed [yes/no]), provider and practice characteristics, and self-rated knowledge, attitudes, and beliefs associated with adoption.

An univariate analysis was performed, the associations between categorical variables were analyzed by means of the chi² test. The level of significance was considered with $p < 0.05$.

Results: A total of 238 surveys were received from 81 centers in Argentina. Female sex: 60.9%; Buenos Aires City: 55.9%, Buenos Aires Province 18.5 %, rest of the country 25.6%. Chief of staff: 13.9%, staff: 58%, resident: 23.6%, others: 4.5%. Age: 52.1% between 36 and 50 years old, younger than 35 years old: 27.7% and older than 51 years: 20.2%.

Fifteen point five percent (15.5%) reported prior used of PrEP. Clinical scenarios with the highest prescription were: serodiscordant couples 77.3%, sex worker 60.9%, transgender patients 32.4%, people who inject drugs 31.1%, MSM 23.2%.

Factors associated with PrEP prescription between physicians were been chief of staff ($p < 0.05$), been an ID specialist ($p < 0.05$), assist more than 200 HIV patients a year ($p < 0.009$) and having prescribed PEP ($p < 0.008$).

Conclusion: Although not yet approved by the local regulatory agency, PrEP is been prescribed off- label by argentine physicians. Adopters were more likely to have experience providing HIV care, been chief of staff and ID specialist. These results could be used to plan future HIV prevention strategies in Argentina.

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Session: VIH y Hepatitis Virales / HIV and Viral Hepatitis

Date: Thursday, March 1, 2018

Time: 15:30-17:30

Room: Retiro BC

Type: Oral Presentation

Dual therapy (ritonavir boosted atazanavir + raltegravir) versus standard triple therapy (ritonavir boosted atazanavir + tenofovir/emtricitabine) in patients failing first line therapy: 48 week results from a randomized pilot study

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Background: Dual therapy has emerged as a novel concept in treatment optimization in naive and suppressed HIV patients. This study aimed at exploring virological response, safety and inflammation markers of a nucleoside-sparing dual regimen consisting of ATV/r+RAL (DT) vs standard therapy of ATV/r+TDF/FTC (TT) among patients failing first NNRTI-containing treatment.

Methods & Materials: Randomized open label pilot study. Primary outcome measures were proportion of subjects with plasma HIV-1 RNA below the limit of detection (<50 copies/uL) and proportion of subjects discontinuing due to adverse events (AEs) during the first 48 weeks. ClinicalTrials.gov Identifier: NCT01829802.

Results: Out of 57 patients screened, 34 were randomized to receive: DT (n: 18) or TT (n: 16). At baseline 80% males, 50% MSM, median age 38 years, CDC stage C:35%, Median pVL: 3.9 Log₁₀, CD4: 289 cells/uL.

At week 48, data from 32 participants (2 did not reach week 48 yet) showed virological response in 69% (n: 11/16) of participants receiving DT and 88% (n: 14/16) receiving TT by FDA snapshot analysis (p=NS) and 73% (DT) and 93% (TT) by per-protocol analysis (p=NS). CD4 cell count median change from baseline to week 48 was +119 and + 52 cell/uL in DT and TT, respectively.

No deaths were recorded. Three SAEs occurred in 2 participants (pneumonia and stroke and, Bell's paralysis), none related to study drugs. Eight Grade 2, probably drug-related AEs were observed: 1 in DT (gastrointestinal) and 7 in TT (5 gastrointestinal, 1 renal stone and 1 rash). Hyperbilirubinemia Grade 2/3 was seen in 77% in DT and 94% in TT, none requiring stopping ART.

Two participants were discontinued due to loss of follow-up, one in each arm. Five participants had virological failure at W48, 4 in DT and 1 in TT, all with low pVL (52-589 copies/uL). One participant developed integrase resistance mutation and suppressed later on TT.

Conclusion: ATV/r+RAL as second-line therapy showed a trend to more frequent virological failure, compared to TT, although the study was unpowered to prove this difference. No major differences were seen in tolerance or toxicity.

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Session: VIH y Hepatitis Virales / HIV and Viral Hepatitis

Date: Thursday, March 1, 2018

Time: 15:30-17:30

Room: Retiro BC

Type: Oral Presentation

HIV viremia, vertical transmission and loss to follow up on HIV pregnant Chilean and immigrant woman: comparative study at 3 years of delivery

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Background: The meaningful rising immigration over the last years in Chile, most of the time on precarious conditions, has brought an increasing incorporation of HIV pregnant woman to HIV perinatal care program. The impact of this situation on HIV vertical transmission risk or treatment failure is not known.

