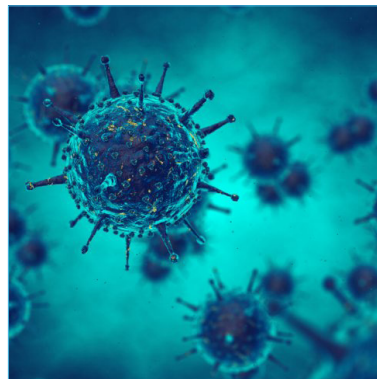


# Poster Presentation

## *Clinical Microbiology & Eye 2018*



7<sup>th</sup> European  
**Clinical Microbiology Congress**  
&  
4<sup>th</sup> International Conference on  
**Ophthalmology and Eye Disorder**  
November 01-02, 2018 | London, UK

7<sup>th</sup> European**Clinical Microbiology Congress**4<sup>th</sup> International Conference on &**Ophthalmology and Eye Disorder**

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**Efficacy and safety of artesunate-amodiaquine for the treatment of uncomplicated *Plasmodium falciparum* malaria in Kigobe health center, in Bujumbura Nord district in Burundi****Ndayikunda Claudette**

University Teaching Hospital of Kamenge, Burundi

**Aim:** To assess the efficacy and safety of artesunate-amodiaquine for the treatment of uncomplicated *P. falciparum* infections in Kigobe health center, in Bujumbura Nord district.

**Background:** The first and second-line treatment for *P. falciparum* in Burundi are respectively artesunate-amodiaquine and quinine+clindamycin. The latest study conducted in 2006, ACPR was 94.8% for artesunate-amodiaquine. This study is to evaluate the efficacy and safety of artesunate-amodiaquine after 10 years of its use.

**Method:** A therapeutic efficacy study was conducted to evaluate the efficacy and safety of artesunate-amodiaquine among patients with uncomplicated falciparum malaria in Kigobe health center, in Bujumbura Nord district. Clinical and parasitological parameters were assessed over a 28-day follow-up period. PCR analysis using *msp1*, *mps2* and *glurp* was conducted to distinguish recrudescence from re-infection. Mutations associated with antimalarial drug resistance in K13 gene (artemisinin resistance), in *dhfr/dhps* gene (pyrimethamine/sulfadoxine resistance), copy number variation in *Pfplasmepsin 2* (*Pfpm2*) gene and *Pfmdr1* (piperaquine and mefloquine resistance) were investigated using PCR analysis and sequencing.

**Result:** A total of 58 patients were enrolled between November 2015 and June 2016. Mean age (SD; range) was 6.3 years (1.8; 2.3-9) and mean weight 19.1 kg (5.4; 10-34). Mean temperature at admission was 38.8°C (1.1; 36.1-40.3) and parasitaemia geometric mean (range) at day 0 was 33 947/ul (2 930-199 800).

Among the 58 patients, 5 were lost to follow-up or withdrawn. Day 3 positivity rate was 0%. ACPR PCR corrected using per protocol analysis was 92.3% (81.5-97.9), LPF 1.9% (0.0-10.3) and LCF 5.8% (1.2-15.9%). No ETF were reported. ACPR PCR corrected using Kaplan Meir analysis was 92.5% (81.3-97.19). Artesunate-amodiaquine was well tolerated. There were no serious adverse reported. Among the 58 isolates analyzed at day 0, all isolates were wild type for K13. All parasites were carrying a single copy of *Pfplasmepsin 2* gene, but 10.3% of the parasites were carrying multiple copy of *pfmdr1*. The prevalence of quintuple mutants (*dhfrN51I+C59R+S108N* and *dhpsK540E+A581G*) was 34.5%.

**Conclusion:** Artesunate-amodiaquine remains efficacious and was well tolerated. There is no evidence of artemisinin resistance and by level of sulfadoxine-pyrimethamine which need to be taken into account for the IPTp policy implementation.

**Speaker Biography**

Ndayikunda Claudette is a laboratory specialist and a Burundian renowned researcher, professor and member of the ASLM team, serving as a member of the East African Public Health Laboratory Network Project operational research. At the university level, she is the head of the Laboratory at CHU Kamenge Hospital in Bujumbura, which is a University Teaching Hospital of Burundi. The Laboratory is Burundi's reference laboratory and here she performs research on HIV/AIDS, Malaria diseases and microbiology as well as medical research. She has published more than 50 papers in reputed journals and has been serving as an editorial board member of 3 journals. She is also engaged in surveillance, education and capacity building in East African community as a deputy chairperson technical working group training and building capacity in Burundi.

