

1st International Conference on (Re-)Emerging Infections Diseases

Abstracts Oral Presentations

1

Potentiality of lytic bacteriophages and their virolysins in lysing multi-drug resistant *Salmonella typhi*

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Background: Bacteriophage virolysins or lytic enzymes are bacterial peptidoglycan hydrolases responsible for lysing bacterial cells. Consequently, they are used as enzybiotics alongside with bacteriophage therapy to remedy multi-drug resistant *Salmonella typhi*.

Objectives: The objective of this study was to evaluate the potentiality of lytic bacteriophages and their virolysins in curing multi-drug resistant *S. typhi*. *S. typhi* was isolated and identified according to WHO and ISO guidelines.

Methods: Antibiotics susceptibilities were tested using CLSI recommendations. Correspondingly, bacteriophage-lysing efficiency was assayed by plaques formation using the double-layer agar technique. Virolysins were extracted using ultracentrifugation and purified by dialysis after buffering in ammonium sulfate. Virolysins activity was determined by measuring the reaction mixtures spectrophotometrically (bacteria incubated as substrate in 37°C for 4 h). The phages and virolysins kinetics exponential rates were calculated using specific differential equations.

Results: Susceptibility data plotted based on antibiogram criteria confirmed that 33% of *S. typhi* isolates were multi-drug resistant. For bacteriophage replication and multiplicity of infection, phages were amplified to produce the maximum particles of titers. The phage titration data fit on sonogram revealed exponential decay of *S. typhi* incubated for 12 h. Meanwhile, the enzyme kinetics exponential decay on double reciprocal plot showed irretrievable relationship of host decay in 4 h.

Conclusion: Since phages depend on their lytic cycle in lysing bacterial host, their enzymes have more capability in decaying the host; besides they are safe and time-saving when used in the treatment of antibiotics resistant *S. typhi*.

2

Anti-Leishmania Donovanii Antibodies Enhance Promastigotes Internalization Into Host Macrophage

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Objectives: This study aimed to demonstrate the role of humoral immunity in Leishmania parasite internalization into host macrophages.

Methods: First, informed consent sera were obtained from 67 parasitologically confirmed visceral leishmaniasis patients reporting to our field treatment centre, Eastern Sudan. Then following titre determination, sera that had a titre of >102,400 were selected for parasite coating. An in vitro parasite internalization system was developed to enhance the Leishmania/ macrophage interactions.

Results: The mean parasite number per monocytes was 626 ± 91 for antibody-coated Leishmania donovani, compared to 412 ± 70 uncoated isolates ($p= 0.01$). On the other hand, the percentage of infected cells was significantly higher for all antibody-coated isolates (100%) compared to uncoated ones (40%). This evidence of high infectivity probably points to the fact that anti-Leishmania antibodies facilitated the parasite uptake by host macrophages and monocytes-derived macrophages (MDM).

Conclusion: Leishmania spp. promastigotes preferentially infect host macrophages, where parasite internalization is facilitated by several host and parasite surface molecules. Moreover, the rate of parasite uptake by MDM was significantly higher compared to monocytes. This could be explained by the fact that the functional capabilities of fully differentiated macrophages differ from monocytes. In conclusion, host humoral immunity probably plays a pivotal role in Leishmania parasites internalization into host macrophages.

3

Outbreak Investigation of Cholera in an Internally Displaced Persons camp in Borno State, North-Eastern Nigeria- August 2017

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Background: Since 2009, the conflict in north-eastern Nigeria has led to a protracted humanitarian crisis affecting 14.8 million people with 1.4 million being displaced and are now living in internally displaced persons (IDP) camps in Borno. In August 2017, a suspected cholera outbreak was reported from an IDP camp in Borno. We investigated to describe the epidemiology, identify risk factors, and recommend preventive measures.

Methods: We defined a suspect case as any resident of Borno, aged ≥ 2 years presenting with acute watery diarrhea and severe dehydration between August 16 and September 23, 2017. We identified cases at the cholera treatment center and at oral rehydration points. We conducted a 1:1 unmatched case-control study using a structured questionnaire to identify risk factors. Stool samples were collected for laboratory investigations.

Results: We recorded 187 cases. 244 (65%) were females. Median age (interquartile range) 20 (5-30) years. Bivariate analysis revealed eating from another household (OR=8.5 [95% CI = 3.0 - 24.7]) and not treating drinking water (OR=8.2 [95% CI = 5.2 - 13.2]) were associated with the outbreak. On multivariate analysis, eating from another household (aOR=13.2 [95% CI = 2.7 - 64.6]) and not treating drinking water (aOR=4.1 [95% CI = 2.0 - 8.5]) emerged as independent risk factors of cholera in the outbreak. Of the 133 stool samples collected, 107 (80%) were rapid diagnostic test positive and 99 (74%) were culture positive for *Vibrio cholerae* respectively.

Conclusion: This was an outbreak of cholera in an IDP camp associated with eating from other households and drinking untreated water. We supported mass risk communication, distributed water treatment tablets, and implemented the first

reactive vaccination with oral cholera vaccines in Nigeria. We recommended health promotion campaigns and provision of adequate safe drinking water in IDP camps to prevent future outbreaks.

4

The predominance of Ethiopian specific Mycobacterium tuberculosis families and minimal contribution of Mycobacterium bovis in tuberculous lymphadenitis patients in Southwest Ethiopia

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Background: Ethiopia has an extremely high rate of extrapulmonary tuberculosis, dominated by tuberculous lymphadenitis (TBLN). However, little is known about Mycobacterium tuberculosis complex (MTBc) lineages responsible for TBLN in Southwest Ethiopia.

Methods: A total of 304 MTBc isolates from TBLN patients in Southwest Ethiopia were genotyped primarily by spoligotyping. Isolates of selected spoligotypes were further analyzed by 15-loci mycobacterial interspersed repetitive unit–variable number tandem repeat (MIRU-VNTR) (n=167) and qPCR-based single nucleotide polymorphism (n=38). Isolates were classified into main phylogenetic lineages and families by using the reference strain collections and identification tools available at MIRU-VNTRplus data base. Resistance to rifampicin was determined by Xpert MTB/RIF.

Results: The majority of isolates (248; 81.6%) belonged to the Euro-American lineage (Lineage 4), with the ill-defined T and Haarlem as largest families comprising 116 (38.2%) and 43 (14.1%) isolates respectively. Of the T family, 108 isolates were classified as being part of the newly described Ethiopian families, namely Ethiopia_2 (n=44), Ethiopia_3 (n=34) and Ethiopia_H37Rv-like (n=30). Other sub-lineages included URAL (n=18), S (n=17), Uganda I (n=16), LAM (n=13), X (n=5), TUR (n=5), Uganda II (n=4) and unknown (n=19). Lineage 3 (Delhi/CAS) was the second most common lineage comprising 44 (14.5%) isolates. Interestingly, six isolates (2%) were belonged to Lineage 7, unique to Ethiopia. Lineage 1 (East-African Indian) and Lineage 2 (Beijing) were represented by 3 and 1 isolates respectively. *M. bovis* was identified in only two (0.7%) TBLN cases. The cluster rate was highest for Ethiopia_3 isolates showing clonal similarity with isolates from North Ethiopia. Lineage 3 was significantly associated with rifampicin resistance.

Conclusions: In TBLN in Southwest Ethiopia, the recently described Ethiopia specific Lineage 4 families were predominant, followed by Lineage 3 and Lineage 4- Haarlem. The contribution of *M. bovis* in TBLN infection is minimal.

5

Mutations and Risk Factors Associated with Drug Resistance Tuberculosis in Ghana

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Background: The control of tuberculosis is hampered by the emergence of drug-resistance strains. This study analysed mycobacterial isolates from Ghana spanning a decade for drug resistance and resistance-conferring mutations as well as associated risk factors.

Methods: Isolates were screened against isoniazid (INH) and rifampicin (RIF) by at least one of three methods; proportion method, micro-plate alamar blue assay and the Genotype MTBDRplus kit. Isolates resistant to at least one of the drugs were further screened against moxifloxacin (MOX) and amikacin (AMK) as well as streptomycin (STR) using the Epsylometer test (Etest) and genotype MTBDRsl version 2. Drug resistance associated genes (*inhApro*, *inhA*, *ahpCpro*, *katG*, *ndh*, *rpoA*, *rpoB*, *rpoC*, *gyrA*, *gyrB*, *eis*, *rrs*, *tap*, *whiB7* and *tlyA*) were PCR amplified and sequenced for mutational analyses.

Results: A total of 3079 genotyped isolates that have been genotyped into species, lineages and sub-lineages were tested against INH and RIF. Isolates resistant to only INH and only RIF (INHr and RIFr) were 268 (8.7%) and 34 (1.1%) respectively whereas 123 (3.9%) were MDR. The *katG* mutations (74.3%) and *inhA* (14.3%) promoter mutations accounted for 88.6% of the observed INH resistance whereas *rpoB* mutations accounted for 96.9% of the observed RIF resistance. INH resistant *Mycobacterium tuberculosis* (Mtbss) isolates were more likely ($p < 0.05$) to harbour *katG* S315T (75.8%) mutations compared to *M. africanum* (Maf; 51.7%) whereas the opposite was true for *inhApro* mutations; Maf (48.3%) compared to Mtbss (26.7%). We identified possible novel compensatory INH resistance mutations in *inhA* (G204D) and *ahpCpro* (-88G/A and -142G/A). One MDR isolate was identified as an XDR (additional resistance to

both MOX and AMK) from which we identified *gyrA* G87C as well as *rrs* A514C & A1401G.

Propensity to acquire INH, RIF and MDR did not statistically differ among the species tested, however, Maf L6 was more likely to be INH resistant ($p < 0.05$) whereas the Ghana sub-lineage of Mtbss L4 was more likely to be INHr, RIFr or MDR ($p < 0.05$). Whereas there was no association of gender with drug resistance, we found age above 50 years to be highly associated with drug resistance ($p < 0.05$).

Conclusion: Our study spanning over 10 years shows points to the possibility of the influence of pathogen genetics and old age on emergence of drug resistance. The identification of XDR MTBC isolate however calls for intensified public education.

6

Local transmission of Chikungunya in Rome and the Lazio Region, Italy: the first outbreak in a metropolitan area in a Western country.

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Background: CHIKV has spread beyond its original tropical locations (Africa and the Indian subcontinent) and, since recently, it has become an emerging issue in temperate regions of Northern Hemisphere. In particular small autochthonous outbreaks occurred, as the consequence of spill over from large ongoing transmission in tropical areas, in continental Europe countries including Italy in 2007 and in France in 2010, in 2014 and eventually in 2017. On September 7th, 2017, the Lazio Regional Service for Surveillance and Control of Infectious Diseases was notified of three potentially autochthonous cases of chikungunya virus (CHIKV) infection in Anzio, a coastal town devoted to internal tourism at 1 hour driving from Rome.

Materials and methods: An outbreak investigation based on an established surveillance system data and molecular analysis of viral variant(s) were conducted.

Results: Between January 1st, 2017 and October 30th, 2017, 391 chikungunya cases were reported. Epidemiological analysis suggested the occurrence of 3 main events of local transmission. The major event involved 309 person who had a direct link with the town of Anzio and its surrounding area. The other two events occurred in people who lived in Rome (68 cases) and Latina (8 cases). Attack rate was highest in Anzio (320.4/100,000 residents); the city of Rome showed attack rates ranging from 1.30 to 13.1/100,000 residents in the different districts and Latina reported an attack rate of 7.13/100,000

residents. The cumulative incidence in the whole region was 6.61 cases/100,000 residents. The 97.2% of cases reported fever, 95.4% reported joint pain, 63.4% developed a skin rash and the 38.9% developed arthritis. On the phylogenetic tree the virus is located on a branch of the IOL sublineage that is distinct from the 2007 Italian autochthonous sequences, and doesn't show the A226V mutation.

Conclusions: This is the first report of a chikungunya outbreak involving a highly populated urban area in a western country. The outbreak probably started in the area of Anzio and spread by continuity to neighbouring villages and then to the metropolitan area of Rome and to the Latina area favoured by the touristic nature of the Anzio area. The low incidence in a metropolitan area is likely to be related to the low *A. albopictus* vectorial competence for the involved CHIKV strain, to the very dry 2017 summer and to the prompt implementation of vector control measure. The new introduction of CHIKV in Italy after ten years, highlights the importance of an integrated multidisciplinary surveillance system of arboviruses infections and the need of increasing the awareness and knowledge in health care workers.

7

Ebola antibody levels in Convalescent Plasma donors over time in Sierra Leone and Guinea.

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Background: Convalescent plasma (CP) was recommended by WHO for therapeutic assessment during the 2014-2016 Ebola outbreak. A trial in Guinea (www.ebola_tx.eu) did not demonstrate efficacy, possibly due to insufficient antibody levels in the transfused CP obtained from serologically unselected survivors. Single and multiple CP donations for trials in Guinea and Sierra Leone (SL) provide an opportunity to investigate antibody levels over time.

Materials and Methods: Three ELISAs based on Mayinga strain Ebola glycoprotein were used to measure Ebola antibody levels in SL donations: IgG-Capture, a simultaneous competitive assay using monoclonal antibody 4G7 (Competitive), and a double antigen bridging assay (DABA). For Guinean donations, levels were measured by a different IgG-capture ELISA to that used in SL, but by the same DABA. Testing by IgG-capture was possible in the field in SL, enabling higher level donors to be identified for apheresis, but not in Guinea. Antibody levels were measured in optical density (IgG Capture; Competitive) or unitage (DABA). The unit of time for analysis was months post virological cure.

Results: Analyses included 314 plasma samples from 116 donors in SL and 85 samples from 58 donors in Guinea. The median (range) time to first donation was 6.9 months (1.0-10.0) in SL and 4.5 months (2.2-10.2) in Guinea.

In SL, only donors with the highest antibody levels at the first donation were invited to donate repeatedly. Amongst the first donations from SL donors, antibody levels appear to be highest in terms of quantity (IgG-Capture) and quality (Competitive) 4 months post discharge from an Ebola treatment unit. Similar results were observed in Guinea. Amongst the first donations of the SL donors, there was no evidence of an association of antibody levels with time since discharge for the IgG Capture assay (linear regression coefficient: 0.01, 95%CI: -0.19, 0.21; p=0.880) or for the Competitive assay (Coef 0.24; 95%CI: -0.13, 0.60; p=0.210). However, there was strong evidence from the DABA that there was a positive association, with an estimated increase of 13.57 units per month (95%CI: 4.69, 22.45; p=0.003). In Guinean donors, a mixed-effects model with a random effect to account for within-donor correlation investigated association in antibody levels over time. There was strong evidence that IgG antibody levels decreased over time (Coef: -0.177, 95%CI: -0.059, -0.295; p=0.005). A similar model for Guinean donors using the DABA suggested an increase of 71.85 units per month (95% CI: 28.55, 115.15; p=0.002).

Conclusions: In general IgG levels decreased over time while affinity and total antibody levels measured by DABA increased over time, appearing to be optimal at 4 months post cure, which is not immediately helpful for an outbreak response. An effective strategy has been to use IgG-Capture and Competitive ELISAs in concert to identify high-level high-affinity individuals in the field early after cure who can repeatedly donate.