Methods & Materials: We analyzed the pregnancy database at Fundación Arriarán, which contains all the HIV+ pregnancy woman deliveries occurred at Hospital San Borja Arriarán since 2002. Baseline characteristics, pregnancy data, prepartum virological response and vertical transmission rates were compared between Chilean and immigrant woman. The data was also analyzed before and after de application of 2012 Chilean guideline for the prevention on vertical transmission. On the subset of patients who continue with antiretroviral therapy (ART) in the postpartum (since 2013) virological failure and loss to follow was evaluated up to three years. For the statistical analysis Chi², T test, Mann-Whitney and Exact Test Fisher were used to compare distributions. Kaplan-Meier survival curves were used to explore differences on postdelivery follow up

Results: 134 pregnancies (128 patients); 80 Chilean and 48 foreigners were included. The median age was 28 and 27 years (p 0.31), the beginning of ART was 18 and 23 weeks (p 0.004), duration of prepartum ART were 136 and 105 days (p 0.007) and the baseline pregnancy viral load (VL) were 644 copies/ml vs 7540 copies/ml (p 0.019) between Chilean and foreign respectively. At delivery 32% of foreigners vs 47% of Chileans had undetectable VL (p 0.07). Of prepartum viremic patients, 41% had high level viremia (>1000 copies/ml). When comparing before and after 2012, there was a 24% increase in undetectability at delivery (61% vs 37%) (p 0,03). It is remarkable that 63% of foreign women never reached undetectability during pregnancy. Vertical transmission reached 3.5% only from Chilean before 2012. At 3 years a 51% and 30% of virologic failure and 57% and 85% of retention was observed on Chilean and immigrant women.

Conclusion: A high rate of suboptimal viral response during pregnancy and loss to follow up after delivery was observed in HIV+ immigrant woman.

Final Abstract Number: SADI 20.005

Session: VIH y Hepatitis Virales / HIV and Viral Hepatitis

Date: Thursday, March 1, 2018

Time: 15:30-17:30

Room: Retiro BC

Type: Oral Presentation

The “no-appointment” patients... another step in the HIV care cascade?

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Background: The success of antiretroviral treatment (ART), in an individual and population basis, requires the achievement and maintenance of viral suppression. Also, engagement and retention in care are needed for better access to ART. Efforts to reduce frequency of missed clinic visits have demonstrated improved efficacy in HIV outcomes. However, some patients fail to take appointments and routinely seek unscheduled attention. Appointments in our centre can be booked by email, telephone or personally and usually take no longer than one week.

Few studies have focused on these “no-appointment” patients and their outcomes. We aimed to explore clinical and demographic characteristics, predictors of having unscheduled visits and virological outcomes of these subjects.

Methods & Materials: All patients who have an HIV-care clinic visit during a five month-period were included. We collected data from medical records on socio-demographic, clinical, virological and immunological characteristics. We defined “no-appointment” patients as those subjects who had at least two unscheduled HIV-care clinic visits during the study period. Logistic regression was used to estimate independent predictors of having unscheduled visits.

Results: A total of 1.689 patients were included, which contributed with 3.215 clinic visits. Overall, median age of participants was 42 years (IQR 33-49), 35.2% were female and 6% transgender women. Of the 699 unscheduled visits, only 8% were for events that deserved urgent attention.

As much as 44.6% of “no-appointment” subjects failed to have an undetectable viral load compared with 36.8% of patients who had scheduled visits.

The odds of having unscheduled visits were higher for women [OR 1.45; CI 1.11-1.89] and patients who did not complete secondary school [OR 1.40; CI 1.07-1.85]. On the other hand, having a formal employment decreased the likelihood of unscheduled visits.

Age (> vs. < 50 years), use of cocaine or marijuana, place of residence (Buenos Aires City vs. suburbs), time from HIV diagnosis, AIDS events and having social insurance were not associated with having unscheduled visits in this cohort.

Conclusion: Unscheduled HIV-care visits were common in our cohort and were associated with a higher proportion of patients with detectable viral load. Additional knowledge is needed to confirm these findings at a larger scale.

Final Abstract Number: SADI 20.006

Session: VIH y Hepatitis Virales / HIV and Viral Hepatitis

Date: Thursday, March 1, 2018

Time: 15:30-17:30

Room: Retiro BC

Type: Oral Presentation

HIV testing after use of non-occupational post exposure prophylaxis (nPEP) in consensual sexual exposure

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Background: PEP is an effective measure to reduce transmission of HIV. There are few studies describing how many individuals are tested for HIV after use of nPEP.

We aimed to describe the proportion of individuals who returned for at least one HIV testing between 4-12 weeks after consensual sexual exposure and received nPEP, and to analyse factors associated with performance of HIV testing.