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Notes:

# Clinical Microbiology Congress

## & 4<sup>th</sup> International Conference on Ophthalmology and Eye Disorder

November 01-02, 2018 | London, UK

### Exposure to manuka honey modules antibiotic susceptibility on wound isolates

Jawahir Mokhtar, Andrew J McBain, Ruth G Ledder and Gavin Humphreys  
The University of Manchester, UK

**Background:** The clinical application of Manuka honey has recently gained momentum, particularly in treatment of chronic wound infections. Changes in antibiotic susceptibility have been observed previously, following the exposure of bacteria to subtherapeutic concentrations of honey, however such findings have been limited to methicillin-resistant *Staphylococcus aureus*, *Streptococcus pyogenes* and *Pseudomonas aeruginosa*. The aim of this study is to assess the modulation of antibiotic sensitivity in a broader panel of chronic wound isolates.

**Methods:** Parent strains (P0) of *Staphylococcus aureus*, MRSA, *Staphylococcus epidermidis*, *S. pyogenes*, *P. aeruginosa*, *Escherichia coli*, *Klebsiella pneumoniae* and *Proteus mirabilis* were passaged ten times in the presence of sub-lethal concentrations of clinical grade Manuka honey to generate strain P10. In order to assess any permanent or transient changes in bacterial susceptibility, the bacteria were grown in honey-free media for a further 10 passages (X10). Antibiotic sensitivity testing was performed using a combination of microdilution and disc diffusion methodologies.

**Results:** Variable changes in bacterial susceptibilities were

noted following subtherapeutic exposure to honey. P10 strains of *S. epidermidis* and *S. pyogenes* exhibited a  $\geq 4$ -fold decrease in their sensitivities to erythromycin and tetracycline in comparison to baseline values. Similarly, *E. coli* displayed a 4-fold reduction in susceptibilities to gentamicin following passaging with honey. In contrast, *K. pneumoniae* and *P. mirabilis* showed notable increases in susceptibility towards both ciprofloxacin and gentamicin after 10 passages in the presence of honey. All changes in MIC, MBC and MBEC were shown to be transient in nature with the exception of *K. pneumoniae* and *P. mirabilis* (X10), which exhibited an MIC to ciprofloxacin  $>4$  fold greater than the parent strains.

**Conclusion:** Wound isolates exposed to clinical grade Manuka honey exhibited transient changes in antibiotic profiles. The underlying mechanism and clinical implications of such changes are unclear and warrant further investigation.

#### Speaker Biography

Jawahir Mokhtar is currently pursuing her PhD at the University of Manchester, UK.

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Notes:

**Analysis of thoracic proteins of female *Aedes togoi*, *Anopheles lesteri* and *Anopheles paraliae*, responsible for nocturnally subperiodic *Brugia malayi* infection**

Watcharatip Dedkhad, Onrapak Reamtong, Wanpen Chaicumpa, Chayanit Hempolchom and Atiporn Saeung  
Chiang Mai university, Thailand

*Brugia malayi* is a mosquito-borne filarial nematodes causing human filariasis lymphatic (LF). Understanding the host responding to *B. malayi* would be useful to prevent the transmission of the disease. The ability of pathogen transmission is depend on the relationship between host and parasite that occurring in the thoracic muscles. However, little is known about mosquito proteins responding during developing processes. We aim to characterize and compare the proteomic profiles of the thoracic proteins of the three mosquito species responsible for nocturnally subperiodic *B. malayi* infections. Highly susceptible (*Aedes togoi*, *Anopheles lesteri*) as well as low susceptible (*Anopheles paraliae*) filariasis vectors were used in this study. The thoraces of *B. malayi*-infected mosquitoes (test group) and uninfected blood meals (control group) of each mosquito species were collected at 96 hours post blood meal. The SDS-PAGE-separated-protein profiles of *B. malayi*-infected *Ae. togoi*, *An. lesteri* and *An. paraliae* showed at least

10, 9 and 8 major protein bands, respectively, whereas 6 major protein bands were found in the control groups. Nano-liquid chromatography mass spectrometry (nanoLC-MS/MS) revealed 22, 9 and 12 previously known proteins in *B. malayi*-infected *Ae. togoi*, *An. lesteri* and *An. paraliae*, respectively. Of interest, peroxiredoxin 5, thioredoxin and superoxide dismutase, were expressed only in *B. malayi*-highly susceptible *Ae. togoi* and *An. lesteri*. This is the first study provides the data on thoracic protein profile responding during *B. malayi* development and demonstrates that antioxidant and detoxifying proteins might play important role and/or provide favorable environment in facilitating further development of the *B. malayi* microfilariae to the human infective stage in the vectors.

**Speaker Biography**

Watcharatip Dedkhad is a PhD student at the Department of Parasitology, Faculty of Medicine, Chiang Mai University, Thailand. She has published 4 papers in reputed journals.