8

Resistance-associated mutations and genotypes in the Hepatitis C Virus NS5B Region in Individuals naive to Sofosbuvir treatment in Cameroon

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Background: Hepatitis C virus has the propensity to mutate into a heterogenous RNA population (quasispecies) as a strategy to adapt to its host immune response leading to seven known genotypes (designated 1 through 7). In 2011, Cameroon recorded a HCV seroprevalence of 1.1% with Genotypes 1, 2 and 4 co-circulating. The HCV nonstructural protein 5B (NS5B) is a RNA-dependent RNA polymerase (RdRp) and exhibits a high mutation rate of approximately 10⁻⁴ substitutions per site and therefore a target to study HCV dynamics. Sofosbuvir, a drug that inhibits the function of RdRp (NS5B nucleotide inhibitor) is among the new direct acting agents (DAA) for treatment of uncomplicated hepatitis C. Currently, low cost combination of sofosbuvir/ribavirin and sofosbuvir/ribavirin/ledispavir are recommended for hepatitis C treatment in Cameroon, based on the medical history and laboratory results of the individual including HCV genotype. The aim of this study was to identify HCV genotypes and known mutations associated to resistance to sofosbuvir in treatment-naive populations.

Methods: Following ethics review by the Cameroon National Ethics Committee, HCV RNA was extracted from plasma specimens of 54 adults aged from 31 to 81 years attending Hepatitis Clinics in Douala and Yaounde from November 2016 to November 2017. After reverse transcription and PCR, the 320 base pair amplicon was sequenced by the Sanger method using the 3130XL DNA analyzer, and the sequences edited using the SeqScape 2.7 version. Mutations that predict resistance to sofosbuvir were identified using Geno2Pheno tool version 0.92 and genotyping by phylogeny.

Results: The S282T mutation, which confers reduced susceptibility to sofosbuvir was not identified in this study. However, the C316N polymorphism of unknown impact on sofosbuvir susceptibility was reported in 7 patients (12.96%). Of the 54 samples, Genotypes 1 (16), 2 (17) and 4 (21) were identified at 29.6%, 31.5% and 38.9% rate, respectively.

Conclusions: Sofosbuvir resistant-associated variants are not common in treatment-naive individuals in Cameroon, indicating that its use in first line regimens are appropriate for the population. Secondly, HCV Genotypes 1, 2 and 4 co-circulate within this population. With the introduction of DAAs, it is important to estimate baseline resistance-associated mutations in treatment-naive populations in order to develop drug resistance surveillance strategies and national treatment guidelines.

9

Emergence of unintended HBV drug resistance and vaccine evasion as the result of HIV co-infection and antiretroviral therapy in Ethiopia

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Background: Hepatitis B virus (HBV) drug resistance and vaccine escape gene mutants were determined in patients with human immunodeficiency virus (HIV) co-infection and antiretroviral therapy (ART) exposure, but unknown HBV status. Moreover, the reciprocal HIV drug resistance profiles were examined in HBV-HIV co-infected patients who developed HBV drug resistance.

Methods: HBV drug resistance and vaccine escape variants were characterized using direct sequencing from a total of 161 HBV positive sera collected from HIV co-infected individuals (with and without ART exposure) and drug naïve HBV mono-infected cases.

Results: HBV drug resistance gene mutations (DRMs) were detected in 21.1% (34) of study participants with an individual frequency of 1.2% rtT184S, 6.2% rtV173L, 10.6% rtL180M, 10.6% rtM204V/I and 8.1% rti233V which confer drug resistance mainly for entecavir, lamivudine and adefovir. The prevalence of the DRMs in HBV-HIV co-infected individuals (with no significance difference among ART status) was higher than mono-infected individuals (41.4% vs. 10.7%). In contrast, none of HIV-1 patients showed no nucleos(t)ide reverse transcriptase inhibitors (NTRIs) drug resistance. However, 62.5% of them developed non NRTIs resistance mutations which confer resistance to nevirapine, efavirenz, etravirine and rilpivirine. The study also revealed higher frequency of vaccine escape mutant variants (sT125S, sA128V, sQ129H/R, sT131I, sC137S, sT143M, sD144D/E, sG145R, sT148P) with the majority of them were more prevalent in HBV-HIV co-infected individuals.

Conclusions: The current HIV-1 therapy without considering HBV diagnosis and treatment in Ethiopia is leading to rather emergence of unintended HBV drug resistance and mutant variants which can evade HBV vaccine-induced

immunity. We recommend HBV testing and co-management as part of routine HIV care programs for a better ART selection. Relatively high level of HIV-1 non NRTIs resistance profiles were observed and highlight further investigation during HBV co-infection.

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Insights on the way forward for combatting Antimicrobial Resistance (AMR) in Africa: Findings from policy consultations on AMR diagnostics during the Launch of the Africa CDC AMR Surveillance Network.

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Background: Recent data suggest that as many as 700,000 people die from AMR annually Worldwide with a projected global annual mortality rate of 10 million by 2050 if nothing urgent is done. Given the magnitude of the AMR emergency, the Africa CDC has launched its AMR surveillance network (AMRSNET) during the Advanced Diagnostics Course in France with the aim of improving detection of antibiotic resistant infections in humans and animals, delaying its emergence, limiting transmission, and mitigating harm among patients infected within the next five years. In an informal policy consultation during that week, policy makers from five African member states were interviewed with respect to their country strategies for combatting AMR and their priorities for the implementation of AMR surveillance as well as diagnostic needs.

Methods: Informal policy consultations were conducted as face-to-face interviews with policy makers from Cameroon, Kenya, Senegal, Tanzania, Zimbabwe. The interviews for policy makers were directed towards the diagnostic priorities to be considered by the AMRSNET. Information was also gathered from break out group discussions with representatives from the ministries of health of the five countries above and, Burkina Faso, Mauritius, and South Africa. The interviews and break out discussions with the country representatives were directed towards obtaining the current state of AMR implementation in the various member states and three immediate actions that should be prioritized by the AMRSNET for in-country implementation.

Results: The policy makers suggested three main AMR diagnostic priorities which include: the need for a simple, rapid test to distinguish bacterial and

viral infection with adequate measures to ensure high uptake among clinicians and health personnel; connectivity of current diagnostics used for AMR for real time data for action; and the selection of affordable technologies for surveillance of Gram negative bacteria to enable impact assessment of antibiotic stewardship programmes. Countries interviewed were at different levels of implementation of AMR control and surveillance. Zimbabwe, Tanzania and Kenya have already launched their national AMR strategic plan while that of Cameroon is still under development. The three immediate actions suggested by the country representatives included: The setting up and stepwise implementation of the WHO-recommended surveillance system adopted to national AMR strategic plans and disease burden; the concomitant formulation and implementation of a multisectoral AMR control policy embracing the One Health concept; the development of financial plans and business models (a strong economic case) to sustain AMR diagnostics and control, and to reduce out of pocket expenses; and capacity building for AMR at all levels of the health care system.

Conclusion: The launch of AMRSNET is a crucial step towards building country capacity to conduct AMR surveillance Africa. Diagnostic technologies, with connectivity, play a pivotal role towards this challenging mission. A stepwise approach with ongoing capacity building will be relevant in the implementation of the surveillance network. An economic case is needed to ensure in-country government support and funding to ensure the sustainability of the national and regional AMR response.

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Reducing the Burden of Post-Caesarean Surgical Site Infection and Antimicrobial Resistance at a Tertiary Hospital in Tanzania

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Background: Surgical site infections (SSIs) are a leading cause of morbidity and mortality among women undergoing caesarean section (CS), especially in low- and middle-income countries (LMICs). Here we report the results of a combined Antimicrobial Stewardship (AMS) program and Infection Prevention and Control (IPC) strategy carried on at the Gynaecology & Obstetric Department of a tertiary hospital in Tanzania.

Materials and methods: We conducted a first survey with the aim to investigate the incidence of post-CS SSI and its determinants in a cohort of pregnant women admitted at Dodoma Regional Referral Hospital (DRRH), Tanzania. Afterwards, a combined IPC intervention and AMS program have been developed including: 1. formal and on-job trainings on IPC (basic infection control principles, hand hygiene, pathogenesis of SSIs, risk factors related to surgical procedures, skin preparation, etc.); 2. evidence-based education on antimicrobial resistance (AMR) and good antimicrobial prescribing practice for SSIs treatment and prophylaxis. A second survey was then performed in order to determine the impact of the intervention. Statistical analysis was performed using the IBM SPSS software version 21, NY, U.S.A.

Results: A total of 464 and 573 women were surveyed before and after the intervention, respectively. After the intervention, skin disinfection with povidone/iodine was performed in the vast majority of cases compared with the pre-intervention group (97% vs 78%, $p < 0.001$), and the antibiotic prophylaxis was administered in a significantly higher number of patients (98% vs 2%, $p < 0.001$). Furthermore, CS were performed by more qualified operators (40% vs 28%, $p = 0.001$), with higher rates of Pfannenstiel skin incisions (29% vs 18%, $p < 0.001$) and of absorbable continuous

intradermic sutures (30% vs 19%, $p < 0.001$). Overall, the total number of post-CS SSIs was 225 (48%) in the pre-intervention group and 95 (17%) in the post intervention one ($p < 0.001$). A lower number of MRSA-SSIs was detected in the post-intervention survey (5% vs 32%, $p < 0.001$).

Conclusion: A multidisciplinary approach including IPC intervention and essential AMS program substantially reduced SSI and AMR rates at the Gynaecology & Obstetric Department of DRRH. Hospitals in LMICs should prioritize their efforts in order to implement AMS programs according to local priorities and available resources.

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β-lactams resistance among Enterobacteriaceae in Morocco

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Background: In Enterobacteriaceae, the main mechanism involved in β-lactams resistance is the production of β-lactamases. These enzymes have been evolving towards genetic diversification, extension of activity and dissemination among many Enterobacteriaceae species until they reached the formation of extended spectrum β-lactamases (ESBL). Community acquired urinary tract infections by these strains represent a major public health problem worldwide due to their diffusion and their multi-resistance to antibiotics. Our study focused on the molecular characterization of ESBLs produced by community acquired uropathogenic enterobacteria isolated in Morocco.

Methods: A total of 3606 uropathogenic strains were collected between 2004 and 2015 from medical analysis laboratories of thirteen Moroccan cities. Overall, 278 (7.71%) isolates were resistant to third generation cephalosporins (C3G). The prevalence of ESBL producing Enterobacteriaceae isolates was 4.65%. This rate was increased significantly from 1.24% in 2004-2009 to 6.1% in 2010-2015. ESBL-producing *Escherichia coli* and *Klebsiella pneumoniae* were the most commonly frequently species isolated. The disk Diffusion susceptibility testing indicated high prevalence of resistance to various antimicrobial agents and 92% of these isolates were Multidrug resistant.

Results: The molecular typing of ESBL produced showed the predominance of CTX-M15 (69.7%) followed by SHV (14.88%) and TEM (7.73%). Plasmid mediated AmpC β-lactamases were detected in 13.7% of isolates. The carbapenemases genes were detected among fifteen carbapenem-resistant strains.

The prevalence of plasmid mediated quinolone resistance genes were 67.3%. Genetic transfer

experiments showed that identified genes were located on Tn3 transposon carried by high molecular weight plasmid

Phylogenetic grouping of ESBL-producing *E. coli* revealed that 34.4% isolates belonged to the virulent phylogroupe B2 and 85% of ESBL-producing *K. pneumoniae* were identified as *K. pneumoniae* phylogenetic group I..

PFGE was performed to determine the genetic relatedness among the *E. coli* isolates and carbapenemase-producing Enterobacteriaceae. PFGE revealed that the *E. coli* isolates comprised seven distinct genotypes; the clonal diffusion was detected in two pulsotypes with high-level similarity (95%). For carbapenemase-producing Enterobacteriaceae isolates, non-epidemiological relationship was detected.

Conclusions: The high prevalence and spread of multidrug resistance in Enterobacteriaceae raises public health concerns due to the very real risk of a therapeutic dead-end. The surveillance of regional and local susceptibilities and mechanisms of resistance are required to mitigate this major public health concern.

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Abstracts Poster Presentations

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The effect of antiretroviral naïve HIV-1 infection on the ability of Natural Killer cells to produce IFN- γ upon exposure to Plasmodium falciparum- infected Erythrocytes.

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Background: In sub-Saharan Africa intense perennial Plasmodium species transmission coincides with areas of high prevalence of human immunodeficiency virus type 1 (HIV) infection. This implies that antiretroviral naïve HIV infected people living within these regions are repeatedly exposed to Plasmodium species infection and consequent malaria. NK cells are known to contribute to malaria immunity through the production of IFN- γ after exposure to Plasmodium falciparum-infected erythrocytes (iRBC). However in antiretroviral naïve HIV-1 infection these functions could be impaired. In this study we assess the ability of NK cells from antiretroviral naïve HIV-1 infected people to respond to iRBC.

Methods: This study was approved by the National ethical committee of Cameroon with administrative authorization number 2015/08/631/CE/CNERSH/S P. Participant's enrolment was voluntary and each participant signed an informed consent. Twenty three (23) ARV naïve HIV-1 infected participants and eighteen (18) HIV-uninfected negative controls aged between 21 to 65 years were recruited to be part of this study. After venous blood drawing, Peripheral Blood Mononuclear Cells (PBMC) were isolated from the whole blood by density gradient centrifugation (using ficoll-hypaque). Magnetically sorted NK cells from anti-retroviral naïve HIV-1 infected people were tested for their ability to response to iRBC following in vitro co-culture. NK cell IFN- γ production after coculture was measured through multiparametric flowcytometry analysis.

Results: Our data show a significant reduction ($p=0.03$) in IFN- γ production by NK cells from antiretroviral naïve HIV-1 infected people after co-culture with iRBCs. This was in contrast to NK cells response from healthy controls which demonstrated elevated IFN- γ production. NK cells IFN- γ production from untreated HIV-1 infected participants correlated inversely with the viral load ($r = -0.5$, $p= 0.02$) and positively with total helper CD4+ T cells count ($r=0.4$, $p= 0.04$).

Conclusions: The reduction of NK cells IFN- γ production observed in ARV naïve HIV-1 infected people was closely related to HIV disease progression, as we observed an inverse correlation between IFN- γ production and plasmatic viral loads. This is probably linked with an effective immune system as lower plasmatic viral load (<2 Log10) usually correlate with the ability of individuals to control the virus. This clearly indicates that antiretroviral naïve HIV-1 infection impairs the ability of NK cells to respond to iRBC. In malaria intense regions there is need to consider people living with HIV as highly vulnerable to malaria and should therefore be offered prophylactic malaria treatment like in pregnant women and children. Thus antiretroviral naïve HIV-1 infection can dampen NK cell mediated immunity to Plasmodium falciparum infection in malaria intense regions. This could in effect escalate morbidity and mortality in people chronically infected with HIV-1.

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Tuberculosis- The Silent Epidemic in Bundibugyo Uganda

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Objectives: The main objective of the study was to determine the Burden and Risk Factors contributing to Tuberculosis infections in Bundibugyo District Uganda.

Tuberculosis (TB) is on the rise among the vulnerable category of people (HIV/AIDS patients, elderly and poor persons) in Bundibugyo. Bundibugyo Hospital data for 2017 indicated that, 19% of the 750 cases tested from the Out Patients Department had tubercle bacillus (Mycobacterium

that causes Tuberculosis in humans), 2% rise from 2016. Inadequate Health Resources, Ineffective Supervision by the respective Health Authorities and Poor Attitudes towards Quality Work by the Health Staff; are some of the contributing risk factors to the problem.

Background: Bundibugyo is a district located 420 km away from Kampala the capital city of Uganda, to the mid-western Uganda. It borders the North-Eastern DRC Congo; it has a population estimate of 241,000 according to Uganda 2014 population census with a growth rate of 3.3% per year.

Uganda was ranked 16th among the 22 countries in Sub-Saharan Africa with high TB burden, (Vision, 29th August 2017), (WHO, 2015). The reports noted that, up to 60,000 people were estimated to be living with Tuberculosis, of which 50% were estimated to be HIV-TB Co-infected. Lack of accurate and reliable data on TB situation was one of the challenges the Uganda faced, (Uganda, 2015). Bundibugyo district Tuberculosis data for 2017 Quarter two review indicated that, TB cure rate was at 4% among the confirmed TB cases, (Bundibugyo, 2017 Quarter 2).