Methods & Materials: Retrospective cohort study. Clinical records of individuals who initiated nPEP between 2010 and 2017 were reviewed. The proportion of patients who were tested for HIV between 4-12 weeks after exposure was calculated. Chi-squared test was used to compare categorical variables.

Results: Between 2010 and 2017, 114 individuals were included, 107 initiated nPEP, 64.9% (74/114) were male. 5.3% transgender, 56.3% MSM. Median age (IQR) was 31 (25-38) years. 69% (76/110) lived in Buenos Aires, 52.5% (42/80) had health insurance, 45% had less than 12 years of education. 45% did not use condom. 53.5% were occasional sexual encounters and 54% recognised their sexual partner as HIV positive. 72% had previously been tested for HIV with a median of 6 (IQR: 2-12) months since the last test.

In 107 who received nPEP, antiretrovirals were: 3TC/AZT (2.8%), 3TC/AZT/EFV (5.6%), 3TC/AZT/LOP/RTV (40.3%), 3TC/TDF/ATV/RTV (29%), 3TC/TDF/DRV/RTV (11.2%), 3TC/TDF/LOP/RTV (9.3%), FTC/TDF/EFV (1.8%).

In 54, 2% of individuals who received nPEP an HIV test was performed between 4-12 weeks after a high risk exposure. All HIV tests were negative.

Having a stable partner (OR=3.7; 95% CI 1.6-8.6 p=0.001), being previously tested for HIV (OR=2.4; CI 1.1-5.8 p=0.04) and recognising intercourse with an HIV positive source (OR=4.2; CI 1.8-9.5 p<0.001) were associated with HIV testing between 4-12 weeks after exposure.

In those (49) who did not return for HIV testing, 23% lived outside Buenos Aires and 32% had been tested before. In 72% sexual intercourse was referred as occasional.

Conclusion: The percentage of HIV testing after nPEP was barely greater than the half of the cohort. Characteristics as occasional sexual intercourse and unawareness of the HIV status of the sexual partner force us to implement retention in care strategies for these individuals.

Final Abstract Number: SADI 20.007

Session: VIH y Hepatitis Virales / HIV and Viral Hepatitis

Date: Thursday, March 1, 2018

Time: 15:30-17:30

Room: Retiro BC

Type: Oral Presentation

Hepatitis C: 184 patients in follow up in the direct acting antiviral era

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Background: Hepatitis C (HCV) is one of the leading causes of chronic liver disease, its estimated prevalence in Argentina is 1.0 a 1.5% and is the main cause for liver transplant.

Since 2013 there are new direct acting antivirals available with high efficacy and safety profile. Patients under these agents achieve a sustained viral response (SVR) above 90-95% and aim at the cure/eradication of the infection and the prevention of the complications of chronic hepatitis.

The first DAAs were approved in 2015 in our country.

The main objectives of the series are to describe the social-demographic characteristics of a series of HCV patients and to analyze the clinical course and response of patients selected for DAA.

Methods & Materials: We conducted an observational, descriptive cross-sectional study.

As of 2015, reactive HCV antibody test patients were assessed during follow up and well as those newly diagnosed at the Infectology service of public and private centers of Mar del Plata, to select those with treatment criteria (\geq Fibrosis 2) according to the current recommendations of the Argentine Ministry of Health.

We used Excel2016 spreadsheet to analyze categorical variables that were described such as absolute rate and percentages.

Results: We evaluated 234 patients with reactive HCV antibody test, male 62%. Were confirmed by PCR 184, 129 co-infected HIV/HCV.

The prevalent genotype was 1a (47%), G3 14%, G4 9%, G2 3%, G1b 12%, G1 8% and 6% pending result.

Only 83 patients met treatment criteria: of them 40(48%) completed full treatment, 6 are now under treatment, 21 are waiting treatment approbation and 16 are under assessment.

Of the 40 patients treated, 24 (60%) attended the follow up visit at 12 weeks post-treatment and had reached the 100% SVR. The 85% received sofosbuvir/daclatasvir and 35% with ribavirine.

Conclusion: Consistent with the findings in the local literature the predominant genotype was G1a.

Only 55% of the patients who met treatment criteria had received DAAs, clearly showing the need to facilitate access to the drugs.

All the patients who completed the post-treatment follow up visit at 12 weeks achieved SVR thus reconfirming the efficacy of DAAs in real life.