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**The role of ActA in peptidoglycan remodelling in *Listeria monocytogenes***

Ohoud S Alhumaidan, Nino Iakochvili, Peter W Andrew and Galina V Mukamolova  
University of Leicester, UK

*Listeria monocytogenes* is a food-borne bacterial pathogen, the causative agent of human listeriosis. It may cause abortion in pregnant women, septicaemia, endocarditis and meningitis in elderly people and immunocompromised patients. *L. monocytogenes* has many virulence factors that enable its replication in macrophages and the escape from the phagolysosome to the cytoplasm. One of these virulence factors is the actin-assembly inducing protein, ActA, that is essential for *L. monocytogenes* intra- and intercellular motility. Recently, the ActA protein has been shown to regulate peptidoglycan (PG) biosynthesis during *L. monocytogenes* replication in macrophages. However, the exact mechanism for this phenomenon is unknown. The central hypothesis of the present study is that ActA possesses peptidoglycan hydrolysing activity. To address this hypothesis three different His-tagged forms of ActA have been expressed in *Escherichia coli*. All versions have been successfully purified using affinity chromatography, gel-filtration and their identity has been confirmed by mass-spectrometry. Peptidoglycan hydrolysing

activity of these proteins has been assessed by application of zymography and digestion of FITC-labelled peptidoglycan. One domain showed significant peptidoglycan-hydrolysing activity as judged by zymography and digestion of FITC-labelled peptidoglycan. Candidate catalytic residues are currently being identified by application of bioinformatics and their function will be verified by site directed mutagenesis. Future experiments such as analysis of muropeptides released from PG by ActA, complementation studies and pull-down assays will shed light on the function of this protein in peptidoglycan remodelling.

**Speaker Biography**

Ohoud S Alhumaidan is a 3<sup>rd</sup> year PhD student in infection, immunity and inflammation department at University of Leicester. She is working under the supervision of Dr. Galina Mukamolova and professor Peter Andrew. Her doctoral research investigates the role of specific protein in *listeria monocytogenes*. She is a member of the microbiology society and she holds master's degree in microbiology from King Saud University, Saudi Arabia, in isolation and characterisation of nasal carriage MRSA among health care staff in a teaching hospital.

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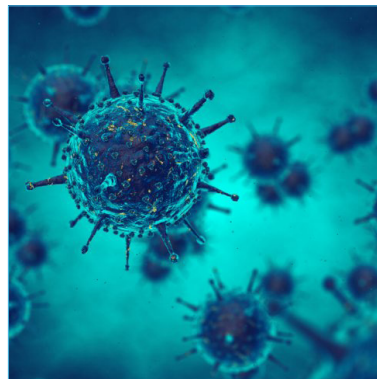


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# Accepted Abstracts

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**Counterfeit drugs set alarm bells ringing: Comparative analysis of drug policies****Abdeen Mustafa Omer**  
Ministry of Health, Sudan

The strategy of price liberalisation and privatisation had been implemented in Sudan over the last decade, and has had a positive result on government deficit. The investment law approved recently has good statements and rules on the above strategy in particular to pharmacy regulations. Under the pressure of the new privatisation policy, the government introduced radical changes in the pharmacy regulations. To improve the effectiveness of the public pharmacy, resources should be switched towards areas of need, reducing inequalities and promoting better health conditions. Medicines are financed either through cost sharing or full private. The role of the private services is significant. A review of reform of financing medicines in

Sudan is given in this communication. Also, it highlights the current drug supply system in the public sector, which is currently responsibility of the Central Medical Supplies Public Corporation (CMS). In Sudan, the researchers did not identify any rigorous evaluations or quantitative studies about the impact of drug regulations on the quality of medicines and how to protect public health against counterfeit or low quality medicines, although it is practically possible. However, the regulations must be continually evaluated to ensure the public health is protected against by marketing high quality medicines rather than commercial interests, and the drug companies are held accountable for their conduct.

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November 01-02, 2018 | London, UK

**The microbiome of insect vectors as hidden reservoirs for pathogens****Ana Carolina M Junqueira**

Federal University of Rio de Janeiro, Brazil

Insects are well-known mechanical and biological vectors of diseases. Flies such as blowflies and houseflies feed and breed in feces and decaying organic matter, where they may acquire a significant part of their microbiome. Likewise, mosquitoes can visit a variety of sites and acquire their microbiome from the environment and hosts where they feed. Flies and mosquitoes are ubiquitous and synanthropic, thus potentially playing an important role in the dispersal of microorganisms to humans, animals and plants. In this study, we investigated the microbiome of major insect vectors in different continents to great depth, including the Oriental latrine blowfly *Chrysomya megacephala*, the common housefly *Musca domestica* and the Asian tiger mosquito *Aedes albopictus*. In total, ~150 individual insects were sequenced through whole genome shotgun (WGS) and we performed an in silico approach to filter the host DNA sequences from datasets. This allowed for genomic and metagenomic analyses of the host-associated microbiome at the

species level. Identification of microorganisms was done with different bioinformatics approaches with varying stringencies. Different insect species segregate based on the microbial diversity and abundance, as shown with PCoA. Legs and wings of flies displayed the largest microbial diversity and were shown to be an important route for microbial dispersion. The environmental sequencing approach used detected a stochastic distribution of human pathogens in flies and mosquitoes. We were able to further analyse pathogens at genomic level, identifying virulence factors of the major causative agent of gastric ulcers, *Helicobacter pylori* and antimicrobial resistance in *Enterobacter cloacae* isolated from mosquitoes. Therefore, our metagenomic approach highlights the potential of insects in dispersing pathogens to humans, plants and animals through neglected epidemiological routes.