Methods: A cross Sectional Retrospective study conducted at Bundibugyo Hospital from 13th Dec 2017 to 5th Jan 2018, covering 12 months (Jan-Dec 2017) was analyzed with special focus on; Out Patients Department (OPD) attendances, TB Suspects sent to the Lab for testing, clinically treated TB cases, HIV-TB Co-infected clients, TB in Children, Knowledge and Attitudes of Health Staff on TB management. Data was analyzed by Epi data and SPSS tools

Results: There were (31,707) patients received in OPD; (750) were identified by clinicians as having signs and symptoms of TB as per the WHO guidelines, and were sent to the Laboratory for testing, this represents 2.4% of OPD attendances. (143) 19.1% were confirmed TB positive by Microscopy and Gene Xpert Laboratory techniques. HIV-TB Co-infection confirmed cases were 6 representing 4.2% of all cases Positive. Other 61 high suspect TB cases of both HIV positive clients and none HIV positive but having Negative Laboratory TB results were treated clinically based on the Clinicians discretion. 2 children under 14 years were confirmed with TB and treated. 4 Multi Drug Resistant Tuberculosis (MDR) were treated in 2017.

Conclusion: The Government should prioritize Tuberculosis and use the approaches currently applied to HIV/AIDS (involving the community,

Health Staff, Implementing Partners and Policy makers) to manage the silent epidemic. Failure by the stakeholders to heed to the ringing bells will lead to the rise in Multi Drug Resistant Tuberculosis (MDR).

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Gastroenteritis Outbreak at Savannah Primary School, Zimbabwe: A case-control study

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Background: Savannah Primary School experienced a gastroenteritis outbreak from the 6th of June to 16th of July 2016. Sixty-one pupils were affected by the outbreak, with 58 cases being recorded between the 30th June and 13th July 2016. A case-control study was conducted to determine the factors for having gastroenteritis among pupils at Savanna Primary School.

Methods: An unmatched 1:1 case-control study was conducted. A case was a pupil who had symptoms of gastroenteritis from the 6th of June 2016 to 23 July 2016. A control was a pupil who was at the school during the week when the outbreak began but did not have symptoms of gastroenteritis. A structured questionnaire was administered to cases and controls and their guardians. Laboratory water quality tests and stool test results were reviewed.

Results: A total of 61 cases and 61 controls were interviewed. The median age among cases was 11 years (First quartile (Q1)=8; Third Quartile (Q3)=12) and 12 years (Q1=9; Q3=13) among controls. Independent factors for having gastroenteritis were having a diarrhea contact at school [adjusted OR (AOR)=8.2, p<0.01] and washing hands in a common bowl [AOR=10.2, p=0.002]. Independent factors for not having gastroenteritis were using soap when hand washing [AOR=0.06, p<0.01] and drinking water stored in a bucket [AOR=0.22, p=0.017].

Conclusions: Poor handwashing practices were responsible for the outbreak. The etiological agent could not be isolated although drinking water at

some storage points had a high coliform count; indicative of fecal contamination. The district was also not prepared to respond to the outbreak. The results will strengthen school public health programmes and district health team preparedness and response.

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Evaluation of Hepatitis B Knowledge among laboratory staff and practices in Bungoma County-Kenya

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Background: Hepatitis B is a serious infection that affects liver and caused by hepatitis B virus (HBV). HB is a serious public health problem and the health professionals are most at risk. It is contagious and easy to be transmitted from one infected individual to another by blood to blood contact, mother to child, unprotected sexual intercourse, sharing of eating utensils and other barber shop and beauty salon equipment. The aim of this study was to assess knowledge and practices about transmissions and prevention of hepatitis B among laboratory in Bungoma County, Kenya.

Methods: A cross sectional study was conducted among 75 laboratory staff in nine facilities in Bungoma County. Self-administered structured questionnaire was used to collect information which included as to whether the staff knew what is Hepatitis B disease; why be vaccinated against Hepatitis B; How Hepatitis B is spread; who should get Hepatitis B vaccine; whether staff has been vaccinated against Hepatitis B; whether staff are aware about the availability of post exposure prophylaxis for Hepatitis B; Whether a facility had included Hepatitis B in its training program and whether the facility has Hepatitis B Vaccination program for its staff.

Results: Out of 75 distributed questionnaires, 75 were returned with a response rate of 100.0%. Only 24% had been vaccinated against Hepatitis B, 100% of laboratory staff knew what is Hepatitis B disease,

93% knew who should get Hepatitis B and 97% knew how Hepatitis B is spread however only 17% of staff were aware of the availability of post exposure prophylaxis for Hepatitis B. 11% of the visited facilities had Hepatitis B vaccination program while none of the visited facilities had included Hepatitis B in the training program.

Conclusion: This study indicates that as much as laboratory staffs are awareness about Hepatitis B, its route of transmission and who should be vaccinated, majority of staff are not aware of availability of post exposure prophylaxis. Similarly, majority of laboratory staff were not vaccinated against Hepatitis B, which makes them vulnerable to the disease. Very few facilities had Hepatitis B vaccination program and none had included Hepatitis B vaccination in there training program which might have contributed to majority of staff not being aware of the post exposure prophylaxis for Hepatitis B vaccination.

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Surveillance Data Analysis on Measles, Anambra State, Nigeria, 2011-2016

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Background: Measles is the leading cause of vaccine preventable deaths among children. Globally there were 134,200 measles death in 2015. Vaccination resulted in a 79% drop in measles deaths between 2000 and 2015 (WHO 2015). In Nigeria, there were 11,856 confirmed; 104 deaths (CFR, 0.41%), 9-59 months were most affected. 62.1 % zero dose (NCDC week 52 epidemiological report 2016). Measles is targeted for elimination and under case based surveillance with laboratory confirmation. We described the surveillance data and assessed the surveillance performance according to measles surveillance indicators.

Method: We conducted a descriptive retrospective review of measles surveillance data from 2011-2016. Data were extracted from integrated disease surveillance and response forms. Incidence was calculated using number of cases/ projected

population. We calculated frequencies and proportions.

Results: A total of 2576 suspected case was reported during the period of which 13.4% (357) were Laboratory confirmed and 2% (52) confirmed by Epi linkage, 7 deaths (CFR 1.7 %). Under 5 age group were the most affected (range: 36.4% - 86.9%). Peak year was 2013 with Incidence of 5/100,000 population. 241 (60%) of confirmed cases had zero vaccine dosage, 136(34%) had one dose, 15(3.8%) had 2 doses or more and 8 (2%) had unknown vaccination status. In 2016, the surveillance system did not meet the set target ($\geq 80\%$) for these indicators; specimen arriving laboratory (lab) within 3 days of collection (9%), lab results reported within 7 days of specimen receipt (39%) , cases with adequate investigation initiated within 3 days of onset of rash (42.5%). This was also the case in 2014 and 2016.

Conclusion: The state is in line with the elimination target of <5 cases/100,000 pop. There is still significant number of unvaccinated children and measles surveillance performance is not adequate.

Recommendations: Immunization team should increase planned outreach sessions per week in order to reach more children. Epidemiology unit should initiate adequate and timely investigation of suspected cases. Nigerian Centre for Disease Control should identify laboratories in every state with capacities to conduct measles investigation and empower them.

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EVD in the Elderly people in Guinea

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Elderly people occupy a prominent position in African societies; however, their potential linkage to high case fatality rate (CFR) in Ebola virus disease (EVD) was often overlooked.

We describe the predictive factors for EVD lethality in elderly.

A total of 2004 adults and 309 elderly patients with confirmed EVD were included in the analysis. The median age (interquartile range) was 35 years (23 - 44) in adults and 65 years (60 -70) in elderly. The proportion of funeral participation was significantly higher in the elderly group compared to the adult. Duration (in days) between the onset of symptoms and admission was significantly longer in elderly. CFR in elderly people was also significantly higher (80.6%) compared to adult group (66.2%).

Funeral participation constituted a risk factor for transmission of EVD in elderly people.

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Outbreak Investigation of Cerebrospinal Meningitis due to Neisseria meningitidis serogroup C, Sokoto, Nigeria - May 2017

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Background: Between 2013 and 2016, consecutive outbreaks of cerebrospinal meningitis (CSM) caused by a new strain of Neisseria meningitidis serogroup C (NmC) led to a reported 7,583 cases and 434 deaths in northwest Nigeria with 1536 cases and 87 deaths from Sokoto state. In March, 2017 a suspected outbreak of CSM was reported from Sokoto. We investigated to describe the epidemiology, identify risk factors, and institute control measures.

Methods: We defined a suspect case as any resident of Sokoto, with sudden onset of fever ($>38.5^{\circ}\text{C}$ rectal or 38.0°C axillary) and one of the following signs; neck stiffness, altered consciousness, vomiting, diarrhea and/or other meningeal signs including bulging fontanelle in toddlers between February 27 and May 3, 2017. We administered case investigation forms and line-listed cases at treatment camps and through active case search in communities. Using a structured questionnaire, we collected socio-demographic and risk factor data and conducted a 1:1 unmatched case-control study. We conducted univariate and multivariate analysis for independent risk factors. Cerebrospinal fluid

(CSF) samples were collected for laboratory investigations. We reviewed and recorded average weekly environmental humidity readings.

Results: There were 133 cases, out of which seventy-three (56%) were female. Median age (interquartile range) 19 (2 - 80) years with attack rate of 97 per 100,000 and case fatality rate of 6%. Socio-economic status (aOR=2.80 [95% CI = 1.61 - 4.87]) and no previous vaccination against CSM (aOR=2.05; [95% CI = 1.05 - 3.99]) emerged as independent risk factors of CSM in the outbreak. Of the 84 CSF samples collected, 11 (13%) had NmC isolated. Average weekly environmental humidity was below 30%.

Conclusion: This was an outbreak of CSM due to NmC associated with no previous vaccination against CSM with background low environmental humidity. We implemented the first reactive vaccination with NmC conjugate vaccines in Sokoto and recommended use of weather forecasting technology to control future outbreaks.

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La prévention IST/VIH et prise en charge HSH migrantes à Paris

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En France une analyse montrait que « le vécu des HSH migrant est caractérisé par une forte pression psychologique, un contrôle social sévère, une grande souffrance, de fréquents rackets, des chantages, une angoisse, un silence, un isolement, une auto stigmatisation, des violences, des rejets, des dénis de justice, une stigmatisation dans les structures de santé dans leurs pays d'origines, entre autres exclusion au sein des familles ». Cette analyse avait aussi identifié un certain nombre de besoins des leaders des associations de HSH en termes de renforcement de capacités et d'accompagnement pour améliorer leur système communautaire par Ardhis en France . C'est dans cette perspective que la mise en place d'une association pour leurs accompagnés dans leurs demandes d'asiles, centre d'écoute, d'orientation et d'offre de services adaptés aux HSH .

L'Ardhis s'est positionné comme un lieu de vie, un espace de rencontre et de socialisation, un cadre de

travail pour les HSH et un centre de référence sur les questions en rapport avec l'homosexualité et d'accompagnement pour l'accès au titre de séjour résident, mais aujourd'hui il met en place un système de soin de santé et de prévention IST/VIH à chaque réunion mensuelle. Le centre est fréquenté par les HSH, bi, gay ,trans on peut également inclure le grand groupe LGBT et les Professionnels de sexe. La gestion et l'animation de prévention IST/VIH est faite par un HSH migrant qui était déjà militant dans son pays d'origine et il est étudiant en France en Santé publique. Le paquet de services offert et tourne autour de trois axes : l'espace convivial, les services de santé et autres. Les services de santé prennent en compte le diagnostic et traitement des IST, le dépistage rapide du VIH (Afrique Arc-En-Ciel de Paris) accompagnement et suivi des HSH séropositifs. Les autres services offerts incluent l'assistance juridique et les consultations psychologiques.

De part sa création de Juin 2017 à Décembre 2017, nous avons enregistré comme nombre de visite 6760 HSH, en ce qui concerne la prise en charge en consultation médicale des ist on note 386 HSH et en conseil dépistage volontaire 301 HSH. La distribution de condom et de gel est de 16276 chacun. Il faut dire que l'impact est considérable au vu des résultats.

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Intégration des professionnelles de sexe (PS) et leurs clients (CPS) au sein d'une Association de lutte contre le VIH/SIDA, dans le district de santé de Nkoldongo au Cameroun : expérience de l'Association EVICAM.

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Issues: L'association Espoir et Vie Cameroun (EVICAM) est une association regroupant en son sein des personnes vivant avec le VIH/SIDA ainsi que leur famille. Créée en 2007 et légalisée sous le N°007171/RDA/JO6/BAPP le 4 juin 2008 par le Préfet du Mfoundi, elle admet en son sein des femmes d'horizons divers sans distinction de religion, d'âge ou de race.

EVICAM vise la promotion du droit et du bien-être des personnes vivants avec le VIH/SIDA ; son but principal est de les aider à vivre positivement et a été retenue dans le cadre de la dispensation communautaire en Avril 2017.

Le Cameroun est bénéficiaire du Nouveau Model de Financement du Fonds Mondial. Dans le cadre de la mise en œuvre des activités y afférentes, la Camnafaw a été retenue par l'Instance de Coordination Nationale comme Récipiendaire Principale (PR) de la société civile en charge des interventions de prévention en direction des jeunes, des hommes ayant les relations sexuelles avec les hommes (HSH), des professionnels de sexe et leurs clients. La mise en œuvre des activités du Grant se fait à travers à travers diverses parties prenantes à savoir les Sous-réceptaires (SR) et les Sous-Sous-réceptaires (SSR). EVICAM a été retenue comme SSR en charge des activités de prévention en direction des PS et CPS dans le district de santé de NKOLDONGO afin d'assurer qu'aux moins 90 % de PS et CPS de cette localité adoptent des comportements à risque réduit.

Descriptions: EVICAM, grâce à la prise en charge psychologique, aide les PS et CPS pendant l'éducation thérapeutique, les groupes de paroles, les causeries éducatives, les causeries interpersonnelle, les visites à domicile et les counselling pré et post test à travers les témoignages de ses membres.

Lessons learned: De décembre 2016 à décembre 2017, nous avons

- pu toucher 3730 Professionnels de sexes à travers les causeries éducatives, les causeries interpersonnelles
- 3486 Clients de professionnels de sexes à travers les causeries éducatives
- 4736 ont bénéficié de du conseil et du dépistage volontaire de VIH
- Les 57 cas positifs ont bénéficié du conseil et la référence vers les CTA. /UPEC et ceux-ci ont bénéficié de l'éducation thérapeutique pour une bonne observance
- 268 PS et CPS ont bénéficié de traitement des IST par l'approche syndromique.

Next steps: La mise en œuvre de ce projet à travers la constitution de la cohorte, les groupe de parole, causerie éducative et les entretiens individuels couplée au visite à domicile a permis à Evicam d'intégrer les PS et CPS en son sein.

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Distribution of Hepatitis C Viral load and Genotypes among Nigerian subjects with chronic infection and Implication for Patient Management

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Background: HCV is highly infectious with no currently available vaccine. Recently, newer direct-acting antivirals (DAAs) are used for its treatment with >90% cure rate. Prior to treatment, it is recommended to confirm HCV infection with either quantitative or qualitative nucleic acid test. Access to these assays and the newer DAAs in Nigeria is limited. However, the use of the available older DAAs and interferon in the country, with their limited efficacy, will require HCV VL and genotype prior to therapy. This study therefore aimed at determining the pattern of HCV VL and genotype in the country, and its implication in patient management.