Final Abstract Number: SADI 20.008

Session: VIH y Hepatitis Virales / HIV and Viral Hepatitis

Date: Thursday, March 1, 2018

Time: 15:30-17:30

Room: Retiro BC

Type: Oral Presentation

Detection of neurocognitive disorders in patients infected with Human Immunodeficiency Virus through fast screening tests

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Background: It's known that cognitive alterations are clinical characteristic of the Human Immunodeficiency Virus (HIV) infection. Exist three clinical categories; dementia associated with HIV (HAD), mild neurocognitive disorder (MND) and asymptomatic neurocognitive disorder (ANI). Fast screening tests used are HIV Dementia Scale (HDS) and International HIV Dementia Scale (IHDS). Minimental test (MMSE) in subcortical disorders is questionable.

The aim of this research is to identify through fast screening tests the presence of cognitive impairment, to know if there is an association with personal risk factors associated with HIV infection and with the antiretroviral regimen received.

Methods & Materials: This is a prospective, analytical, research accomplished at the Rawson Hospital of Córdoba in 2016. Three screening tests (HDS, IHDS and MMSE) were performed in patients between 18 and 60 years old with reactive serology for HIV. Exclusion criteria were patients with previous or current opportunistic infections of CNS, concomitant psychiatric disorders, current use of drugs, alcoholism, traumatic brain injury (TBI) and previous neurosurgery.

Results: We included 51 patients, average age 38 ± 12.2 years old with a range between 19 - 67. The 61% were men. More than 50% did not complete high school and that was associated with cognitive impairment ($p: 0,03$). Underweight influenced cognitive deterioration ($p: 0,02$). Current LTCD4 + level was <200 cells / μ l in the 35.2%. The 18% of the patients were not on HAART. The 26.1% had a detectable viral load.

Conclusion: We conclude that different levels of neurocognitive deterioration depends on test used. A significant association was found between the low educational level and a lower score on the HDS test. Association was found between the low LTCD4 + count and the presence of cognitive impairment in the MMSE, but not in the rest. It was found that underweight influences the presence of cognitive impairment in our sample.

Most of the patients were with HAART and a low percentage had detectable viral load for HIV.

Association wasn't found between detectable viral load and the development of cognitive deterioration in this sample.

All treated patients had at least one antiretroviral drug in their scheme with good penetration through the BBB.

Final Abstract Number: SADI 20.009

Session: VIH y Hepatitis Virales / HIV and Viral Hepatitis

Date: Thursday, March 1, 2018

Time: 15:30-17:30

Room: Retiro BC

Type: Electronic/Moderated Poster Presentation

The interplay between intrahepatic lymphocyte populations and Hepatitis B virus antigens related to liver damage in chronic hepatitis

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Background: Chronic hepatitis B virus (HBV) infection is still a global health problem. Even though it is well known that adaptative immune response plays an important role in the pathogenesis of chronic infection, the impact of each immune cell population in liver damage and viral surveillance is still a matter of debate.

Our aim was to elucidate the interplay between the immune response and viral activity in the context of liver damage.

Methods & Materials: Immunostaining was performed in 23 liver biopsies from CHB treatment naïve patients (40% HBeAg-positive) to: 1) characterize liver infiltrate [Th (CD4+), Th1 (Tbet+), Th17 (IL-17A+), Treg (Foxp3+), and CTL (CD8+)] [portal quantification: immunostained/total lymphocytes; lobular quantification: immunostained lymphocytes in 10 fields; (400x)], 2) evaluate the Hepatitis B surface antigen (HBsAg) expression (presence was determined). Inflammatory activity and fibrosis were assessed using the modified Knodell scoring system (Histological Activity Index, HAI) and METAVIR.

Results: All studied populations were observed in portal/periportal infiltrates with predominance of Th {Th [0.65 (0.33-0.77)] >CTL [0.54 (0.16-0.74)] >Treg [0.09 (0.00-0.25)] >Th1 [0.07 (0-0.20)] >Th17 [0.05 (0-0.20)]}. However, only CTL were present in the intralobular area [2.77 (0.01-0.25)]. Concerning liver damage, Th17 frequency was increased in cases with more severe fibrosis (p=0.04), while Th in cases with severe hepatitis (p=0.02) mostly due to Treg (p=0.02). The frequency of intralobular CTL also depicted association with severe hepatitis (p=0.02). Regarding HBV antigen profile, only 62% of cases showed presence of HBsAg, being its absence associated with a higher number of Treg (p=0.02) and severe hepatitis (p=0.01). Moreover, HBe Ag-positive cases exhibited higher Treg and Th frequencies (p=0.0002 and p=0.037; respectively).

Conclusion: Although Treg population was highly represented in the infiltrate, they were not related to liver damage. In contrast, intrahepatic Th17 mediated fibrosis severity. The presence of CTL in the intralobular area may indicate a relationship between them and hepatocytes denoting their contribution to hepatitis severity. Finally, our results suggest that the presence of a regulatory microenvironment enhances viral replication. This hypothesis is supported by the fact that a higher Treg frequency was observed in the context of absence HBsAg as well as among HBeAg-positive cases.