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**Clinical Microbiology Congress****Ophthalmology and Eye Disorder**

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**War on terror cells: Novel sources of antimicrobials****Naveed Ahmed Khan**

Sunway University, Malaysia

With the worsening trends of drug resistance, there is a need for newer and more powerful antimicrobial agents. The search for new compounds originating from natural resources is a promising research area. We hypothesized that animals living in polluted environments are potential source of novel antimicrobial molecules. Under polluted milieus, organisms such as cockroaches encounter different types of microbes, including superbugs. Such creatures survive the onslaught of superbugs and are able to ward off disease by producing antimicrobial substances. Here, we characterized antibacterial properties in extracts of various body organs of cockroaches (*Periplaneta americana*) and showed potent antibacterial activity in crude brain extract against methicillin-resistant *Staphylococcus aureus* and neuropathogenic *E. coli* K1. The size-exclusion spin columns revealed that the active compound(s) are less than 10 kDa in molecular mass. Using cytotoxicity

assays, it was observed that pre-treatment of bacteria with lysates inhibited bacteria-mediated host cell cytotoxicity. Using spectra obtained with LC-MS on Agilent 1290 infinity liquid chromatograph, coupled with an Agilent 6460 triple quadruple mass spectrometer, tissues lysates were analyzed. Among hundreds of compounds, only a few homologous compounds were identified that contained isoquinoline group, chromene derivatives, thiazine groups, imidazoles, pyrrole containing analogs, sulfonamides, furanones, flavanones and known to possess broad-spectrum antimicrobial properties and possess anti-inflammatory, anti-tumour and analgesic properties. Further identification, characterization and functional studies using individual compounds can act as a breakthrough in developing novel therapeutics against various pathogens including superbugs.

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**Detection and management of highly pathogenic avian influenza A/H5N1 clade 2.3.2.1c virus in poultry in Cameroon, 2016–2017****Abel Wade**

Laboratoire National Veterinaire, Cameroon

In May 2016, highly pathogenic avian influenza virus (HPAIV) of the subtype A/H5N1 was detected in Cameroon in an industrial poultry farm at Mvog-Betsi, Yaounde (Centre region), with a recorded sudden increase of deaths among chickens, and an overall mortality rate of 75%. The virus spread further and caused new outbreaks in some parts of the country. In total, 21 outbreaks were confirmed from May 2016 to March 2017 (six in the Centre, six in the West, eight in the South and one in the Adamaoua regions). This resulted in an estimated total loss of 138,252 birds (44,451 deaths due to infection and 93,801 stamped out). Only domestic birds (chicken, ducks and geese) were affected in farms as well as in poultry markets. The outbreaks occurred in three waves, the first from May to

June 2016, the second in September 2016 and the last wave in March 2017. A multi-sectorial management were used to control the outbreaks. The topology of the phylogeny based on the haemagglutinin gene segment indicated that the causative H5N1 viruses fall within the genetic clade 2.3.2.1c, sharing a same group with the A/H5N1 viruses collected in Niger in 2015 and 2016. More importantly, the gene constellation of four representative viruses showed evidence of H5N1/H9N2 intra-clade reassortment. Additional epidemiological and genetic data from affected countries in West Africa are needed to better trace the origin, spread and evolution of A/H5N1 in Cameroon.

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**Zika virus infection new threat in global health****Saber Mosaad Hegazy**  
Al Azhar University, Egypt

In this abstract we will show the history of virus, classification, properties of virus including virion properties, virus replication, Similarities and differences between other members in the same genus. As skin is the first line of body defense against infection we examined infected skin to see the histopathology as a marker of infection regarding viral molecular pathogenesis molecular epidemiology, evolution and phylogenetic analysis. Referring to symptoms of virus as a primary indicator for infection since the symptoms appeared only in 20% of infected people, including the most common symptoms such as (microcephaly, guillian barre syndrome). There is no doubt that the vector has a critical

role in spreading the virus, so we will talk about transmission and mode of transmission. Detection of virus by different ways (serology and RT-PCR).

Control of vector by using:

1. Traditional technique like using repellent and chemicals.
2. Advanced biological ways for control (modifying of some vector genes, production of new off spring generation) and
3. Finally treatment.

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**Genomic features, novel antibiotic resistance genes and pan-genome analysis of clinical multidrug-resistant *Acinetobacter baumannii* strains in Vietnam hospital****Si-Tuan Nguyen**

Thongnhat Dongnai General Hospital, Vietnam

**Background:** *Acinetobacter baumannii* is an important nosocomial pathogen that can develop multidrug resistance. In this study, we sought to explore the genomic properties, phylogenetic relationships and comparative genomics of this pathogen through strain DMS06669 and DMS06670 (isolated from the sputum of two male patients with hospital-acquired pneumonia).