Methods: This was a retrospective study that involved data abstraction from an electronic database (File Maker Pro version 12), of an accredited reference laboratory in Nigeria. Data between June 2013 and May 2017 were abstracted from records of adult subjects' ≥18 years with HCV VL and genotype results. Abstracted data were de-linked and analysed using Microsoft Excel 2010 and SPSS v20.

Results: Within the timeframe of the study, 392 subjects had baseline VL results available and 143 (36.5 %) had genotype in addition while 26/392 (6.6%) had multiple VL assessments. Of these, 230/392 (58.7%) had detectable VL results with higher prevalence in males (63.6%) and in those within the age groups of ≥51 (46.6%) and 41-50 (22.2%) years. The median VL among the 230 subjects was 407,430 (IQR: 90,215 - 1,403,162) IU/mL. Distribution of genotypes for 101 samples with detectable VL showed that genotype 1 and 4

had the highest prevalence of 63.4% and 14.9% respectively.

Conclusion: HCV viraemia was found more in males and subjects above 40 years of age. Though the genotypes 1 and 4 have the highest prevalence, fewer subjects were able to access multiple assessments therefore, access to the newer DAAs, particularly the pangenotypic antivirals are still required to improve management of HCV infection in Nigeria.

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Survey of causative agents for acute respiratory infections among patients in Khartoum- State, Sudan, 2010—2011

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Objective: This study was carried out to determine causative agents of acute respiratory illness of patients in Khartoum State, Sudan.

Methods: Four hundred patients experiencing respiratory infections within January-March 2010 and January-March 2011 were admitted at Khartoum Hospital and had their throat swab samples subjected to multiplex real-time RT-PCR to detect influenza viruses (including subtypes) and other viral agents. Isolation, nucleotide sequence and phylogenetic analysis on some influenza viruses based on the HA gene were done.

Results: Out of 400 patients, 66 were found to have influenza viruses (35, 27, 2, and 2 with types A, B, C, and A and B co-infections, respectively). Influenza viruses were detected in 28, 33 and 5 patients in the age groups <1, 1–10, and 11–30 years old, respectively but none in the 31– 50 years old group. Out of 334 patients negative for influenza viruses, 27, 14, and 2 were positive for human respiratory syncytial virus, rhinovirus and adenovirus, respectively. Phylogenetic tree on influenza

A(H1N1)pdm09 subtype shows that Sudan strains belong to the same clade and are related to those strains from several countries such as USA, Japan, Italy, United Kingdom, Germany, Russia, Greece, Denmark, Taiwan, Turkey and Kenya. Seasonal A H3 subtypes have close similarity to strains from Singapore, Brazil, Canada, Denmark, USA and Nicaragua. For influenza B, Sudan strains belong to two different clades, and just like influenza A (H1N1)pdm09 and A H3 subtypes, seem to be part of worldwide endemic population (Kenya, USA, Brazil, Russia, Taiwan and Singapore).

Conclusions: In Sudan, the existence of respiratory viruses in patients with acute respiratory infection was confirmed and characterized for the first time by using molecular techniques.

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Capacity Building on Reproduction Health for Adolescents as a Prevention Strategy of Risk Behaviors Related to This Critical Development Phase: Experience from a Site of Albert Royer National Hospital Centre of Fann (Senegal)

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Background: A statistical review shows, in different countries including Senegal, a more and more important share of infected adolescents in patient cohorts who benefit from aftercare. At Albert Royer National Hospital Centre (NHCAR), the estimated rate is 51% of the active stream of patients in 2015 against 30% in 2012. With ESTHER's support, sexual and reproduction health training sessions are organized for the adolescents benefiting from aftercare in order to give them some senses of responsibility. Indeed, adolescence is a very complex maturation phase with multiple implications related to sexuality, transgression, risk taking, etc.

Objective: The objective of this study is to describe and evaluate the impact of the training sessions (held in March and December) on the dynamic of behavior change of these adolescents.

Method: Regarding the training component, participatory approach was preferred with a methodology centered on plenary sessions, focus groups and role plays. Data collection lasted two days (on day1 13 units of the concerned population were interviewed and day2 14) through questionnaires filling followed by in-depth interviews of the two cohorts of concerned adolescents who were previously informed about their HIV-positive status.

Results: The socio-demographic profile of respondents is as follows: 27 young single adults (14 females and 13 males), 16 of them living with their custodians and 11 with one of the biological parents (window or divorced). First trends show the positive impact on: (i) self-knowledge (mastering of body, puberty, identity, and sexual access change mechanisms); (ii) knowledge of sexually transmitted infections (STI) (contamination modes, clinical signs, prevention means, integration of socio-cultural values, etc.); (iii) importance of self-esteem observance and reinforcement (23 out of 27 respondents feel confident and less inhibited); (iv) improvement of communications framework with parents; and (v) elaboration of life projects professional as well as conjugal. These results confirm the importance of training sessions that focus on the link between responsible behavior, observance and life project.

Conclusion: Capacity building for adolescents in the grip of multiple difficulties, most of the time exacerbated by their HIV-positive status, could be a mean of effective prevention for risk behaviors, provide that not only they are more empowered but also all concerned actors are involved, especially parents and/or custodians.

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Human papillomavirus knowledge and acceptability to be vaccinated for prevention against cervical cancer among Moroccan adolescents and young adults.

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Background: Human papillomavirus (HPV) infection is estimated to play an etiologic role in 99.7% of cervical cancer. Vaccines can prevent up to 70% of the cervical cancer caused by HPV 16 and 18. The present study was designed to define the knowledge of HPV and HPV vaccine acceptability among Moroccan youth.

Methods: A nationwide anonymous questionnaire with a sample of 688 adolescents (12-17 years) and 356 young adults (18-30 years) was organized, that asked about HPV, origin of cervical cancer, Papanicolaou (Pap) test, and acceptability of HPV vaccine. Data were analyzed using univariate and multivariate logistic regression methods.

Results: Overall, a low frequency (213/1044 = 20%) of HPV knowledge was observed among the studied population. A multivariate model analysis showed that age, educational level, and knowledge of the Pap test remained significantly associated factors with HPV knowledge. Additionally, only 27% (282/1044) of participants were willing to accept HPV vaccination. Highest acceptability was observed among young adults compared with adolescents (166/356 = 46.6% vs 116/688 = 16.9%). Sixty-two percent (103/165) of male participants accepted the HPV vaccine compared with only 20.4% (179/879) of female participants. Educational level, type of school, and knowledge of the Pap test were associated factors with HPV vaccine acceptability in a multivariate model analysis.

Conclusions: The present study showed a low level of HPV knowledge and HPV vaccine acceptability among Moroccan youth. Promotion of activities and sensitization are required to maximize public awareness in the future. This objective can be achieved with the use of media, active efforts by health care providers, and introduction of sexual education in school programs.

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Comprehensive HIV Prevention: A situational and Response Analysis of HIV Prevention among Most-at-Risk-Adolescents (MARA) in Wollega University, Nekemte, Ethiopia

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Background: Adolescents are often at higher risk to acquire HIV infection and they are categorized under the Most at Risk Population Segments (MARPS) due to their inclination to be engaged in risky sexual behaviors and their sense of no vulnerability. The aim of this study was to assess the situation and response to HIV/AIDS prevention and knowledge, attitude and practice (KAP) of students towards HIV/AIDS in Wollega University.

Methods: A cross-sectional study was conducted in Wollega University regular students (2nd year and above) from February to June 2017. A multistage sampling technique was utilized to identify study participants and students were randomly enrolled from the selected colleges with proportional allocation. Structured questionnaires, document review and key informant in-depth interviews were used to collect data. Knowledge, attitude and practice were categorized as “low, medium, high”, “favorable/unfavorable” and “risky/safe”, respectively based on mean and median scores. Qualitative data were summarized manually. SPSS version 24 software was used for data analysis and EpiData 3.1.1 was used for data entry.

Results: Limited commitment, limited budget, lack of strong monitoring and evaluation, and lack of communication around sexual and reproductive health issues, limited manpower, and limited impact assessing studies are the main barriers facing the HIV/AIDS prevention activities in Wollega University. About 11% of students had a high level of knowledge. The median practice of the respondents was 6 (range: 1-11) from 12 practice-related questions and 68.2% had risky sexual practices. The mean (SD) attitude of the respondents was 4.8±2.6 from 10 attitude related questions and 467 (46%) had unfavorable attitudes towards HIV/AIDS prevention and transmission. Students with low level of knowledge were 1.69

times more likely to practice risky sexual activities compared to students with medium level of knowledge [OR, 95% CI: 1.69(1.21,2.38), P=0.002] and 2.77 times more likely to practice risky sexual activities when compared to students with high level of knowledge [OR, 95% CI: 2.77(1.69,4.55), P<0.001].

Conclusion: The situation of HIV/AIDS prevention in the campus looks comprehensive but needs improvements. The students had moderate KAPs about HIV/AIDS prevention and transmission. Knowledge significantly contributed to the level attitudes and practices. Future researches involving nationally representative samples for both males and females, impact assessments, school-attending and out-of-school adolescents could contribute substantially to HIV/AIDS prevention.

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Unprecedented Pneumonic Plague Epidemic, Madagascar, 2017

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Background: *Yersinia pestis* was the cause of many devastating plague outbreaks, epidemics and three pandemics throughout history. It continues to threaten the Malagasy population with plague recrudescence between September and April (around 300 cases per year). In 2017, Madagascar experienced a large epidemic of Pneumonic Plague (PP). Here, we report the onset of this PP epidemic, its evolution and the challenges during responses.

An alert, triggered by unknown successive deaths occurred in a plague-free area, has been received on September 11, 2017 through the sentinel surveillance of fever of the Institut Pasteur (IPM) and the Ministry of Public Health (MoPH). Plague was identified on one dead case, occurring in Antananarivo (the capital city), by rapid diagnostic test (RDT, locally-produced by IPM). Five unnoticed plague suspected deaths occurred during the 15 days period between the index case disease onset and the alert. This delay coupling with the displacement of infected people and their contacts

induced the extension of the PP epidemic throughout many areas (plague-free and endemic area) targeted a national and international response.

Between August 1st and November 27, 2480 clinically-suspected plague cases were reported, of which 1915 (77%) were PP cases. Confirmed or probable cases represented 24% of PP. Among 114 administrative districts, 49 had reported PP cases with a PP hotspot mainly identified in Antananarivo, the capital city and Toamasina, the main seaport. The PP case fatality rate was 7%.

Contact identification and rapid confirmation remained a challenge for a pneumonic plague epidemic throughout its history until now. For this epidemic, they are respectively due to its occurrence in urban and highly populated area and the difficulties encountered with sputum sample biological analyses. However, these epidemics allowed the implementation of additional molecular diagnostic tools and strengthen the country capacities for multisectorial responses. Lesson learned will help us to tackle responses for the next seasons and highlights the need to strengthen research on plague to eliminate the disease.

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Evaluation of Fluorescent Thin Layer Chromatography (f-TLC) as a diagnostic tool for mycolactone detection in patients with Buruli ulcer, Ghana

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Background: Buruli ulcer, a neglected tropical disease caused by *Mycobacterium ulcerans* affects mainly people living in poor rural communities who have little or no access to health facilities and reference laboratories in Africa with the highest

burden in West Africa. Laboratory confirmation of clinically suspected cases has become an important step in management of the disease following introduction of antibiotics by the WHO. As proposed, early diagnosis reduces treatment costs and prevents disabilities. Current diagnosis relies on PCR, which is only available in reference laboratories far away from endemic districts. The need for a point-of-care diagnostic test is a priority. Prof Kishi and colleagues (Harvard University, USA) have recently developed fluorescent thin layer chromatography (f-TLC) as an innovative diagnostic tool to detect mycolactone - a toxin responsible for the pathology associated with this disease. We evaluated the performance of f-TLC against standard IS2404 PCR as a diagnostic tool for Buruli ulcer. We also established the perception of health workers involved in the management of the disease on the introduction of the new technique.

Methods: This was an observational cross-sectional study involving patients who reported to two Buruli ulcer treatment centers in the Ashanti region of Ghana between the period February 2016 and November 2017. We compared results of simultaneous samples that were collected from all patients before treatment and analyzed by both f-TLC and PCR. Health workers were interviewed using questionnaires. Data were analysed using Graphpad prism after entry into Microsoft Excel; contingency analysis using fisher exact test was used to determine sensitivity and specificity. Frequencies were tested using column statistics.

Results: One hundred and seven (107) patients made of 48 males and 59 females were included. The overall sensitivity of the f-TLC technique was 58% and specificity was 74%. When the result was stratified by the type of sample taken, the sensitivity was comparable for FNA (57%) and swab (58%). Similarly, specificity was 75% for FNA and 73% for swabs. Positive predictive value for the test was 78% and the negative predictive value was 52%. Evaluations from the health workers indicated 58% of them see BU management to have improved following implementation of the f-TLC point-of-care test. 48% of the respondents identified with the ease of use and 32% noted that it was time saving.

Conclusion: We have shown that f-TLC is capable of confirming suspected cases of Buruli ulcer within an endemic country suggesting the possibility of its use as a point a care test even though to a lesser extent when compared to IS2404 PCR. The simplicity of the technique, its affordability and positive perception by health workers makes it a potentially implementable diagnostic tool in the district level.

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Towards Providing an Affordable and Sustainable Laboratory Information System for Tuberculosis Laboratories in Developing Countries: Successful Implementation of TBLIS Laboratory Information System in Tuberculosis Laboratories in Africa

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Background: Tuberculosis (TB) is one of the most deadly infectious diseases in the world. A recent alarming rise in cases of drug-resistant TB (DR-TB), multidrug-resistant TB (MDR-TB) and extensively drug-resistant tuberculosis (XDR-TB) make it very much an issue of the present.

Drug resistant TB requires lengthy treatment with multiple drugs and specialized laboratory testing usually performed at regional, national or even supranational level laboratories. Drug resistant tuberculosis patients in resource-poor settings experience large delays in starting appropriate treatment and may not be monitored appropriately due to overburdened laboratory systems, delays in communication of test results, and missing or error-prone laboratory data.

Timely and quality laboratory reporting of TB is important for prompt initiation of appropriate medical therapy for TB patients and rapid public health response.

We developed and implemented TBLIS, an electronic laboratory information management system for tuberculosis laboratories, to improve the quality of TB laboratory data, timeliness of results reporting, monitoring of patient treatment outcomes and effective patient care, materials and inventory management among others.

Methods: A gap analysis in information management in TB laboratories was conducted in three tuberculosis laboratories in Uganda in 2012. Development and piloting of TBLIS was done throughout 2013 and 2014 using Uganda National TB Reference Laboratory (NTRL) as the case study.

Throughout 2016 and 2017, the system was scaled up to other TB laboratories across Africa.

Results: Successful implementation of TBLIS was achieved in Uganda NTRL in 2014. The system facilitated input, storage, analysis, reporting and security of data for patients, specimen and test results. It has enabled monitoring of laboratory processes in real-time, met information management requirements for all the standards followed by the laboratory including ISO 15189, and was very useful in managing laboratory data for the Uganda TB Prevalence Survey 2014/15. Due to the vacuum it has filled and its effectiveness in facilitating TB laboratory information management, TBLIS has been scaled up for implementation in five other TB laboratories in Uganda, Somaliland, Tanzania and South Sudan in a period of 2 years. There has been tremendous improvement in information management operations and audit scores in these six laboratories where TBLIS is implemented.

Conclusion: TBLIS is a novel model that can support TB laboratory information management with its unique requirements in developing countries in a limited resource setting. The system is appropriate for implementation for both TB patient care and research laboratories and can support laboratory accreditation. We propose TBLIS as a tested option for information management in tuberculosis laboratories and other TB care and control programmes.

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Evaluation of a multi-pathogen tropical fever prototype test for the diagnosis of acute arboviral and malarial infections.