Final Abstract Number: SADI 21.002

Session: Control de Infecciones / Infection Control

Date: Thursday, March 1, 2018

Time: 15:30-17:30

Room: La Pampa

Type: Oral Presentation

Mobile phones: a potential source of nosocomial infection?

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Background: Mobile phones are widely used and are integrated into the professional practice of healthcare workers, even in critical areas and operating rooms. Recent studies suggest that these devices are reservoirs for pathogens with potential to cause nosocomial infections.

Main objective: To evaluate the bacterial colonization rate of mobile phones of healthcare workers.

Secondary objectives: To determine if disinfection with alcohol 70% is useful to reduce the bacterial colonization of telephones and know the perception of healthcare workers regarding the colonization of their phones and the impact that may have on their clinical/surgical practice.

Methods & Materials: 45 mobile phones of the healthcare workers were included, 20 of operating room and 25 of other areas. A trained investigator took swabs from the front and back of the devices (Group A), then the telephones were cleaned with 70% alcohol and 10 minutes later, they were swabbed again with the same technique (Group B). The samples were transported in Stuart's medium and planted on CLDE agar. The colonies were manually identified and confirmed with Phoenix BD automated equipment. Simultaneously 171 healthcare workers answered an anonymous survey about the use, cleaning and perception of colonization of mobile phones.

Results: 35/45 samples of group A (78%) and 4/45 of group B (9%) developed pathogenic bacteria. 6 cases in group A were polymicrobial, the others developed: *methicilin-sensitive CoNS* 23%, *methicilin-resistant CoNS* 18%, *nonfermenting Gram-negative bacilli* 28%, *MSSA* 5%. Alcohol disinfection reduced bacterial colonization by 69%; IC95% (50-86%) $p < 0.0001$.

92% of workers answered that the cell phone helps them solve work issues, 92% said they clean the phone and of them 58% once a day, 83% with alcohol. 86% think that their phone is contaminated but only 41% believe that this has clinical impact.

Conclusion: Mobile phones of healthcare workers have a high rate of colonization with bacteria potentially causing nosocomial infections. Disinfection with 70% alcohol was effective in reducing bacterial colonization. For the most part, healthcare workers think that mobile phones are contaminated, but less than half believe that this has a clinical impact. We believe that guidelines are necessary to protocolize the type and frequency of cleaning cell phones.

Final Abstract Number: SADI 21.003

Session: Control de Infecciones / Infection Control

Date: Thursday, March 1, 2018

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Room: La Pampa

Type: Oral Presentation

A prospective study on active surveillance of bacterial colonization in oncohaematological patients and its association with bacteraemias

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Background: In recent years, a significant increase in invasive infections by multi-drug resistant bacteria (MDR) in oncohaematological (OH) patients has been documented in our country, mainly those caused by gram-negative bacilli, such as KPC. Research has proved connection between colonization and bacteraemia by MDR. Active surveillance of colonization might help identify patients at risk. Objective: analyse the relation between MDR colonization and bacteraemia by the same MDR previously detected in a swab test.

Methods & Materials: Active surveillance data of MDR colonization and bacteraemic infections (MRSA, VRE, Carbapenemase producing *Klebsiella pneumoniae* (KPC), *Acinetobacter baumannii*, *Pseudomonas aeruginosa*) was collected prospectively from OH hospitalised patients from April 2016 to September 2017. Nasal, rectal, axillary and inguinal swabs were carried out on admission and once weekly until discharge.

The results of the categorical variables are shown as percentages, and the ones of numeric variables as mean and standard deviation. In order to compare proportions, the chi-square test was used. Relative risk (RR) was calculated as well as confidence intervals (CI) for 95%. A $p < 0.05$ has been considered significant.

Results: 913 surveillance swabs were carried out in 212 patients. 55% men, average age: 53.2 years old. Underlying diseases: NHL 30%, MM 22%, AML 18%, ALL 12%, MDS 5%, HL 4%, others 9%. Initial swabs were positive in 17/212 (8%) patients. Follow-up monitoring swabs were made in 137 patients, out of which 37/137 (25%) were positive.

We documented 17 bacteraemias/51 colonized patients (33%), 8/17 bacteraemias (47%) caused by MDR, and 56 bacteraemias/161 non-colonized patients (34.7%), 10/56 (17%) caused by MDR ($p = 0.03$). The association between colonization by MDR and MDR bacteraemia was significant: $p = 0.02$; OR: 4.08; IC 95%: 1.2 – 13.21; PPV: 47%; NPV: 82%; S: 44% y E: 83%. Only in the subgroup of patients colonized by KPC there was a significant association with bacteraemia caused by the same bacteria: $p = 0.0001$; RR: 6; IC 95%: 2.9- 12.1; PPV: 85%; NPV: 85%; S: 42% y E: 97%.