**Methods:** Whole genome analysis of *A. baumannii* DMS0669 and DMS06670 included *de novo* assembly; gene prediction; functional annotation to public databases; phylogenetic tree construction by average nucleotide identity; pan-genome analysis and antibiotics resistance genes identification. Antibiotics resistance genes *in-vitro* were isolated by PCR and re-confirmed by improved Sanger method.

**Results:** The data showed that a total of 19 possible antibiotic resistance genes, conferring resistance to eight distinct classes of antibiotics, were identified in two strains. Nine of these genes have not previously been reported to occur in *A. baumannii*. Comparative analysis of 23 available genomes of *A. baumannii* revealed an open pan-genome consisting of 15,883 genes. All antibiotics resistance genes were isolated.

**Conclusions:** Our results provide important information regarding mechanisms that may contribute to antibiotic resistance in the DMS06669 and DMS06670 strain and have implications for treatment of patients infected with *A. baumannii*.

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**Occult hepatitis B infection, a real challenge for low incoming countries****Bivigou Mboumba Berthold**

Centre International de Recherches Médicales de Franceville, Gabon

Occult hepatitis B infection (OBI) is defined as the presence of low level of HBV DNA in the serum and/or hepatic cells without HBsAg in the serum. These patients are at risk for HBV reactivation in immunosuppressed state or in treatment of cancers and autoimmune diseases. This reactivation can lead to fulminant hepatitis B form, or high level of hepatic injury. The transmission of OBI may appear mainly in blood transfusion context. In HCV endemic area like in sub-Saharan countries, OBI could be responsible for the acceleration of chronic hepatitis C virus (HCV) progression and interfere with treatment response. The prevalence of HBOs varies from 1 to 87%, depending on studied population, the sensitivity of the tests used for diagnostic and the nature of the sample used. OBI is significantly associated with the endemicity of HBV infection, but is not limited to hyper-endemic countries for HBV. OBI may appear in many different clinical conditions such as: a) transmission by blood transfusion and mainly liver

transplantation, causing typical hepatitis B in newly infected individuals; b) the development of an immunosuppressive status may induce OBI reactivation and development of acute and sometimes fulminant hepatitis; c) a large body of data suggests that OBI can contribute to the progression of the chronic liver disease toward cirrhosis, in particular in HCV-infected patients and d) much evidence suggests that OBI can be involved in hepatocellular carcinoma (HCC) development. The diagnostic of this infection is only possible by using high sensitive and specific PCR technique with a low limit of detection (LLOD <10 IU/mL). However, this technique remains a challenge in low and middle income countries like sub-Saharan countries where HBV prevalence is high. Propositions of molecular diagnostic of OBI in sub-Saharan countries are in exploration by African researchers.

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**Screening, identification and antimicrobial activity of mycoparasitic fungus (*Aspergillus* sp.) from Philippine aglibut sweet tamarind****Crisanto A Miclat**

Saint Joseph Thare School, Philippines

Due to the increasing resistance of pathogenic microorganisms, *Aspergillus* sp. isolated from aglibut sweet tamarind's bark of Pampanga State Agricultural University was evaluated for potential mycoparasitism and antimicrobial activity. The micrograph obtained from Scanning Electron Microscopy (SEM) analysis reveals that *Aspergillus* sp. is a potential mycoparasite; further, its identity was 99% which was confirmed through 18s rDNA of its ITS1 forward and ITS4 reverse sequences by Polymerase Chain Reaction (PCR) amplification and sequencing. Moreover, Thin-layer Chromatography (TLC) was used to identify the bioactive compounds of *Aspergillus* sp. The chemical groups such as

glycosidic flavonoid, alkaloid and anthrones were also present which can express the desired activity. Complete Randomized Design (CRD) was carried out with the following treatments; T1 (suspensions) - control (DMSO) and + control (streptomycin for bacteria: Ketoconazole for fungus). Paper-disc diffusion confirms that the suspensions of *Aspergillus* sp. have significant antimicrobial potential as shown in the zones of inhibition in *S. aureus* and *S. cerevisiae* but with lower activity in *E. coli*. Thus, *Aspergillus* sp. is a potential mycoparasite and source of new drugs and drug products.

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**Direct evidence of viral infection and mitochondrial alterations in the brain of fetuses at high risk for schizophrenia****Segundo Mesa Castillo**

Psychiatric Hospital of Havana, Cuba

There is increasing evidences that favor the prenatal beginning of schizophrenia. These evidences point toward intra-uterine environmental factors that act specifically during the second pregnancy trimester producing a direct damage of the brain of the fetus. The current available technology doesn't allow observing what is happening at cellular level since the human brain is not exposed to a direct analysis in that stage of the life in subjects at high risk of developing schizophrenia. Methods. In 1977, we began a direct electron microscopic research of the brain of fetuses at high risk from schizophrenic mothers in order to finding differences at cellular level in relation to controls.

**Results:** In these studies we have observed within the nuclei of neurons the presence of complete and incomplete viral particles that reacted in positive form with antibodies to herpes simplex

hominis type I [HSV1] virus and mitochondria alterations.