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Background: Arboviruses are spreading rapidly and globally, and cause sporadic and unpredictable outbreaks. Due to similarities in clinical presentation and overlapping geographical distribution, broad and simultaneous screening for different arboviruses and co-circulating pathogens (e.g. Plasmodium) is required to identify the origin of disease in febrile patients living in or visiting endemic regions.

Materials and Methods: We have developed a multiplex PCR assay that allows simultaneous detection of several arboviruses and Plasmodium in one test cartridge on an automated molecular diagnostics platform (IdyllaTM, Biocartis). This sample-to-result molecular platform is easy-to-use, and requires minimal hands-on time. The assay has 14 targets: dengue virus (DENV)-1, -2, -3, -4; Chikungunya virus (CHIKV), Zika virus (ZIKV), West Nile virus (WNV), Yellow fever virus (YFV), Japanese encephalitis virus (JEV), Tick born encephalitis virus (TBEV), Plasmodium falciparum, P. ovale, P. vivax, and P. malariae besides sample and internal controls. We have evaluated a prototype version of this IdyllaTM assay on clinical and mock samples in a reference laboratory in a non-endemic setting (Institute of Tropical Medicine (ITM), Belgium) and on acute phase serum samples from febrile patients in a mobile laboratory (ML) in an endemic setting (Senegal) during an ongoing DENV outbreak.

Results: Results were compared with the reference PCR tests routinely used in both settings.

Results A total of 165 Tropical Fever cartridges were evaluated, 131 at the ITM and 34 at the ML in Senegal. In total, 109 clinical samples (65 whole blood, 43 serum, 1 urine), 43 mock samples (whole blood or serum spiked with reference material) and 13 external quality control samples were tested. All 11 negative samples, were also negative with the

prototype test. For 26 whole blood samples (15,7%) there was an error during the extraction which resulted in an incomplete assay (no PCR result), 1 sample gave an invalid test result (no internal PCR control signal).

At the ITM, 19/20 DENV-positive and 10/11 CHIKV-positive samples tested positive with the prototype test. All YFV (6/6), JEV (7/7), TBEV (8/8), and WNV (5/5) samples tested positive. For ZIKV, 3 out of 7 samples tested positive. For Plasmodium, 18/20 P. falciparum, 9/12 P. ovale, 7/9 P. vivax, and 9/9 P. malariae samples tested positive. The 5 negative samples tested also negative with the prototype assay.

In the ML in Senegal, 17/17 DENV positive samples (3 DENV-2, 14 DENV-1), and 6 of the 11 P. falciparum samples tested positive. The missed P. falciparum samples had a Ct-value > 36 with the reference PCR. The 6 samples that were negative by reference testing tested also negative with the Tropical Fever assay on the IdyllaTM platform. Overall, target positivity was 101/114 (88%) at the ITM and 23/28 (82%) at the ML in Senegal.

Conclusions: Preliminary testing demonstrated good performance of the Tropical Fever prototype assay. Further optimization to improve the extraction protocol and ZIKV and P. falciparum detection are ongoing. The multi-pathogen Tropical Fever assay is a promising tool for the differential diagnosis of febrile illness for people living in or traveling to endemic regions.

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Hepatitis B virus vaccination status and associated factors among healthcare workers in Shashemene Zonal Town, Shashemene, Ethiopia: a cross sectional study

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Background: Hepatitis B virus (HBV) remains a major global health problem. More than three-quarters of HBV infection occur in Asia, the Middle

East and Africa. Healthcare workers (HCWs) are at risk of acquiring HBV, hepatitis C (HCV) and human immunodeficiency virus (HIV) infections via exposure to patients' blood and bodily fluids. HBV infection is a recognized occupational hazard, and non-immune health professionals are at risk of acquiring the infection from their work. This study was intended to assess the level of HBV vaccination status and factors affecting the vaccination status of health care workers in Shashemene Zonal Town.

Methods: Institution based cross-sectional study was conducted and a simple random sampling technique was

used to select study subjects. A total of 423 HCWs were enrolled in the study. A structured and pre-tested questionnaire was used to collect the required information through a face to face interview. Finally, data were processed and analyzed using Epi info version 7 and SPSS version 21. Both bivariate and multivariable logistic regression analyses were used to assess the effect of the various factors on vaccination status of HCWs. p value ≤ 0.05 at 95% CI was considered statistically significant.

Results: Overall, 53 (12.9%) respondents were found to be fully vaccinated. The multivariable logistic regression showed that, those respondents who are female, had ≥ 10 years of work experience and those working at governmental health care institutions were significantly associated with vaccination status (AOR = 3.84, 12.51, 2.45 respectively).

Conclusion: Our study revealed that vaccination status of subjects was below the WHO's estimation of vaccination rate among HCWs in developing countries and was very poor when compared with other countries. This is a serious public health problem and challenge for a country with high prevalence of hepatitis B infection.

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Microbiological Analysis of Hemodialysis Water at the Douala General Hospital, Cameroon

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Background and Objective: Rigorous control of the microbiological quality of water in hemodialysis services is important because the immune system of patients with chronic renal failure is weakened. The objective of this study was to determine the microbiological quality of water for hemodialysis in Nephrology Unit of the Douala Général Hospital in order to improve the disinfection strategy.

Materials and Methods: Twelve water samples were collected each month at different sites of the hemodialysis circuits A (inlet of filters), B (Outlet of filters / inlet of Reverse Osmosis (RO) device) and C (outlet of the RO device / close to the generator) between November 2015 and February 2016 to be analyzed. The bacteria were isolated after filtration of 100 ml of water at each site through nitrocellulose membrane with 0.45 μm microporosity deposited on the surface of the Tryptone Glucose Extract Agar (TGEA) and then incubated at room temperature (20 to 22°C) for 7 days. After transplanting to different environments, pure bacterial isolates were identified by their cultural characters and marketed biochemical galleries.

Results: The colony count was well above the required international standards (>100 CFU / ml), for the hemodialysis water with a percentage of 50% of non-compliance. Among the bacteria identified, seven (07) were Gram-negative bacilli including *Pseudomonas fluorescens*, and *Klebsiella pneumoniae* subsp *ozaenae*, three (03) Gram-positive bacilli all *Bacillus* sp and three (03) Gram-positive cocci all of coagulase-negative staphylococci. The most frequently isolated bacterial genera were *Pseudomonas* sp (38,5%), *Staphylococcus* sp (23%), *Bacillus* sp (23%) and *Klebsiella* sp (15,5%).

Conclusion: The high bacteriological contamination of the hemodialysis water with the detection of a

variety of bacteria shows that the disinfection procedure of the distribution loop is not efficient and cannot prevent the development of a biofilm. A higher frequency of disinfection (almost every week), an increase of the concentration and time of contact of the chlorine disinfection product or the use of peracetic acid and a regular monitoring can contribute to improve the quality of the hemodialysis water at the Douala General Hospital to ensure a better quality of life for patients undergoing this treatment.

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Comparison of Incidence of Catastrophic Health Expenditure among Tuberculosis Patients in Public and Private Health Facilities in Kaduna State, Nigeria, 2016

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Background: Despite providing free tuberculosis (TB) diagnosis and treatment services, TB patients still incur financial hardship while seeking for care. Involving private health facilities through Public-Private Mix (PPM) has been identified by World Health Organization as a strategy for eliminating catastrophic health expenditure (CHE) due to TB. There is paucity of studies comparing the incidence of CHE in public and private health facilities in Nigeria. We therefore compared the incidence of CHE due to TB among patients in public and private health facilities rendering TB Directly Observed Treatment Short-course (DOTS) services in Kaduna State.

Methods: We conducted a comparative longitudinal study in 2016, recruiting 274 pulmonary TB patients, 137 from public health facilities and 137 from private health facilities using a multi-stage sampling technique. Data was collected using a questionnaire adapted from a tool developed by USAID and was analysed using SPSS

version 23.0 software. CHE was measured using a threshold of out of pocket (OOP) health expenditure >40% of non-food expenditure. Bi-variate and multi-variate analysis were used to identify risk factors by estimating the adjusted odds ratio (AOR) and 95% confidence interval (CI).

Results: The average cost per TB patient successfully treated from the patient's perspective was US\$485.7 in private health facilities and US\$262.9 in public health facilities ($t = -2.79$; $p = 0.006$). After controlling for the effects of potential confounders, there was a statistically significant difference in the incidence of CHE due to TB between patients in public health facilities (21.20%) and private health facilities (13.10%) (AOR = 2.87; 95% CI, 1.22 – 6.73).

Conclusion: The incidence of CHE due to TB was higher in public health facilities compared to private health facilities. We recommend that efforts to reduce OOP expenditure (e.g. home management of TB) among TB patients in public health facilities in Kaduna State should be explored.

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Evaluation of hepatic function of Hepatitis C Antibodies (HCVAc) positives patients in community area: case of Otou Village-Yaounde

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Background: In Cameroon the prevalence of Hepatitis C is higher than Hepatitis B (13% against 12,2%). In community area, if positive to HCV antibodies HCVAc (immunochromatography or ELISA), it is recommended a confirmation by HCV viroload, only done by a reference laboratory and judged most often expensive by the patients in addition of a long time waiting results. This situation increases the number of lost to follow-up, patients early diagnosed HCVAc positive who vanished into thin air without HCV RNA confirmation and came back generally later on at the last stage of the

disease with severe hepatic complications. In community area, the kinetic dosage of transaminases (SGOT/SGPT), easily accessible, is launched after HCV RNA confirmation. This study was to evaluate the liver function of patients with positives HCV antibodies.

Methods: A cross-sectional, prospective study took place from December to February 2017 at Sainte Monique pediatric and gynecologic Centre, located at Otou village, Yaounde. HCV antibodies (immunochromatography), HBsAg, high blood sugar (one touch glucometer), the kinetic titration of ALAT/ASAT were simultaneously done to each participant. Significant threshold 5%.

Results and discussion: 102 residents of Otou village were enrolled, mean age 38,39 [1.98 [min 12; max 72]. The prevalence of HCV antibodies was 15,68% (16/102) with a dominance of women 17,86% (15/84). Patients aged [52 ; 72] 38,46% (5/13), widows and single had the highest prevalence of HCVAc. 40,26% of the study population suffered from hepatic failure (ASAT+ALAT couple abnormal). Besides, liver failure touched more HCVAc positives subjects than HCVAc negative (66, 67% Vs. 33,87%, $p=0,02$). Furthermore, the hepatic function was gradually destroyed with the age and subjects aged [52-73] were the most involved ($p=0,028$). 59,80% (61/102) had a ASAT/ALAT quotient >2 (probably alcoholic liver failure) while 30,39% (31/102) was suffering from acute liver failure (ASAT/ALAT quotient <1).

Conclusions and recommendations: The presence of HCV antibodies and the age of the participants are significant factor of the hepatic failure. It would be judicious in a community context to intensify the systematic control of hepatic function of HCV antibodies positives especially aged subjects with or without HCV viral load confirmation results.

HIV Disclosure Status and it's Determinants among HIV-Infected adults in a Tertiary Health Facility in North-Western Nigeria, 2017

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Background: HIV/AIDS remains a major global public health problem and Nigeria accounts for the second largest population of people living with HIV/AIDS worldwide. Disclosure of HIV status especially to sexual partners is key to the prevention and control of HIV/AIDS. We therefore assessed HIV disclosure status and its determinants among HIV-infected adults attending anti-retroviral therapy (ART) clinic in Ahmadu Bello University Teaching Hospital (ABUTH), Kaduna State, North-Western Nigeria.

Methods: A cross-sectional study design was used. We recruited 217 HIV-infected adults attending ART clinic in ABUTH using a systematic sampling technique. Data on socio-demographic characteristics, disclosure status and potential factors associated with disclosure were collected using a pre-tested semi-structured interviewer-administered questionnaire and analyzed using SPSS version 23.0 software. Bi-variate and multi-variate analysis were used to identify the determinants of disclosure status by estimating adjusted odds ratio (AOR) and 95% confidence interval (CI).

Results: Out of 217 HIV-infected adults, 133 (61.4%) were female, 120 (55.3%) were married and 88 (40.6%) were within the first and second wealth quintiles. The mean age of the HIV-infected adults was 31.4 years (+8.5 years). One hundred and fifty (67.3%) of the HIV-infected adults had disclosed their status out of which 115 (76.7%) disclosed to their sexual partner. HIV-infected adults were more likely to disclose their status when they are female (AOR = 6.9; 95% CI, 2.7-17.5), married (AOR = 2.6; 95% CI, 1.1-6.1), diagnosed with HIV for > 2 years (AOR = 3.6; 95% CI, 1.4-9.4), feel it is important to disclose their status (AOR = 6.5; 95% CI, 2.2-19.6) and on anti-retroviral (ARV) drugs (AOR = 5.6; 95% CI, 1.3-25).

Conclusion: About two-third of HIV-infected adults had disclosed their HIV status, mostly to their sexual partner. Disclosure was associated with being a female, married, diagnosed with HIV for > 2 years, feeling it is important to disclose HIV status and on ARV drugs. We recommend improved disclosure counseling particularly among male HIV-infected adults that are not married and newly diagnosed.

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African coalItion for Epidemic Research, Response and Training

ALERRT Consortium^{1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21}

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Background: ALERRT (African coalItion for Epidemic Research, Response and Training) aims to reduce the public health and socio-economic impact of disease outbreaks in Sub Saharan Africa (SSA) by building a sustainable clinical and laboratory research preparedness and response network. ALERRT consists of 21 partner organisations from 13 countries (4 European and 9 African). ALERRT has been awarded a five-year, €10,000,000 grant from EDCTP starting on 01 December 2017

Methods: ALERRT will establish a clinical research network that can design and rapidly implement ICH-compliant, high quality, large-scale, multi-site clinical studies in preparation for and response to outbreaks in Sub-Saharan Africa (SSA). A laboratory

network will also be established and will include mechanisms for diagnostic outreach, bio-banking, and platforms for the evaluation of new diagnostic technologies. ALERRT will develop and implement an ICT infrastructure to provide scalable, robust and GCP-compliant data management capabilities suitable for resource-poor settings in SSA. ALERRT will work to alleviate the administrative, regulatory and ethical bottlenecks that can slow the initiation of research by establishing a 'response framework'. This will ensure that ALERRT can act swiftly to respond to disease outbreaks by initiating fit-for-purpose clinical and laboratory research. The operational research capacity of the ALERRT network will be enhanced and maintained through a training and capacity development programme. Furthermore, in order to ensure that its activities are locally and internationally acceptable, ALERRT will set up systems of community engagement for clinical trials and outbreak responses. ALERRT's organisational and operational readiness will be developed, tested and trained by conducting 'warm-base' clinical studies. The 'warm base' studies will focus on febrile illnesses, generating clinical and health-system evidence to improve patient care.

Results: The overall anticipated impact of ALERRT is to enhance global clinical research preparedness and response capacity for infectious diseases with epidemic or pandemic potential, by establishing a fully operational clinical research preparedness and response network for SSA. The network will be able to provide accelerated evidence for the optimal clinical management of patients and to guide the rapid research and public health response to any infectious disease outbreak in SSA. The ALERRT clinical research platform will also actively support the development of new diagnostics, drugs and vaccines for priority pathogens as proposed by the WHO Blueprint and CEPI.

Conclusions: ALERRT combines the strengths of leading African and European partners in (re-)emerging and epidemic-prone infectious disease clinical research, preparedness and response. It builds on efforts by the EDCTP Networks of Excellence WANETAM, CANTAM and EACCR, and internationally well-embedded research and training partners with extensive operational experience in outbreak preparedness and response, and the associated challenges in SSA.

