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Management of MDR-TB at the University Hospital of Kinshasa

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Background: MDR-TB is a great concern in the fight against TB in many underdeveloped countries.

To assess the management of MDR-TB at The University hospital of Kinshasa.

Methods & Materials: Retrospective analysis of charts of patients with drug resistant TB admitted at the Kinshasa University hospital from January 1st to December 31st 2006.**Results:** Out of 256 with chronic TB, 76 has performed a culture for sensitivity test and 45 (59.21%), predominantly aged between 20 and 49 years old, where really MDR-TB. The main treatment regimen applied was the combination of Kanamycine+ Ofloxacin+ Prothionamide+ Ethambutol+ Pyrazinamide, with recovery in 51.3%, and mortality rate of 22.86%. Treatment failure was observed in 5.71% of patients; and sputum culture conversion at the 3rd month of treatment was 51.7%.**Conclusion:** MDR-TB screening is still weak in our milieu. The standardized treatment regimen seems to be accurate with a good bacteriological conversion after a 3 months treatment.<http://dx.doi.org/10.1016/j.ijid.2014.03.1119>**Type: Poster Presentation**

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The new PCR-protocol for identification of *Salmonella* spp. and typing of *S. enterica* enteritidis, *S. enterica* typhimurium, *S. typhi*, *S. dublin*, *S. gallinarum* in the food safety system

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Background: Salmonellosis is one of the most dangerous diseases that is caused by *Salmonella* agents, and has a wide spectrum of clinical manifestations - from asymptomatic to severe septic forms. In the majority of *Salmonella* infection cases, the *enterica* subspecies serovars are isolated from animals and humans. According to the FAO, 20% of poultry products in the world are contaminated with salmonella. Every year on the planet 21 million cases of typhoid fever are registered where 216 thousand are lethal. Traditional microbiological methods for *Salmonella* typ-ing (cultivation) is usually stretched out in time. This necessitates the development of modern methodology of food safety. Goal: Development of a multiplex PCR protocol enabling identification of *Salmonella* spp. and typing of *Enterisa Salmonella Enteritidis*, *Salmonella Enterisa Typhimurium*, *Salmonella Typhi*, *Salmonella Dublin*, *Salmonella Gallinarum*.**Methods & Materials:** For amplification the following primers were used: *Salmonella* spp.: Salm3-Salm4 (Ferretti, 2001); *Salmonella enteritidis*: SentF-SentR (Agron, 2001); *Salmonella typhimurium*: StypF-StypR (O'Regan, 2008); *Salmonella Typhi*: StyphiF-StyphiR (Kumar, 2008); *Salmonella Dublin*: SdubF-SdubR; *Salmonella Gallinarum*: SgalF-SgalR (Akiba, 2011).

Optimization of multiplex PCR protocol was performed according to Elnifro (Elnifro, 2000).

Results: To determine optimal PCR temperature options, the assay was performed at different temperatures of primers annealing: 58 °C, 60 °C, 63 °C and 65 °C. The result of this was to determine the best amplification mode: Initial denaturation - 94 °C-2 min; Denaturation - 94 °C-45s; Annealing - 63 °C-45s; Extension - 72 °C-60s (40 cycles); Final extension - 72 °C-5 min. The optimal composition of the reaction mixture for multiplex PCR was: 10 × DreamTaq Buffer 2.5 µl, dNTP Mix, 2 mM each 2.5 µl, 25 mM MgCl₂ 0.5 µl, Primers 20pM, Template DNA 5.0 µl, DremTaq DNA Polymerase 2.0 µl Water, nuclease-free 3.5 µl. The resulting protocol allowed the detection of DNA in the *Salmonella* spp. samples as well as the simultaneous typing of *Salmonella Enterica Enteritidis*, *Salmonella Enterica Typhimurium*, *Salmonella Typhi*, *Salmonella Dublin*, *Salmonella Gallinarum*. At the same time with PCR amplification, the simultaneous amplification of all the 6 expected fragments occurred.**Conclusion:** The developed protocol is promising for the biological control of food safety, as well as in routine investigations.<http://dx.doi.org/10.1016/j.ijid.2014.03.1120>**Type: Poster Presentation**

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Aetiology of community-acquired pneumonia in HIV-infected South African adultsW.C. Albrich¹, J.-N. Telles², P.V. Adrian³, M. Messaoudi², N. van Niekerk³, G. Paranhos-Baccala², S. Madhi⁴, K. Klugman⁵¹ Cantonal Hospital St. Gallen, St. Gallen, Switzerland² Fondation Merieux, Lyons, France³ University of the Witwatersrand, Bertsham, South Africa⁴ National Institute for Communicable Diseases (NICD), Johannesburg, South Africa⁵ Emory University, Atlanta, GA, USA**Background:** Few recent comprehensive studies are available on the aetiology of community-acquired pneumonia (CAP) in HIV-infected adults which include bacterial and viral organisms in developing countries.**Methods & Materials:** Induced sputum, blood cultures, urine, nasopharyngeal swabs (NPS) and aspirates (NPA) were collected from HIV-infected adults hospitalized with radiologically confirmed pneumonia with symptoms of ≤14 days not currently