**Conclusion:** The importance of these findings can have practical applications in the prevention of the illness keeping in mind its direct relation to the aetiology and physiopathology of schizophrenia. A study of the gametes or the amniotic fluid cells in women at risk of having a schizophrenic offspring is considered. Of being observed the same alterations that those observed previously in the cells of the brain of the studied foetuses, it would intend to these women in risk of having a schizophrenia descendant, previous information of the results, the voluntary medical interruption of the pregnancy or an early anti HSV1 viral treatment as preventive measure of the later development of the illness.

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**Human RAD9B variant 2 regulates the phosphorylation of CHK2 kinase****Yogendra Kumar Verma**  
Bangor University, United Kingdom

**H**uman RAD9A and RAD9B protein are two isoforms of the DNA lesion response protein RAD9. RAD9A and Rad9B form the Rad9-Rad1-Hus1 checkpoint ring at sites of DNA damage. The RAD9 protein participates in the DNA repair process through regulating cell cycle checkpoints and the apoptotic pathway. The checkpoint kinases CHK1 and CHK2 are associated with single and double stranded DNA damage jointly with ATR and ATM kinase, respectively. RAD9A and RAD9B isoforms differ from each other by their amino acid sequence; RAD9B is larger than RAD9A. So far it is unknown why human cells express to related

Rad9 proteins. The RAD9B gene encodes four protein splice variants and the results presented here identify splice variant 2 as a regulator of CHK2 phosphorylation. Only over-expression of variant 2 but not variant 1 in HEK293 cells results in the hyper-phosphorylation of CHK2 in undamaged cells. It is still not yet clear which kinase is involved in the aberrant modification of CHK2. This is the first evidence identifying a specific function for Rad9B and more specifically for one of its protein variants.

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***Salmonella* Typhimurium and *Salmonella* Enteritidis infections in sporadic diarrhea in children: Source tracing and resistance to third-generation cephalosporins and ciprofloxacin****Zhouqiu Wei**

Children's Hospital of Fudan University, China

**Objectives:** This study is aimed to trace the transmission source of *Salmonella* Typhimurium and *Salmonella* Enteritidis strains associated with enteric infections in Shanghainese children, and understand the molecular mechanism of resistance to third-generation cephalosporins and ciprofloxacin.

**Methods:** The profiles of pulsed-field gel electrophoresis (PFGE) were compared among the isolates from children, animal and environment. Antimicrobial susceptibility was determined using the minimal inhibitory concentrations and Kirby-Bauer disk diffusion method. Genes mediating extended-spectrum  $\beta$ -lactamase (ESBL) producing were identified using PCR and sequencing.

**Results:** Based on PFGE patterns, 49 (33.1%) of 148 human *Salmonella* Typhimurium isolates in the dominant PFGE clusters were genetically related to the isolates from poultry source, environment water, aquatic products and reptiles and 97(97.0%) of 100 human *Salmonella* Enteritidis isolates were

genetically related to isolates from poultry and water. The rates of resistance to ceftriaxone among clinical *Salmonella* Typhimurium and *Salmonella* Enteritidis isolates were 42.0% and 14.2%, respectively. Besides, 35.1% of clinical *Salmonella* Typhimurium isolates were resistant to ciprofloxacin. The rates of resistance to cefotaxime and ciprofloxacin among *Salmonella* Typhimurium isolates from freshwater food animals and *Salmonella* Enteritidis isolates from pork meat were 13% and 69.6%, and 18.2% and 9.1%, respectively. Of the 64 ESBL/AmpC-producing strains, CTX-M, TEM, DHA and CMY were found in 86.0%, 62.5%, 7.8%, 3.1% and 3.1% of isolates, respectively.

**Conclusions:** The transmission sources of *Salmonella* Typhimurium and *Salmonella* Enteritidis infections in Shanghainese children were diverse. The high prevalence of resistance to third-generation cephalosporins and ciprofloxacin mediated by multiple molecular mechanisms need continuous attention and intervention.

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**3D Technology applied in the rehabilitation of patients with loss of ocular globe****Marcela Felizzola Cristancho**

Fundacion Universitaria San Martin, Colombia

**Objective:** To demonstrate the effectiveness of 3D technology in the ocular rehabilitation of patients with total or partial loss of the eyeball.

**Material and Methods:** A unicentric prospective clinical trial was performed, with patients with total and partial loss of the ocular globe. In total there were 8 cavities studied, during a period of 15 months. These patients were evaluated with the Proofel protocol and adapted with ocular prostheses made based on the topographic interpretation of the cavity (visualization technique and wax modeling of previous models), taking quantitative measurements, evaluation of the three adaptation criteria: Mobility, symmetry and aesthetics and parameterization of the final devices.

Once the patients were adapted, the information gathering stage for the three-dimensional reconstruction of the cavities under study began, with the use of a high-tech scanner capable

of capturing complex geometries, sharp edges, thin slits and with a resolution of up to 0.1 mm, the necessary images were captured and then exported by means of files to a 3D design computer program where computer aided design was made, which was later printed by computer-aided manufacture, this impression becoming the model of the prosthesis future for each patient.