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Drug resistance among women attending antenatal clinics in Ghana

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Background: Initial evidence from resource-limited countries using the WHO HIV drug resistance (HIVDR) threshold survey suggests that transmission of drug-resistance strains is likely to be limited. However, as access to ART is expanded, increased emergence of HIVDR is feared as a potential consequence. We have performed a surveillance survey of transmitted HIVDR among recently infected persons in the geographic setting of Accra, Ghana.

Methods: As part of a cross-sectional survey, 2 large voluntary counseling and testing centers in Accra enrolled 50 newly HIV-diagnosed, antiretroviral drug-naïve adults aged 18 to 25 years. Virus from plasma samples with >1,000 HIV RNA copies/mL (Roche Amplicor v1.5) were sequenced in the pol gene. Transmitted drug resistance-associated mutations (TDRM) were identified according to the WHO 2009 Surveillance DRM list, using Stanford CPR tool (v 5.0 beta). Phylogenetic relationships of the newly characterized viruses were estimated by comparison with HIV-1 reference sequences from the Los Alamos database, by using the ClustalW alignment program implemented.

Results: Subtypes were predominantly D (39/70, 55.7%), A (29/70, 41.4%), and C (2/70; 2, 9%). Seven nucleotide sequences harbored a major TDRM (3 NNRTI, 3 NRTI, and 1 PI- associated mutation); HIVDR point prevalence was 10.0% (95%CI 4.1% to 19.5%). The identified TDRM were D67G (1.3%), L210W (2.6%); G190A (1.3%); G190S (1.3%); K101E (1.3%), and N88D (1.3%) for PI.

Conclusions: In Accra the capital city of Ghana, we found a rate of transmitted HIVDR, which, according to the WHO threshold survey method, falls into the moderate (5 to 15%) category. This is a considerable increase compared to the rate of <5% estimated in the 2006-7 survey among women attending an antenatal clinic in Mamobi. As ART programs expand throughout Africa, incident infections should be monitored for the presence of transmitted drug resistance in order to guide ART regimen policies.

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Prevalence and Drug Susceptibility Pattern of Group B Streptococci (GBS) among Pregnant Women Attending Antenatal Care (ANC) in Nekemte Referral Hospital (NRH), Nekemte, Ethiopia

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Background: Maternal colonization with GBS in the genitourinary or gastrointestinal tracts is the primary risk factor for disease. Maternal infections of GBS constitute one of the leading pathogens associated with both early and late-onset neonatal sepsis. The aim of this study was to determine the prevalence and drug susceptibility pattern of Group B Streptococci (GBS) among pregnant women.

Materials and Methods: A cross sectional study was conducted in Nekemte referral hospital (NRH) between March and May, 2016 on a total of 180 pregnant women. Vaginal swabs were aseptically collected from each pregnant woman using sterile cotton swabs, inoculated in 1.5 ml Todd Hewitt broth (supplemented with colistin and nalidixic acid) and sub-cultured on 5% sheep blood agar. Gram staining, Bacitracin sensitivity test, CAMP test and Drug susceptibility tests were performed. Data on socio-demographic characteristics and associated risk factors were collected using structured questionnaires. Cleaned and coded data were analyzed by SPSS software version 20. P value < 0.05 was used as a significance level.

Results: The median age of the participants was 24.5 years (range: 16-38) and 86% participants were urban residents. The total prevalence of maternal GBS colonization from vaginal swab culture was 12.2% (22/180). The prevalence of GBS colonization rate was significantly higher in those pregnant women above 37 weeks of gestation [AOR, 95% CI: 2.1(1.2, 11.6), P= 0.03] and married ones [AOR, 95% CI: 3.2(1.8, 11.6), P< 0.021]. Twenty (91%) of GBS isolates were sensitive to vancomycin and the highest resistance was observed against penicillin G (77.3%).

Conclusion: The prevalence of GBS colonization in this study is significantly high and differed by

gestational age and marital status. None of the GBS isolates were resistant to vancomycin but higher resistance was shown against Penicillin G. Screening of pregnant women for GBS colonization, large scale longitudinal studies with molecular characterization of GBS in both mothers and neonates is recommended. Further, antimicrobial prescriptions should be made based on antimicrobial susceptibility test results.

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In Vitro Antibacterial Activity and Acute Toxicity of the Extracts of *Annona senegalensis* (annonaceae), a Medicinal Plant of Cameroonian Pharmacopoeia

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Background: The resistance of pathogens to antibiotics is increasing worldwide because of various environmental and genetic changes. However, natural substances have become sources of new antibiotics. This work aimed to isolate and characterize multiresistant microbes and to determine their sensitivity profile to the various aqueous and hydro-ethanol extracts of *Annona senegalensis*, a Cameroonian medicinal plant.

Methods: The antibacterial activity was determined using the diffusion method followed by microdilution to elucidate the inhibition parameters. The safety of the most active extract was determined using the Organization for Economic Co-operation and Development (OECD) 410 protocol, and the biochemical and histopathological parameters were investigated.

Results: During the period of June to December, 325 samples were collected from cytoculture (81.84%) and pro-culture (18.15%). In these samples, we obtained 13% and 11% positive cultures, respectively, in which the following bacteria were isolated and characterized: *Klebsiella pneumoniae*

pneumoniae, *K. pneumoniae ozaenae*, *E. coli*, *K. oxytoca*, *Enterobacter sakazaki*, *Salmonella sp*, and *Klebsiella spp*. The results of the sensitivity profile of bacteria to these antibiotics showed the following resistances: *E. coli* to Amoxicillin (100%), Amoxicillin + Clavulanic Acid (83.33%), Cefotaxime (52.94%), Ceftazidime (44%), Nitrofurane (57.14%), and Norfloxacin (45.45%). The lowest resistance was noted for Aztreonam (25.00%) and Imipenem (13.64%). With regard to the susceptibility of the multi-resistant bacteria strains to *A. senegalensis* extracts, the diameter of the inhibition zone was between 11.33 and 19.5 mm depending on the type of extract and the bacterial strain. The hydro-ethanolic extract of *A. senegalensis* was the most active with a diameter of 19.5 mm for the reference bacteria strain (*Pseudomonas CIPI7525*) and 16.33 mm for an isolated multi-resistance strain (*K. pneumoniae pneumoniae*). However, none of the four extracts showed inhibitory activity against *K. pneumoniae ozaenae*. The inhibition parameters varied from 1.56 to 25 µg/µL for the MIC and 1.56 to 50 µg/µL for the MBC, respectively. All the extracts tested were bactericidal. The results of the acute toxicity of the bark hydroalcoholic extract showed no significant variation in AST, ALT, creatinine, and lipid profile in the assay and control groups, with both females and males demonstrating that the extract had very weak toxicity.

Conclusion: The hydro-ethanolic extract of the bark of *A. Senegalensis* showed antibacterial activities on the microbes responsible for urinary and diarrheal infections such as *S. aureus*, *S. typhi*, *K. pneumoniae*, *P. aeruginosa*, and *E. coli* and is not toxic.

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Intestinal carriage of vancomycin resistant-Enterococcus in community setting in Casablanca

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Background: Enterococci rank among leading cause of community acquired infections. This study aimed to determine the prevalence of intestinal carriage and to perform a phenotypic and genotypic characterization of vancomycin resistant Enterococcus (VRE) in community in Casablanca, Morocco.

Methods: During 6 months (2014), 113 fecal samples were examined for the presence of Enterococci. Antibiotic susceptibility of isolates was realized by disk diffusion method. Phenotypic and genotypic identification of species were performed and vanA, vanB and vanC genes were detected by PCR.

Results: We isolated 100 strains collected from community population of 80 persons. 55% of isolates were identified as *E. faecium* and 45 % as *E. faecalis*. The resistance profile shows that 88% of strains were multiresistant. The prevalence of fecal carriage of VRE was 21% (n =21), which 8(17.77%) strains were *E. faecalis* and 13 (23.63%) were *E. faecium*. PCR analysis revealed that 14strains were resistant to vancomycinby possession of vanA gene.

Conclusion: The emergence of VRE and the high rate of colonization by multiresistant enterococciare alarming. Strict measure must be required to control the further spread of these strains in Moroccan community.

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Prevalence of current patterns and predictive trends of multidrug-resistant *Salmonella* Typhi in Sudan

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Background: Enteric fever has persistence of great impact in Sudanese public health especially during rainy season when the causative agent *Salmonella* enterica serovar Typhi possesses pan endemic patterns in most regions of Sudan - Khartoum.

Objectives: The present study aims to assess the recent state of antibiotics susceptibility of *Salmonella* Typhi with special concern to multidrug

resistance strains and predict the emergence of new resistant patterns and outbreaks.

Methods: *Salmonella* Typhi strains were isolated and identified according to the guidelines of the International Standardization Organization and the World Health Organization. The antibiotics susceptibilities were tested using the recommendations of the Clinical Laboratories Standards Institute. Predictions of emerging resistant bacteria patterns and outbreaks in Sudan were done using logistic regression, forecasting linear equations and in silico simulations models.

Results: A total of 124 antibiotics resistant *Salmonella* Typhi strains categorized in 12 average groups were isolated, different patterns of resistance statistically calculated by ($y = ax - b$). Minimum bactericidal concentration's predication of resistance was given the exponential trend ($y = n \text{ ex}$) and the predictive coefficient $R^2 > 0 < 1$ are approximately alike. It was assumed that resistant bacteria occurred with a constant rate of antibiotic doses during the whole experimental period. Thus, the number of sensitive bacteria decreases at the same rate as resistant occur following term to the modified predictive model which solved computationally.

Conclusion: This study assesses the prediction of multi-drug resistance among *S. Typhi* isolates by applying low cost materials and simple statistical methods suitable for the most frequently used antibiotics as typhoid empirical therapy. Therefore, bacterial surveillance systems should be implemented to present data on the aetiology and current antimicrobial drug resistance patterns of community-acquired agents causing outbreaks.

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Sentinel surveillance of HIV-1 drug resistance and genetic diversity reveals disparities by region and by urban/rural settings among antiretroviral therapy initiators in Cameroon

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Background: Scale-up of antiretroviral therapy (ART) is accompanied by an increasing risk of HIV drug resistance (HIVDR) emergence and transmission. In a context where pre-treatment HIV-1 drug resistance (PDR) is $\geq 10\%$ for non-nucleoside reverse-transcriptase inhibitors (NNRTIs) and without access to dolutegravir-based first-line regimens, ART-guided by resistance testing is highly recommended. Thus, understanding the burden and patterns of PDR in different geographical settings of countries like Cameroon could help in prioritising public health actions for effective ART programme performance. Thus, in order to limit the emergence of HIVDR, we aimed to evaluate burdens and patterns of PDR and HIV-1 genetic diversity in different regions and to compare PDR in urban versus rural settings of Cameroon.

Methods: A sentinel surveillance study was conducted from 2014 to 2017 in 5 regions of Cameroon (Centre, East, Littoral, North, and Northwest). Amongst patients initiating ART, sequencing of HIV-1 protease/reverse transcriptase was performed. PDR mutations were interpreted following the Stanford HIVDR database v.8.3 (<https://hivdb.stanford.edu/>) and HIV-1 phylogenetic analysis was performed using MEGA v.6. PDR and genetic variability were analysed according to geographical settings, and p-value <0.05 was considered statistically significant.

Results: A total of 231 patients initiating ART were enrolled (15-65 years old; 65% female; 5-1286 CD4 cells/mm³); with 61, 53, 43, 41 and 33 sequences from the Northwest, Centre, East, Littoral and North region, respectively. Overall burden of PDR was 7.8% (18/231), with varying trends between drug-classes: 6.1% (14/231) NNRTI-DRMs (driven by K103N [7], E138A/G/K [4], A98AG [2], Y181C [2], K238T [2]); 2.2% (5/231) NRTI-DRMs (driven by M184V/I [3], M41L [2], K65R [2]); and 0.4% (1/231) PI-DRM (L90M). Of note, increasing burden of PDR was observed from the North (0%), Littoral (7.3%), Centre (7.5%), Northwest (9.8%), to East (11.6%); following similar trends of NNRTI-DRMs across regions (0%, 4.9%, 5.7%, 8.2%, and 9.3% respectively [see Figure 1]). PDR was higher in urban (11.3%) versus rural settings (8.2); p=0.592. Globally, a wide genetic diversity of HIV-1 was found, and CRF02_AG was the predominant subtype (64.1%[148/231]) ranging from 42.4% in the North to 72.1% in the Northwest region (Figure 2). Burden of PDR was similar between CRF02_AG (8.1%[12/148]) and non-AG (7.2%[6/83]), p=0.811.

Conclusion: Burden of PDR is considerably different in these regions of Cameroon, with slightly higher burden in urban settings. Interestingly, with $<10\%$ burden of NNRTI-resistance in all settings, current first-line ART remain widely effective at population-level. However, there is need to limit emerging HIVDR by strengthening monitoring approaches preferentially in urban settings, as well as in the regions where overall PDR is $\geq 5\%$ (Littoral, Centre, Northwest, East regions). Moreover, understanding further the significance of the predominant CRF02_AG viral strain on ART response is warranted in this context of wide HIV-1 genetic variability.

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Status of rabies in Addis Ababa, Ethiopia, 2012 – 2016: Retrospective cross sectional study.

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Background: Rabies is a highly fatal viral disease of all warm blooded animals including human globally. Around 59,000 people die due to rabies annually world-wide; most are children under the age of 15

(CDC, 2017). In Ethiopia, there are an estimated 2700 deaths per year. It is 100% fatal once clinical signs have begun. It is also 100% preventable with appropriate medical care. However, effective rabies control program still remains to be a reality and needs to be strengthened.

Objective: To describe the distribution, trend and magnitude of rabies in Addis Ababa in the years 2012 – 2016.

Methods: A retrospective data were used from the Ethiopian Public Health Institute rabies case record book registered in the years 2012 to 2016. All humans and animals that came to the Institute Zoonoses research case team from each sub cities of Addis Ababa with rabies exposures were considered for the cross-sectional study. Microsoft excel and spss version 20 were used for the data analysis.

Results: A total of 6927 human rabies exposures were reported at Ethiopian Public Health Institute during 2012-2016, giving a mean annual incidence of ~46 human rabies exposures per 100,000 (55.6% males, 44.4% females). Out of these, 6199 (89.5%) and 573 (8.27%) were exposed to suspected dogs and cats respectively. Among the total animal bites, 3810 (55%) were bitten on the lower extremities. Eighty percent of the dogs were not vaccinated. Out of 1638 animal brains investigated in the laboratory with Fluorescent Antibody Technique, 1010 (61.7%) were confirmed rabies positive. Among the laboratory confirmed positive rabies cases; high percentage of the animals came from Yeka 210 (21%) and lower number from Kirkos sub city 35 (3.5%).

Conclusion: The principal vector of rabies in Addis Ababa is dog. Effective rabies management and control based on confirmed cases, and mass-immunization and control of free roaming dog populations is recommended.

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Trends in Non-Neonatal Tetanus Morbidity and Mortality, Ethiopia- September 2012- August 2016

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Background: Tetanus is a vaccine-preventable disease with high morbidity and mortality in developing countries. In 2015, an estimated 209,000 tetanus infections with 59,000 deaths occurred globally. Although infants in Ethiopia are routinely vaccinated against tetanus, booster doses of vaccine needed to provide lifelong protection are only provided to pregnant women and women of childbearing age to prevent neonatal tetanus. Ethiopia eliminated neonatal tetanus in 2017, but cases of tetanus still occur in other age groups. Our analysis aimed to highlight the magnitude of tetanus in Ethiopia over the past five years to inform policymakers and stakeholders.

Methods: We conducted a retrospective analysis of nationwide reports of inpatients and outpatients diagnosed with tetanus from the Health Management Information System from September 11, 2012 to August 28, 2016. Neonatal tetanus was not included. Incidence, case fatality and mortality rates were calculated using Epi Info 7.2.1.