receiving treatment for tuberculosis in Soweto, South Africa. A composite diagnostic standard for *Streptococcus pneumoniae* was considered positive if any of routine blood culture, good quality sputum culture or Gram stain, urinary immunochromatographic testing (ICT) for pneumococcal C-polysaccharide (Binax® Now) or *lytA* real-time (rt) PCR on blood were positive for pneumococcus or *lytA* rtPCR on NPS was ≥ 8000 copies/ml. Other bacterial aetiologies were identified by routine blood cultures and sputum cultures, *mycobacterium tuberculosis* (TB) was assessed by acid-fast staining of sputum. Multiplex rtPCR for respiratory viruses and atypical bacterial pathogens (Fast-track diagnostics Respiratory pathogens plus) was used on NPA and triplex rtPCR for *S. pneumoniae*, *Staphylococcus aureus* and *Haemophilus influenzae* from whole blood.

Results: Among 280 HIV-infected persons with CAP, pneumococcus was the most frequently identified organism (n = 151 [53.9%], of which 79 [28.2%] were mono-infections; 75 [26.8%] by molecular diagnostics only), followed by TB (n = 69 [24.6%], of which 39 [13.9%] were mono-infections). 48 (17.1%) viral or mycoplasma infections were identified (10 as mono-infections, 38 as combinations mostly with pneumococcus [n = 32]). *Staphylococcus aureus* and *Haemophilus influenzae* were frequently detected in the nasopharynx, but only rarely isolated from blood or sputum cultures. Up to 5 different organisms were simultaneously present. No aetiology was identified in 22.9% of patients.

Conclusion: Using a combination of traditional and molecular methods, an infectious aetiology could be identified in the majority of episodes of acute CAP in HIV-infected South African adults. A large proportion was attributable to polymicrobial infections, most of which included the pneumococcus or tuberculosis. Viral mono-infections were relatively infrequent. Further work is necessary to delineate the utility of bacterial or viral identification from nasopharyngeal specimens as diagnostic tools in CAP.

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Common causes of bacterial meningitis at Mthatha Hospital Complex, Eastern Cape South Africa

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Background: The Mthatha hospital complex serves as a primary and referral centre to children in the OR Tambo district in the Eastern Cape. The aim was to determine the common bacteriological causes of meningitis in children who present at the hospital.

Methods & Materials: A retrospective cross sectional study was done. The study from January 2012–December 2012. Cerebrospinal fluids obtained from children in paediatric wards and outpatients of

Nelson Mandela and Mthatha general paediatric wards were analysed to identify the most common causes of bacterial meningitis. Children admitted to the neonatal unit were excluded. The age group analysed were 1 month–12 years.

Results: 182 patients met the study criteria. 14/182 (7.7%) had a positive gram stain. CSF culture was positive in 11/182 (6.0%). Only one patient had a bacterial PCR done as part of new NICD criteria for CSFs with more than 100 white blood cells. It was positive for *Neisseria meningitidis* serogroup Y. Bacterial antigens which are done at the on-site lab were positive in 8/182 (4.3%).

The most prevalent organism was *Streptococcus pneumoniae* (46%) followed by *Neisseria meningitidis* (23%). *Streptococcus* group B (1/182–7%), *Streptococcus* group D (1/182–7%), *E. coli* (1/182–7%), *Haemophilus influenzae* (1/182–6%) and *Proteus mirabilis* (7%). *Neisseria* targeted the older children typically 10–11 yr olds.

Conclusion: The most prevalent organism was *Streptococcus pneumoniae*. Currently there is a PCV13 vaccine available. Vaccines against *Neisseria meningitidis* do not form part of the public immunisation programme. More surveillance and studies are needed. The presence of Hib vaccine in the immunisation schedule has led to a decline in H influenzae. CSF PCR could help identify organisms in patients with pleocytosis but negative gram stain and culture. Other causes of patients with CSF pleocytosis include TB meningitis, viral meningitis but these were not part of the study. As a referral centre most children presenting to the hospital have already received an initial dose of antibiotic as part of integrated management of childhood illnesses or a course of antibiotics at their local hospital could sterilise the CSF which could yield to the lower yield of positive CSF cultures and antigens. Use of PCR might help us identify more pathogens.

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The role of *Chlamydia pneumoniae* in the etiopathogenesis of schizophrenia and brain-derived neurotrophic factor (BDNF), neurotrophins like neurotrophin 3 (NT3) levels: A worldwide retrospective study

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Background: It's known that, in the occurrence of a neuropsychiatric disease like schizophrenia, multifactors such as genetic predisposition, neurodevelopmental disorders, social and environmental factors play a role. It was suggested that the synthesis of neurodevelopmental factors such as brain-derived neurotrophic