The parameters of the devices in use and those obtained by 3D printing were analyzed, complemented by a survey that allowed comparing the two techniques from the patients.

**Results:** Safe technology for the health of patients, objective, reliable, comfortable, zero contact, with a minimum exposure time to collect accurate information about the cavity, for use in all types of patients with total or partial loss of the balloon ocular.

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*Notes:*

7<sup>th</sup> European**Clinical Microbiology Congress**4<sup>th</sup> International Conference on &**Ophthalmology and Eye Disorder**

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**Evolution of high-level aminoglycoside resistance in *Escherichia coli* under high and low mutation supply rates****Claudia Ibacache-Quiroga**

National Center for Biotechnology, Spain

Antibiotic resistance is a major concern in public health worldwide, generating 25,000 death per year only in Europe, thus there is much interest in characterizing the mutational pathways through which susceptible bacteria evolve resistance. Among most important antibiotics in human health are those that belong to the aminoglycoside family, whose are effective for the treatment of infections caused by gram negative pathogens like *Escherichia coli*. The usage of experimental evolution to explore the mutational pathways toward aminoglycoside resistance, using gentamicin as a model, under low and high mutation supply rates, allowed to identify that normo and hypermutable strains of *Escherichia coli* are able to develop resistance to drug dosages > 1,000 fold higher than the minimal inhibitory concentration for their ancestors. In this approach, this level of

resistance has been associated with changes in susceptibility to other antibiotics. Whole-genome sequencing of gentamicin-resistant strains revealed that all resistant derivatives presented diverse mutations in five common genetic elements: *fhuA*, *fusA* and the *atpIBEFHAGDC*, *cyoABCDE* and *potABCD* operons. In contrast to recent studies, in this study the mutation supply rate mainly affected the speed (tempo) but not the pattern (mode) of evolution: Both backgrounds acquired the mutations in the same order, although the hypermutator strain did it faster. This observation is compatible with the adaptive landscape for high-level gentamicin resistance being relatively smooth, with few local maxima; which might be a common feature among antibiotics for which resistance involves multiple loci.

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**The *in-vitro* anti-methicillin resistant *Staphylococcus aureus* (MRSA) activity of *Garcinia binucao* (Choisy)****Alyanna Maachah P Hipe**

University of Santo Tomas, Philippines

The use of antibiotics has paved the way for the health improvement of the people, but its use and misuse have also caused several problems which has alarmed the clinical community. Natural products, specifically underutilized and indigenous fruits of the Philippines may have promising effects compared to chemically synthesized antibiotics. *Garcinia binucao*, an evergreen fruit tree, is abundant in the Visayas region and its only known function is as a souring agent among the locals. This study shall identify Batuan's bioactive compounds and screen the fruit and leaf extract against

methicillin-resistant *Staphylococcus aureus* (MRSA), a clinically significant multi-drug resistant pathogen. The fruits and leaves will be procured in Jaro, Iloilo and will be extracted using ethanol and methanol. These crude extracts will be prepared for an antimicrobial susceptibility assay and a time-kill assay. Transmission electron microscopy will be done to observe cell ultrastructure on the extract's exposure to MRSA which, may shed light on the extract's possible mechanism of action.

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**Prevalence of enterovirus serotypes in children with encephalitis/meningitis in Shanghai, China, 2016~2017****Jingjing Li**

Children's Hospital of Fudan University, China

**Background:** Enterovirus (EV) is a major cause of viral encephalitis/meningitis. This study aimed to investigate the prevalence of enterovirus-associated encephalitis/meningitis and the distribution of enterovirus serotypes in children with encephalitis/meningitis in Shanghai during 2016~2017.

**Methods:** We collected cerebrospinal fluid specimens from pediatric patients with encephalitis/meningitis and stool specimens from children with viral encephalitis/meningitis followed with hand-foot-mouth disease (HFMD) during 2016~2017. The nested RT-PCR and sequencing were performed to identify the enteroviruses and serotypes.

**Results:** During 2016~2017, we obtained 295 non-duplicated cerebrospinal fluid specimens from children with clinically diagnosis viral encephalitis/meningitis, and enterovirus was positive in 163 (55.25%) specimens. Of which, 139 and 156 specimens were taken from inpatients and outpatients, respectively. Enterovirus was positive in 66 (47.48%) and 97 (62.18%) cerebrospinal fluid specimens from inpatients and outpatients, respectively. Among inpatients with viral encephalitis/meningitis, 11 serotypes were identified including Echovirus 30 (E30, 42.42%), Coxsackievirus A6 (CV-A6, 12.12%), CV-A5 (10.61%), E6 (9.09%), E11 (7.58%), CV-A2 (4.55%), E9 (4.55%), CV-B5 (4.55%), CV-A10 (1.52%), CV-B3 (1.52%), E14

(1.52%). Among outpatients with viral encephalitis/meningitis, 13 serotypes were identified, including CV-A6 (31.96%), E30 (23.71%), CV-A10 (14.43%), E6 (7.22%), E9 (5.15%), CV-A2 (4.12%), CV-A9 (4.12%), CV-A5 (3.09%), CV-B5 (2.06%), EV-A71 (2.06%), E14 (1.03%), CV-B4 (1.03%). Of the 5 cases with critically severe encephalitis who all survived, E9, CV-A2 and E6 was identified in 2 cases and 1 case, respectively. Among 163 EV-associated encephalitis/meningitis cases, children aged >4 years old accounted for the most cases with 79.14% (129/163).