Results: A total of 30,625 tetanus patients were registered; 26,903(88%) were outpatients, 15,255(49.8%) were male, and 16,101 (52.5%) were ≥15 years. The largest number of patients was reported in 2013 (16,242, 53%). Incidence per 100,000 was (6.86) 2012, (19.1) 2013, (2.88) 2014, (4.61) 2015, (2.56) 2016. Overall incidence of tetanus was 7.2 per 100,000, with Afar Region being the most-affected (95.2per 100,000). The national case-fatality rate was 3.8%. The mean annual tetanus mortality rate was 0.15 per 100,000. Among 669 deaths, 482 (72%) were males. The annual mortality rate was the highest in Southern Nation Nationalities and Peoples Region (0.56 per 100,000).

Conclusion: Although the control and prevention of tetanus is on the right track, morbidity and mortality due to tetanus remains significant with thousands of cases and hundreds of deaths reported every year. The incidence and mortality of tetanus can be reduced further by early detection and treatment of tetanus, improved and expanded immunization services, and health education focusing on good wound care.

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Mortality and virologic outcomes between two and five years of antiretroviral treatment initiated during the first year of life: experience of the 1240 ANRS-PEDIACAM study (Cameroon)

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Background: In most of the studies, virologic response is assessed during the first 2 years of antiretroviral treatment initiated in HIV-infected infants. Instead, early initiation of antiretroviral therapy exposes infants to very long-lasting treatment. Moreover, maintaining viral suppression in children is very difficult. We aimed to describe virologic response and mortality after two years of antiretroviral treatment initiated during the first year of life, and identify factors associated with success in a Sub-Saharan Country (Cameroon).

Methods: We included 149 children of the ANRS 12140-PEDIACAM study still alive after two years of antiretroviral treatment initiated during the first year of life. The study population was organized in two groups according to virologic status at two years of antiretroviral treatment initiation: 1) group 1: children with viral load <400 copies/mL; 2) group 2: children with viral load ≥400 copies/mL or whose viral load was not measured. The probability of maintaining virologic success between two and five years antiretroviral treatment in group 1, or achieving virologic success at least once in group 2, was estimated using survival models. The study of factors associated with viral load <400 copies/mL in children still alive at five years of antiretroviral treatment (versus ≥ 400 copies/mL or not measured) was performed using univariate and multivariate logistic regression.

Results: At five years of early antiretroviral treatment, viral load was suppressed in 66,4% [58.7-74.1]) of the 144 children still alive and in care, but viral load was not measured in 15.4%. Five deaths (3.3% [IC95%: 0.4-6.2]) were recorded during the study period. Among the children with viral suppression at two years of treatment initiation, the probability of maintaining viral suppression at five years of treatment was 64.0% [48.5-79.6]. Among the children with detectable or unknown viral load at 2 years of treatment initiation, the probability of achieving viral load < 400 copies/mL at least once between two and five years of treatment initiation was 76,0% [53,5-98,5]. The only factor associated with viral suppression at five years of treatment initiation was virologic success at two years of treatment initiation.

Conclusion: The probability of maintaining viral suppression between two and five years of early initiated antiretroviral treatment in HIV-infected children is unsatisfactory, stressing difficulties of parents for daily long-term adherence to treatment. Thus, it is necessary to routinely monitor viral load and resistance to antiretroviral drugs in order to optimize treatment response in Sub-Saharan African children.

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Seroprevalence of leptospirosis among high risk individuals in Morocco

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Background: Leptospirosis is an anthropozoonotic re-emerging infectious disease whose prevalence is often underestimated in most developing countries.

Globally, this re-emergence sickness is likely influenced by environmental conditions, such as occupation, urbanization and poverty. Lack of basic sanitation, poor housing conditions and limited access to education and health increase the risk of human infection in urban areas.

The aim of this study was to investigate the Seroprevalence of leptospirosis among high risk individuals in Casablanca (Morocco).

Materials and Methods: In cross-sectional study, 490 blood samples (97.6% males) from people were carried out in 3 high risk occupational sites: the biggest slaughterhouse meat (n=208), a poultry market (n=121) and the fish market (n=161) during 2014. 125 blood samples from people in the general population were also provided. The sera were screened with in-House IgG and IgM enzyme-linked immunosorbent assay (ELISA) to detect the presence of anti *Leptospira*. Positive samples were tested by Micro Agglutination Technique (MAT) using a panel of 24 serovar culture and cut point of 1:25.

Results: The seroprevalence of 10.4% (13/125) in the control group was found significantly lower than the overall seroprevalence of 24.1% (118/490) in the high risk groups of which 7.3% (36/490), 13.7% (67/490) and 3.1% (15/490) were positive for anti-*Leptospira* -IgM, -IgG and both -IgG/-IgM antibodies, respectively. Most of the positive patients were occupationally involved with poultry (37.2%), followed by the market fish (26.1%) and the slaughterhouse meat (14.9%). Among all ELISA positive workers sera, 20.3% (n=24) had positive MAT responses, the most common serogroup was *Icterohaemorrhagiae*, which was seen in 7 (29.1%), followed by *Javanica* in 4 (16.7%). *Australis* was seen in 2 (8.3%) and *Sejroe* (*Hardo Prajitno*), *Mini* and *Panama* in one each (4.2%). In the remaining 8 samples sera, MAT showed equal titer against more than one serovar (undetermined serogroup). Of which, 5 seropositive sera had two agglutinations with *Icterohaemorrhagiae* serogroup, serogroups found in these 5 associations were *Javanica* (3 cases), *Louisiana* (3 cases), *Canicola* (2 cases), *Mini* (1 case), *Batavia* (1 case) and *Javanica* (1 case). In the remaining 3 undetermined serogroups, MAT showed equal titer against only two serogroups, *Icterohaemorrhagiae* with *Canicola* or *Louisiana* and *Panama* with *Mini*.

Conclusion: The present results indicated that leptospirosis is a potential health hazard of occupational groups in Casablanca. The prevention of occupational human exposure is recognized as a basic control measure.

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Better surveillance data for better action: lessons learnt in using multiple HIV surveillance data systems to inform policy and guide public health program planning

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Better surveillance data are useful to lobby for policy change, mobilize resources, planning, improve programming and implementation, and measure performance of public health responses. Many countries have now systems to collect high-quality surveillance data. In many low-income countries, however, more efforts are put into the collection of data than ensuring effective use of data and transforming analytics results into actionable insights. These often limit the capacity of countries for planning at the policy level: who is affected or at most risk, what is the extent of the problem, how is the disease spread, and what comes next. It also makes difficult to assess the public health impact of health outcomes, determine and measure geographical trends, or facilitate micro-level planning.

Pakistan has been conducting HIV surveillance since 2005, with four rounds of surveillance data being collected among key populations across 19 major cities between 2005-2011. The number of cities and key populations surveyed in each round varied. Each round of surveillance began with in-depth mapping to estimate the size, distribution and operational typology of key populations in each city. All four rounds of data were utilized extensively to better understand heterogeneity in HIV transmission dynamics among key populations in order to inform policy and better plan intervention programs. Combined with epidemiological approaches, simple to complex mathematical modelling approaches were used to gain insights into underlying epidemiological factors driving epidemics in each major city.

The aim of this article is to share the experiences and lessons learnt during the process of developing

and utilizing multiple HIV surveillance data systems to inform policy and guide public health program planning in Pakistan.

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Epidemiological studies on the disease and vector of *Mansonella perstans* in the Asante-Akim North district of Ghana

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Background: Large parts of African and South American countries are colonized by *Mansonella* a very common but poorly described filarial nematode. Blood-sucking flies of the genus *Culicoides* are suspected to be the vector of *Mansonella perstans* but no study in Ghana has confirmed that it can transmit the parasite. An epidemiological survey was conducted in eight communities in the Asante-Akim North district of Ghana to determine the prevalence of *M. perstans* and the diversity of *Culicoides* spp that could be potential vectors for transmission.

Method: A total of 1,216 residents comprising 601 males and 615 females with an age range of 9 years and above, participated in the study after an informed consent. 100µl of finger-prick blood from all participants was taken and examined for microfilariae of *M. perstans*. *Culicoides* flies were investigated in the study communities for *M. perstans*. The different *Culicoides* spp in the study communities were determined using the CDC light trap and human landing catches (HLC).

Results: The average prevalence of *M. perstans* was 33.2% with the range between 1.6% and 72.3%. The prevalence of the parasite among the males was 57.2% and females 42.8%. Microfilariae were detected among all the age groups with the highest prevalence in the 30-39years age group. In all, 2,194 *Culicoides* species (spp) were collected at the end of the study. Light trap collections gave diverse species with HLC giving only one species (*C. inornatipennis*). Investigations of seasonal abundance revealed a

higher prevalence in the rainy season (58.7%). Biting activities had a peak period between 5-6pm. No *Culicoides* spp was found positive for *M. perstans* and its vector still requires identification.

Conclusion: *M. perstans* has been detected in the Asante-Akim North District of Ghana with high prevalence. *Culicoides inornatipennis* was identified as the most anthropophilic and is likely to be the responsible vector species for transmission. However, further studies should be carried out to determine the actual responsible vector species; and conducted in other parts of the country to determine the actual prevalence of the disease.

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Building Laboratory Capacity to Detect and Characterize Pathogens of Public and Global Health Security Concern in Kenya

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Since 1979, multiple CDC Kenya programs have developed diagnostic expertise and laboratory capacity in Kenya. In 2004, CDC's Global Disease Detection (GDD) program within the Division of Global Health Protection Kenya (DGHP-Kenya) initiated close collaboration with Kenya Medical Research Institute (KEMRI), to build on previous efforts by malaria, HIV and tuberculosis programs and support the expansion of the diagnostic expertise and capacity in KEMRI and the Ministry of Health. First, DGHP-Kenya developed diagnostic capacity for diarrheal, respiratory, zoonotic and febrile illnesses to understand the etiologies and human health burden of these common illnesses in settings like informal urban settlements, remote rural areas and refugee camps where infectious diseases diagnostics were not previously available. Second, we have evaluated and implemented new diagnostic technologies such Taqman Array Cards (TAC) to detect emerging or reemerging pathogens such as Rift Valley fever, Ebola, chikungunya, and

Zika viruses and have recently added next generation sequencer (NGS) for detection of new emerging pathogens. Third, with support from DGHP-Kenya, KEMRI provides rapid laboratory diagnostic support to Kenya and the regional countries during outbreak investigations. Fourth, DGHP-Kenya has been assisting the Kenya National Public Health laboratory-National Influenza Center to obtain World Health Organization (WHO) certification and the microbiology reference laboratory in obtaining ISO15189 accreditation. Fifth, we have supported biosafety and biosecurity curriculum development to help Kenyan laboratories safely and appropriately manage infectious pathogens. As a result of these efforts, DGHP-Kenya has supported the establishment of > 100 assays for 153 pathogens for surveillance, disease outbreak investigations and research in Kenya, provided reference laboratory support for the investigations of 205 outbreaks from 2007-2016, and detected 2 pathogens not previously diagnosed in Kenya. Lastly, laboratory data from population-based surveillance have supported evidenced-based decisions such as the introduction of rotavirus and pneumococcal vaccines in Kenya and a recommendation for future influenza vaccination. These achievements, in collaboration with existing programs, the CDC Divisions of Global HIV and TB (DGHT) and Division of Parasitic Diseases and Malaria (DPDM), have significantly improved public health in Kenya and the region resulting in more rapid detection and control of infectious disease outbreaks and other public health threats at their source, thereby enhancing global health security.

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The link between human resource management practices, health workforce and patient outcomes in sub-Saharan Africa: systematic review

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Background: Many studies found that human resources management (HRM) is key for improving quality of care and strengthening health system globally. Sub-Saharan Africa (SSA) is confronting

problems related to HRM practices and a high burden of disease in the world but performs a disproportionately low quality of health care. Poor HRM practices and low performance of health workers are among the major causes for this gap. Closing this gap requires bundles of HRM interventions for improving employee outcomes, patient outcomes and organizational outcomes. Although SSA is confronting the burdens, there is scant documentation on the link between HRM and performance in healthcare sector, health professionals' and patient outcomes in hospitals. This calls for the present study which is the first at its kind in the region. The study aims to review literature on "how the human resources management-in the broad sense- related to health workforce outcome, patient outcomes, and hospital performance in general, in sub-Saharan Africa?"

Methods: We searched seven data bases (Embase, Medline Ovid, Web of Science, Cochrane, PubMed, CINAHL & Google Scholar) for all relevant papers using detailed search strategy and terms, which resulted in 2251 hits of titles and abstracts. In-depth screening and judgment was made for meeting the eligibility for being selected using PRISMA diagram by three researchers as per the inclusion and exclusion criteria. We extracted, collated and synthesized data on participants, interventions, outcomes, methods and settings. Data abstraction table was developed to summarize each selected papers to answer the research question which was defined using PICO frame.

Results: The research resulted in 354 full texts, of which 111 papers met all inclusion criteria were included and analyzed. Despite variations among studies, dimensions of HR practices, in a single or bundles form of skills-enhancement, motivation-enhancement- and empowerment-enhancement practices, and aspects of health workforce outcomes (e.g. job satisfaction, turnover, task performance, motivation) patient experiences(satisfaction, clinical outcomes), and hospital performance (e.g., quality of care, efficiency, waiting time, staff shortage, safety) were identified. The overwhelming majority of studies shown variations in implementing HRM practices which led to variations in work performance of health workforce or employees (individually or teams) and patient outcomes among hospitals within and among the countries. Almost all studies identified some kind of link between HRM practices and performance.

Conclusions: Despite variations were reported across studies, evidences show that effective HRM

practices are instrumental for better capacity of employees and hospitals to deliver quality healthcare. The study also identified that poor HRM practices led to poor performance skills of employees, patient outcomes were not found according to the international standards. There is a room for improvement of HRM practices, which intern requires interventions to improve employee performance in hospitals and ultimately enhance patient outcomes. Therefore, policy makers and health systems planners should design and implement sound HR policy and adapt contextualized HRM model or practices to enhance employee outcomes and improve patient and organizational outcomes in hospital sector in sub-Saharan Africa. For better generalization and understanding, we strongly suggest empirical study of examining the association between HRM practices, employee performance, patient outcomes and hospital performance in a selected country/ies of Africa.

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Intestinal Parasitosis in Relation to CD4+T Cells Levels and Anemia among HAART Initiated and HAART Naïve Pediatric HIV Patients in Model ART Center, Addis Ababa, Ethiopia

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Background: Intestinal parasites (IPs) are major concerns in most developing countries where HIV/AIDS cases are concentrated and almost 80% of AIDS patients die of AIDS-related infections. In the absence of highly active antiretroviral therapy (HAART), HIV/AIDS patients in developing countries unfortunately continue to suffer from the consequences of opportunistic and other intestinal parasites. The aim of the study was to determine the prevalence of intestinal parasites in relation to CD4+ T cells levels and anemia among HAART initiated and HAART naïve pediatric HIV patients in a Model ART center in Addis Ababa, Ethiopia.

Methods: A prospective comparative cross-sectional study was conducted among HAART initiated and HAART naïve pediatric HIV/AIDS patients attending a model ART center at Zewditu Memorial Hospital between August 05, 2013 and November 25, 2013. A total of 180 (79 HAART initiated and 101 HAART naïve) children were included by using consecutive sampling. Stool specimen was collected and processed using direct wet mount, formol-ether concentration and modified Ziehl-Neelsen staining techniques. A structured questionnaire was used to collect data on socio-demographic and associated risk factors. CD4+ T cells and complete blood counts were performed using BD FACScalibur and Cell-Dyn 1800, respectively. The data was analyzed by SPSS version 16 software. Logistic regressions were applied to assess any association between explanatory factors and outcome variables. P values < 0.05 were taken as statistically significant.