Conclusion: In our OH-patient population, we found association between colonization and bacteraemia by KPC. Surveillance of MDR colonization, particularly KPC, would allow to select the best empirical treatment, and reduce associated mortality.

Final Abstract Number: SADI 21.004

Session: Control de Infecciones / Infection Control

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Room: La Pampa

Type: Electronic/Moderated Poster Presentation

Infection control program in elderly adults center

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Background: The National Program of Epidemiology and Control of the Hospital Infections (VIHDA) was created in 2004 in Argentina to decrease hospital infections (HI). Our elderly care center is adhered from the 2012.

To analyze the HI rates for 5 years and to describe the different measures of infection control.

Methods & Materials: Descriptive retrospective quasiexperimental study. We use the Program VIHDA software to analyze the Ventilator associated Pneumonia (VAP), Central Catheter related infections (CCRI) and Catheter Urinary Tract Infection (CUTI) rates by 1000 day - procedure in the intensive care unit since January-2012 to October-2017. The general and specific strategies were classified in periods, describing the strengths and weaknesses of the implemented measures.

Results: VAP rates was 29,49 in 2012, 14,45 in 2013, 22,34 in 2014, 6,36 in 2015 and 12,81 in 2016.

CCRI rates was 14,84 in 2012, 7,98 in 2013, 5,03 in 2014, 8,3 in 2015 and 10,84 in 2016.

CUTI rates was 11,01 in 2012, 7,30 in 2013, 5,95 in 2014, 0,45 in 2015 and 1,88 in 2016.

The VAP, CCRI, CUTI rates until October, 2017 is 9,21; 11,5; 3 respectively.

In the Diagnosis and Implementation period, the rates measured up and there were applied packages strategies for HI prevention. In Intensification period, we adapted the prevention's measures, training personal, preventive universal isolation, monitoring of the empirical initial treatments (EIT) to decrease VAP's rate. In 2015 descended 28,46 %. In Monitoring period, we supervise the compliances to packages of measures and EIT because VAP's rate increased in 50 %. Even this way, we continued working to control CCRI's rates especially.

Conclusion: The strength of the Diagnosis and Implementation period was institutional information to develop measures adapted to the local epidemiology despite difficulties in the adherence to the Procedures Manual. In the Intensification period education was reinforce but also there was limited human resource. In the Monitoring period the opportune load of information was achieved but the human and economic resource is still enough.

In our experience the software implementation is useful to decrease HI.

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Session: Control de Infecciones / Infection Control

Date: Thursday, March 1, 2018

Time: 15:30-17:30

Room: La Pampa

Type: Oral Presentation

Costs reduction and resources optimization: Change of isolation policy

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Background: Contact precautions (CP) are effective measures to prevent the spread of multidrug-resistant microorganism (MDRO). The use of personal protective equipment (PPE) is essential to guarantee effectiveness. This strategy entails a cost, adverse events for the patient and difficulties in compliance. On the other hand, it has been shown that the greater the number of isolated patients, the less adherence.

Objective: To determine the economic impact and infection rate after isolation policy change.

Methods & Materials: Quasi-experimental study, before and after, observational, from January 2014 to September 2017 in a general university hospital located in Buenos Aires province with 197 beds (15 intensive care adults, 19 coronary care unit, 10 pediatric intensive care, 15 Neonatology and 8 Bone Marrow Transplantation). Since 2014, universal isolation was established in adult ICU and PC for patients colonized / infected by KPC, Resistant Enterococcus vancomycin (EVR), Methicillin-resistant Staphylococcus aureus (MRSA), Clostridium difficile (CD) and extended-spectrum beta lactamases (ESBL) producing Enterobacteriaceae in the rest of the hospital.

In July of 2016, the CPs for ESBL and EVR, and universal isolation were suspended. Infections by EVR and ESBL were measured pre intervention (2014-june 2016) and post-intervention (july 2016- sept 2017). The costs in the 1st semester 2016 were compared with 2nd semester 2016

Results: Regarding EVR, in the first period there were 23 infections / 25,482 discharges (0.18 infections/1000 patients days) vs. second period with 6 infections / 14023 discharges (0.086 infections /1000 patients days). The difference between both periods was not statistically significant (p0.14). In patients with ESBL infections there were 61 / 25,482 discharges (0.42 infections/1000 patients days) vs 11/1,4023 discharges (0.06 infections/1000 patients days), the difference is significant in favour of the reduction of infections (p0.0005). We saved \$ 540,000 between 1st and 2nd semestre 2016.