Besides, we obtained 61 stool specimens from children with viral encephalitis/meningitis followed with HFMD. And EV was positive in 56 (91.80%) specimens. 11 serotypes were identified including EV-A71 (85.71%), CV-A2 (5.36%), CV-A16 (23.57%), CV-A6 (3.57%), CV-A5 (1.79%). All encephalitis/meningitis followed with HFMD were mild cases. Of which, children aged <4 years old accounted for the most cases with 73.22% (41/56).

**Conclusion:** Multiple enterovirus serotypes co-circulated among children in Shanghai. Non-EV-A71 enteroviruses were responsible for viral encephalitis/meningitis and E30 and CV-A6 were frequent serotype responsible for encephalitis/meningitis. And school children were more susceptible to EV-associated encephalitis/meningitis than preschool child.

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**Wavefron- Guided LASIK vs. SMILE: Which is better?****Mounir Khalifa**

Tanta University, Egypt

SMILE technique has been suggested to be an alternative to laser in situ keratomileusis (LASIK) for the correction of myopia, with some advantages. As the SMILE technique is an all-in-one femto second laser procedure, the complications associated with flap-cutting are avoided. Furthermore, as there is no superficial cut, the impact on sub-basal nerve plexus is minor, with less incidence of postoperative dry eye signs

and symptoms in the initial postoperative period. However, the benefit of the SMILE technique over LASIK in terms of postoperative visual acuity, refraction and visual quality is not clear. This presentation will discuss pros & cons of each technique as a treatment for low, moderate and high myopia with astigmatism.

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## Orbital immature teratoma: A rare entity with diagnostic challenges

**Hind M Alkatan**

King Saud University-Medical City, Saudi Arabia

Childhood orbital teratomas are congenital lesions that presents most often at birth with progressive, severe unilateral proptosis. Due to the rarity of such tumors, the diagnosis is often missed with delay in the patient's management. We are presenting a unique case of an immature

right orbital teratoma with extensive growth in a full-term newly born baby boy. In this case report, we provide description of the clinical findings, initial misdiagnosis and the eventual management with review of similar reported cases.

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**Clinical features of cytomegalovirus endotheliitis/anterior uveitis****Oya Donmez**

Bayindir Hospital, Turkey

Cytomegalovirus is a rare but, increasingly recognized cause of corneal endotheliitis that requires strong clinical suspicion for diagnosis. We report the clinical characteristics and follow up of twelve cases of CMV endotheliitis/anterior uveitis. Six male and six female patients were included. The mean age at the time of diagnosis was  $37.2 \pm 17.2$  (15-74) years and mean follow-up time was  $40.5 \pm 24.04$  (10-72) months. The mean number of attacks were  $4.7 \pm 4.5$  (1-16). The time between the first attack and CMV diagnosis was  $17.1 \pm 11.3$  (5-36) months. Diagnostic tap was performed in 10 cases in whom quantitative PCR analysis were positive for CMV. The focal corneal endotheliitis with localised edema was present in 8 (66.7), diffuse iris atrophy in 7 (58.3%), cataract in 10 (83.3%), intraocular pressure rise during acute attacks and keratic precipitates in all cases. Specular microscopy demonstrated significantly lower endothelial cells in affected eyes. ( $2288 \pm 357$ ) compared to the fellow eyes ( $3224 \pm 335$ ). Keratic precipitates (KP) was medium-sized either localised around the endotheliitis or at the lower two thirds

of corneal endothelium. Inferiorly localised pigmented KPs were present in 75% of the patients. The mean IOP during the attacks was  $35.5 \pm 11.8$  (15-60) mmHg and treated with medical therapy and 2 patients required glaucoma surgery. Five patients have visually impairing cataract and underwent surgery. All patients were given systemic antiviral treatment (valaciclovir or valganciclovir) and topical antiviral ophthalmic gel (ganciclovir). Duration of systemic treatment was  $10.8 \pm 8.5$  months, all patients showed favorable improvement while reinstatement was necessary in two patients due to recurrent attacks. Focal corneal endotheliitis with localised corneal edema, inferiorly pigmented KP and, intraocular pressure rise during attacks are characteristic features of CMV anterior uveitis. Early diagnosis and treatments are crucial to reduce the number of attacks, severity of the disease and prevent sight threatening complications.

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