Conclusion: Changing isolation policy, made it possible to maintain low infection rate by ESBL and EVR with significant expenses' savings.

Comment: the change of the isolation policy improved the satisfaction of the staff.

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Type: Oral Presentation

Impact of an antimicrobial stewardship program at a university hospital of respiratory diseases

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Background: Antimicrobial Stewardship Programs (ASP's) have the potential to reduce antimicrobial exposure and decrease microbial resistance, and to decrease costs. The objective of this study was to characterize the overall impact of an ASP on antimicrobial utilization, antimicrobial resistance and mortality rates.

Methods & Materials: Quasi-experimental study, before and after ASP implementation, from January to May 2016 and from January to May 2017 respectively, in an 8-bed adult intensive care unit at a university hospital of respiratory diseases. ASP included: elaboration of local guides (LG's); empiric therapy according to LG's; taking cultures before starting antibiotic therapy (AT); de-escalation of therapy as soon as culture results were available; discontinuation of AT if evidence of infection was absent; short courses of AT. Outcomes for analyses included: retrospective data for antimicrobial utilization measured as defined daily doses (DDD); bacterial susceptibilities of the first five most frequent organisms isolated in each period; and mortality rates for all causes and for infectious causes according to ICD-10 classification.

Results: The overall reduction of all antibiotic utilization was 19%, including a decrease by 81% in meropenem use, 11% for imipenem, 39% for ciprofloxacin, 93% for ceftriaxone, 23% for ceftazidime and 33% for vancomycin. The most frequently isolated organism in the ASP period were *Pseudomonas aeruginosa*, with a reduction by 50% of *Acinetobacter baumannii*, the most frequent isolation in the pre-ASP period. *Pseudomonas aeruginosa* showed resistance to ceftazidime and cefepime in 55% of the cases in the pre-ASP period, whereas only 5% were resistant to the same antibiotics in the ASP period. The susceptibility pattern of *Klebsiella pneumoniae* in the pre-ASP period was 50% KPC and 83% ESBL, in the ASP period there was no carbapenem resistance and 75% ESBL. There was a 71% reduction in overall mortality rates and a 35% reduction in mortality due to infectious causes in the ASP period.

Conclusion: There were limitations in this study due to missing individual patient data. There is a trend towards a decrease in the utilization of antibiotics and a shift of the epidemiological and susceptibility patterns of multidrug resistance organisms. The implementation of ASP was not accompanied by an increase in mortality.

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Type: Oral Presentation

Carbapenemases in the UCI: A constant challenge

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Background: Carbapenemase-producing enterobacteria (CPE) infections increase morbi-mortality and hospital costs ,becoming a serious problem for public health and a constant challenge for the health team.

Argentina has a prevalence of 10%, including the three classes of carbapenemases (OXA, NDM and KPC) with different patterns of sensitivity and geographical distribution.

In the last decade we have observed an exponential increase in CPE infections mainly in the ICU, hence affecting empirical treatments (ET)and limiting de-escalation and therapeutic options.

Objective: To analyze the CPE infections in the ICU and the impact of the ET.

Methods & Materials: Retrospective analysis of case series from January-September 2017 in 2 intensive care unit medical surgical (UCIA - UCIB) in a general hospital in Buenos Aires city (20 beds). We analyzed the episodes of CPE infections, demographic characteristics of the affected population, adequate ET, in vitro sensitivity and evolution. Adequate ET was defined when at least one drug was sensitive in vitro.

Results: There were 485 discharges (3934 patient days) during the analyzed period, episodes of infections 45.7% (222) with 19%(42) by CPE. The number of patients with CPE infections was 36; 61% men, mean age 55 and reason for admission was distributed as follows: liver disease or transplant 19%, neurology 19%, intraabdominal 17%, respiratory 14%; mean APACHE 20, mortality 52.7% (47% related to CPE infection). KPC Colonization 70%. CPE infections were urinary 55%, bloodstream 31%, abdominal 14.4%, respiratory 9.5%. Time from admission to CPE infections was 21 days. Treatment analysis showed: adequate empirical treatment 57%, two or more drugs 63% (24) (mero-col 45.8%, mero-amika 12.5%), definitive treatment combined amikacin 46%, fosfomicin 46%, tigeciclin 21.4%, colistin 25%, monotherapy 39% (mainly in urinary infection). In vitro results: Sensible (S) fosfomicin 78.5%, amikacin 52%, Tigecycline 90%, colistin 21%, meropenem (MIC <16) 4.7%.

Conclusion: CPE infections is one of most important challenges in ICU patients with prolonged stay who are seriously ill and colonized by KPC. Half received adequate combined empirical treatment, with fosfomicin and tigecycline being the most active drugs in vitro. The mortality associated to the infection continues being high, so this data analysis is very useful to improve initial treatments.

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MediPIET (2014-2017) a network for strengthening capacities for global health security through a regional field epidemiology training programme in the Mediterranean and Black Sea regions

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Background: Cross-border threats increase globally every day. Infectious diseases (Ebola, Zika, MERS-CoV) but also chemical or other hazards showed recently that global efforts are needed for early detect, control and prevent of public health threats all over the world. Inter-country collaboration is crucial for a better response. MediPIET - an EU-funded project - is a Regional Field Epidemiology Training Programme (RFETP) involving 18 countries from 3 WHO Regions.

Aim: MediPIET created a network of epidemiologists and PH institutions able to collaborate and contribute to Global Health Security.

Methods & Materials: Development tools for the network: training infrastructure and participatory body. A training infrastructure: fellowship addressed to junior and train-the-trainers (ToT's) addressed to senior, as well as a yearly bases conference that allows sharing of knowledge and networking. Appraised national PH institutions become training sites.

The two-year fellowship programme includes 10-weeks of theoretical –plus-practical sessions and the two-years-on-job-training under the mentorship of seniors. It includes learning duties as: outbreak investigations, surveillance systems and research project development, international assignments and scientific writing.

The seniors involved in ToT's gain knowledge, skills, methodology on learning-by-doing and monitoring tools that place them as pillars of the strategy for strengthening institutional capacities.

The training centre forum (TCF) gathers the countries PHI and provides technical guidance to the programme by establishing training priorities, curriculum development as networking elements. Each country creates its MediPIET National Committee involving different health related sectors: Chemical, biological and Radio Nuclear Centres of Excellence focal points (CBRN-FP).

Results: This 4-years MediPIET achieved to train 22 fellows, 325 external participants in the training modules, 250 seniors, to establish 8 training sites +4 appraised (with supervisors and experts for fellows supporting), 3 scientific conferences organized with a total of 352 abstracts submitted, 350 participants and involving international organizations, networks, individuals. A regional network is established.

Conclusion: Fruitful regional collaboration has been established that otherwise would never occurred due to the different cultures, languages but with common environment and threats.

It is highly recommended to use a Regional FETP for increasing the critical mass and improving regional collaboration for global health security.

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Type: Oral Presentation

Antimicrobial efficacy of highly micronized aerosols of pure, stable HOCl for decontamination of environmental surfaces

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Background: Electrolytically-generated hypochlorous acid produced on-site as a mist or applied as a coarse aerial spray from a liquid reservoir is effective in the inactivation of both noroviruses and spores of *C. difficile* on contaminated coupons and environmental surfaces. However, times of exposure and dwell times in both studies were inconveniently long, undermining the practicality of this approach. We recently demonstrated rapid, high level inactivation of infectious prion proteins and bacterial spores with pure, stable HOCl. We hypothesized that aerial applications of this solution in fine droplet form might be sufficiently potent to accomplish decontamination in attractively short contact times.

Methods & Materials: We used spray nozzles receiving a flow of pressurized air (55 psi) through six 0.078 mm channels to create droplets of HOCl in the 1-8 micron range, delivered to the tip from a reservoir by gravity flow. The resulting “dry mist” was used to expose coupons coated with dried-down inocula of *Staph. aureus*, *Candida albicans*, and spores of *Bacillus subtilis*, and *Aspergillus niger* for 5-30 secs followed by a dwell period (10-15 mins for *S.a*, *C,a*, 20 for *B.s*, 30 for *A.n*) before neutralization with sodium thiosulfate, and recovery of remaining viable organisms by culture.

Results: Inactivation of *S.aureus* and *C.albicans* was achieved at the level of 5-6 LRV with 15 secs of mist exposure. Thirty seconds of misting was required for *B.subtilis* to reach 4 LRV, but for *Aspergillus* the LRV was 2. (The fungal spore preparation contained much more organic material compared to the *Bacillus* suspension). Active Cl content of the droplets delivered to the coupon surfaces declined by as much as >50% from that in the reservoir: from 350 ppm down to 100-150 ppm at the point of delivery to the coupon at 0.5 m, and to <100 ppm at 1 m from the nozzle tip.

Conclusion: These findings support the potential utility of dry misting as a means of efficiently delivering micronized HOCl to points of contamination. They suggest that further contact and dwell time definition could result in an attractive protocol for environmental sanitation in healthcare.