Results: The overall prevalence of IPs was 37.8% where 27.8% of HAART initiated and 45.5% of HAART naïve pediatric HIV/AIDS patients were infected (p < 0.05). *Cryptosporidium* species, *E. histolytica/dispar*, Hook worm and *Taenia* species were IPs associated with CD4+ T cell counts <350 cells/μL in HAART naïve patients. The overall prevalence of anemia was 10% in HAART and 31.7% in non-HAART groups. Hook worm, *S. stercoralis* and *H. nana* were helminthes significantly associated with anemia in non-HAART patients [AOR, 95% CI: 4.5(1.3, 15.2), P<0.05]. The prevalence of IPs in non-HAART patients was significantly associated with eating unwashed/raw fruit [AOR, 95%CI: 6.3(1.2, 25.6), P<0.05], open field defecation [AOR, 95%CI: 9.3(1.6, 53.6), P<0.05] and diarrhea [AOR, 95%CI: 5.2(1.3, 21.3), P<0.05]. IPs significantly increased in rural residents [AOR, 95%CI: 0.4(0.1, 0.9, P<0.05)].

Conclusion: The overall prevalence of intestinal parasites significantly differed by HAART status and *Cryptosporidium* species were found only in HAART naïve patients with low CD4+ T cell counts. Anemia was also more prevalent and significantly associated with IPs in non-HAART patients. This study identified some environmental and associated risk factors for intestinal parasitic infections. Therefore, Public health measures should continue to emphasize the importance of environmental and personal hygiene to protect HIV/AIDS patients from infections with intestinal parasites and maximize the benefits of HAART.

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The burden of HCV and HIV co-infection among pregnant women in Ethiopia: a single-center experience

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Background: Both Hepatitis C virus (HCV) and Human immunodeficiency (HIV) infection is a leading cause of major burden to public health worldwide. Very particularly, the seriousness and impact is considered to be great in Africa continent. Despite their devastating consequences, there are only very limited research based evidence on HCV and HIV co-infection ; particularly, in Ethiopia. The major aim of the study was to evaluate the prevalence of and examine the potential risk factors for HCV and HIV infection among pregnant women seeking antenatal care in Addis Ababa, Ethiopia.

Methods: Facility- based cross-sectional study was conducted during July to October 2014 to investigate HCV and HIV co-infection and associated risk factors among pregnant women at Public hospital Addis Ababa Ethiopia. Structured questionnaire was used to gather information on socio-demographic characteristics and risk factors. Serum sample was used to test anti-HCV and HIV antibody. Data was analyzed, organized and managed using descriptive statistics. Association of exposure variables with HCV status was evaluated using bi-variate and multivariate logistic regression. P-value < = 0.05 declared as cut-off value showing significant association.

Results: The prevalence rate of anti-HCV positivity was 2 (0.93%). HCV positivity was higher among participants who have attended primary school. Higher age specific HCV (3.2%) and HIV prevalence was observed among participants in the older age group (30+ years). Screening for HIV indicated that 9 (4.2%) of the participants were positive for HIV and from the 9 HIV positive cases, 1 participant was positive for Anti- HCV antibody. The prevalence of HIV/HCV co-infection was 11%. Statistically significant association was not observed between the assessed participant socio-demographic characteristics and risk factors for HCV and HIV infections.

Conclusion: The research finding noted that the prevalence of HCV was low. However, the study populations were exposed for potential risk factors. Hence, we should work aggressively to further strengthen the prevention of mother-to-child transmission of the deadly virus.

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Etiological study of severe acute respiratory infection in Chinese adults

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Background: Etiological study of severe acute respiratory infection in Chinese adults (China-SARI study) was a prospective, multicenter, active surveillance study, which is a part of International Severe Acute Respiratory and Emerging Infection Consortium (ISARIC) surveillance network. At present, there are 45 hospitals taking part in this network, covering 20 provinces, autonomous regions and municipalities. By collecting the clinical and experimental information of SARI cases and building a bank for clinical samples, this platform can monitor and forewarn the occurrence, treatment and pathogenic characters of SARI. It can help to improve the ability of SARI monitoring in China and promote the molecular epidemiologic research of SARI and associated pathogens. it is also meaningful in providing a way to discover the pathogens of emerging and orphan infection diseases. We also set up a website named "China Severe Acute Respiratory-tract Infection Surveillance Platform (CSP)", which was online in January, 2013. As well as, the website is bilingual to enhance international communication and cooperation.

Methods: Up to now, 45 hospitals have joined this network, including 27 tertiary hospitals and 18 secondary hospitals. The data of adult cases of severe acute lower respiratory tract infection (including the cases of severe pneumonia) have been inputted in the China-SARI Information Management System. the lower respiratory tract specimens (tracheal aspirate and bronchoalveolar lavage) and blood specimens were collected from these patients. The lower respiratory tract

specimens were examined using multiplex real-time reverse transcription polymerase chain reaction (RT-PCR), which can detect many virus including influenza virus (IFV A and B), human coronavirus (CoV OC43, 229E, NL63 and HKU1), parainfluenza virus (PIV 1-4), metapneumovirus (MPV A and B), rhinovirus (HRV), enterovirus (EV), respiratory syncytial virus (RSV A and B), adenovirus(ADV), bocavirus (BoV) and parechovirus. Loop primer-mediated isothermal amplification (LAMP) targeting *Streptococcus pneumoniae*, *Staphylococcus aureus*, *Haemophilus influenzae*, *Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Acinetobacter baumannii*, *Stenotrophomonas maltophilia*, *Legionella pneumophila*, *Mycoplasma pneumoniae*, *Chlamydia pneumoniae* and *Mycobacterium tuberculosis* were performed on the specimens simultaneously.

Results: From January 2013 to January 2016, we obtained 302 patients who had radiographic evidence of pneumonia and whose lower respiratory tract specimens were available for both bacterial and viral testing. The median age of the patients was 56 years (range 16 to 97). Pathogen was detected in 65%, one or more viruses in 16%, bacteria and atypical pathogen in 41%, mixed infection in 8%. The most common pathogens were *Mycoplasma pneumoniae* (in 14% of patients), rhinovirus (8%), influenza virus (8%), *Klebsiella pneumoniae* (8%) and *Streptococcus pneumoniae* (7%).

Conclusions: *Mycoplasma pneumoniae*, rhinovirus, influenza virus, *Klebsiella pneumoniae* and *Streptococcus pneumoniae* are usually found in adult SARI. No pathogen was detected in 35% of patients although using molecular diagnostic tests. The findings contribute baseline data on SARI study in China.

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Identification of Dengue and Chikungunya cases among suspected cases of Yellow fever in the Democratic Republic of Congo

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For more than 95% of acute febrile jaundice cases identified through surveillance for yellow fever, a re-emerging arthropod-borne viral disease, no etiological exploration is ever done. The aim of this study was to test for other arthropod-borne viruses that can induce the same symptoms in patients enrolled in the yellow fever surveillance in the Democratic Republic of the Congo (DRC). Of 652 patients included in the surveillance of yellow fever in DRC from January 2010 to January 2012, 453 patients that tested negative for yellow fever virus IgM antibodies were selected for the study. Real-time PCR was performed for the detection of dengue, West Nile, Chikungunya, O'nyong-nyong, Rift Valley fever, Zika and yellow fever viruses. The average age of patients was 22.1 years. We reported sixteen cases (3.5%) of dengue (serotypes 1 and 2) and two cases (0.4%) of Chikungunya. Three patients were co-infected with the two serotypes of dengue virus. Three cases of dengue were found in early July 2010 from the city of Titule (Oriental province) during a laboratory-confirmed outbreak of yellow fever, suggesting simultaneous circulation of dengue and yellow fever viruses. This study showed that dengue and Chikungunya viruses are potential causes of acute febrile jaundice in the DRC and highlights the need to consider dengue and Chikungunya diagnosis in the integrated disease surveillance and response program in the DRC. A prospective study is necessary to establish the epidemiology of these diseases

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Suspected Outbreak of Lassa Fever in Plateau State, North-central, Nigeria, 2011-2016: A Retrospective Assessment of Data.

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Background: Lassa fever is an acute viral hemorrhagic illness caused by the arenavirus, Lassa virus, which is endemic in West Africa. The reservoir of Lassa virus is a multimammate rat widely distributed across sub-Saharan Africa. Outbreaks have been reported in Nigeria since 2012. Plateau State and all neighboring States have consistently reported suspected cases annually since 2012. We analyzed the records with the following objectives:

- To describe and determine the extent of suspected measles outbreak
- To identify the population most affected and determine the annual trend in the suspected outbreak

Method: Line list of suspected Lassa fever cases in Plateau State (2011-2016), based on WHO case definition for suspected case was obtained. The variables recorded were LGA, age, sex, date of onset, outcome and severity. Descriptive epidemiology was performed with variables expressed in frequency, proportions and percentage to describe the outbreak. A line graph was used to demonstrate annual disease trend for the period.

Result: A total of 104 cases were reported with 11(10.6%) from neighboring States. Male constituted 53.8%(56) of cases and the mean age was 27 years. CFR was 21.2%. The epidemic curve shows an intermittent outbreak. Jos North recorded highest number of cases while Jos South recorded highest mortality. Only 71(68.3%) of cases were laboratory confirmed. Bivariate analysis showed odds of death of 1.95 (95% C.I=0.71-5.35) among males compared to females and when stratified by age, adjusted OR=0.89.

Conclusion: An intermittent outbreak (CFR of 21.2%) occurred between 2011 and 2016 in Plateau State. Cases clustered around November of the previous year and March of the following year. Males were mostly affected and the odd of death

among males compared to females was confounded by age.

Recommendations:

1. Effort should be made to confirm all suspected cases through prompt laboratory testing.
2. An analytical study should be conducted in the State to identify risk factors for the recurrent cases of Lassa fever in the State

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Prevalence of Toxoplasmosis and risks factors among pregnant women in semi-urban area : case of “cite-verte” health district, Yaounde Cameroon

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Background: Toxoplasmosis is a parasitic disease caused by toxoplasma gondii. infections with toxoplasmosis usually cause no obvious symptoms in adults. In those with weak immune system, severe symptoms may occur. if infected during pregnancy, congenital toxoplasmosis with birth defect or unwanted abortion may affect the children. we notice nowadays a new outbreak of this infection with a particular tropism in hot tropical region. In Cameroon, the prevalence of this infection differs across the country and depends on a number of risk factor. This survey was conducted to evaluate the speed of the prevalence and risks factors of toxoplasmosis among pregnant women at “cit -verte” health district, Yaounde Cameroon.

Methods: A cross-sectional, prospective study has been carried out from December to February 2016 at “cit -verte” health district, Yaounde, a semi-communal area in the Center Region of Cameroon. Toxoplasma Immunocomb IgM and IgG antibodies were simultaneous done at each participant after getting inform consent and the authorization of the head of district. Data were analysed with Epi info 4.0. $p > 0, 05$, the difference was statistically significant.

Results: We enrolled 34 pregnant Women aged between 17 and 45 years, mean age 27,2 (1,8. The prevalence of toxoplasmosis was 32, 4 (with 14, 7% (5/34) of IgM and 23,5% of IgG(8/34). The most represented age bracket was [17-27[with 47, 05% (16/34) and this same age bracket was the most affected 50% (8/16). Women at the first and third trimester of pregnancy were the most involved (40% each other). Besides, 55,55% of affected women got a cat against only 24% (6/25) of affected pregnant without (difference non statistically significant, $p>0.05$). 76, 5% (26/34) of pregnant were ignoring the existence of this disease and Food has been incriminated as a main factor of risk in the quasi totality of participant especially women eating meat sold along the street.

Conclusions: The prevalence of toxoplasmosis remain high in this study (32, 4%) due to the young age of these pregnant women, the term of pregnancy, the link with a cat, foods and the knowledge on the disease. So, we recommend to intensify the strategies of information, education and communication against the risk factors of transmission and why not to do the serological test of toxoplasma be financially accessible for all the pregnant women in Cameroun.

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The Church and Traditional Birth Attendants (TBAs) as twin pathways to delayed HIV testing of pregnant women in rural Nigeria

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Nigeria has the second highest estimated number of maternal deaths after India and responsible for 30% of the global burden of Mother-to-Child Transmission of HIV (MTCT). According to UNAIDS (2013), MTCT is the main route of paediatrics HIV infection. It accounts for over 90% of all paediatrics (children less than 15 years) infection and ranks amongst the highest number of new HIV infections in children in the world. A growing body of knowledge has mostly focused on the role of African church groups in hampering support to people living with HIV and AIDS and contributing to HIV/AIDS-related stigma.

This study is situated within the phenomenological research model which is centered on the lived experiences of those interviewed and employed a qualitative analysis that utilized semi-structured interviews conducted with healthcare staff and caregivers of HIV positive children (0-5 years) in Bori zonal hospital in Rivers State, Nigeria.

The methodological finding reveals that Churches have the best well organised and recognized community networks in Nigerian communities and consequently potentially exercise a great influence over them. Their constant moralistic attitudes, reinforcement of conservative gender ideologies and wholesome integration of health and faith into the ministry is influencing their flock's late uptake of HIV and AIDS-related services.

Traditional Birth Attendant (TBA) is also exacerbating the delayed HIV testing of pregnant women in the rural communities in Nigeria. With no formal training (but generally respected because they are elderly community women), TBAs play a vital part in maternal and child health by bridging the gap and support the delivery of babies in communities far removed from health facilities. By relying on child deliveries for sustenance, they see formal medical facilities as competitors.

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Aetiology of Hepatitis Among Jaundiced Patients Presenting to a Tertiary Hospital in Ghana

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Background: Viral hepatitis continues to play significant role in causing morbidity and mortality in sub-Saharan Africa. Apart from the few population based studies available, not many have investigated the burden of these viruses in jaundiced patients. Among the few studies, hepatitis E is the least studied among jaundiced patients. This study was aimed at describing the frequency, distribution and risk of the different hepatitis viruses among jaundiced patients reporting to the second largest teaching hospital in Ghana.

Methods: From November, 2015 to April, 2017, a cross-sectional study was conducted among jaundiced patients attending the Komfo Anokye Teaching Hospital. Between 3-5 ml of blood was collected from each patient and screened for various causes of viral hepatitis using both serologic and molecular-based assays. Environmental, socio-demographic and clinical information were also collected from patients and others extracted from their medical records.

Results: In the 155 patients recruited, hepatitis B was the most prevalent [54.2% (95% CI = 46.0% - 62.2%)] followed by hepatitis E [32.9% (95% CI = 25.6 - 40.9%)]. Most cases of hepatitis E occurred as co-infections with hepatitis B (18%), with the predominant clinical feature being hepatocellular carcinoma. Risk factor variable analysis showed middle and older aged individuals were more at risk of hepatitis B exposure whereas younger age groups (<18 years) were more at risk of hepatitis E virus infection.

Conclusion: Hepatitis viruses are still important in the viral aetiology of jaundice in Ghana. Hepatitis B and hepatitis E co-infections could play significant roles in causing severe disease. A more aggressive approach needs to be adopted in order to reduce the morbidity and mortality associated with hepatitis causing viruses in Ghana and other developing countries.

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Diagnostic Performance of Direct Wet Mount Microscopy in Detecting Intestinal Helminthes among Pregnant Women Attending ante-natal Care (ANC) in East Wollega, Oromia, Ethiopia

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Background: Although several diagnostic tests are available to diagnose intestinal helminths, the direct wet mount is commonly used as a reliable diagnostic method for the diagnosis of intestinal parasitic infections generally in Africa and particularly in Ethiopia. The aim of this study was to evaluate the diagnostic performance of direct wet mount microscopy in detecting intestinal helminths in pregnant women.

Materials and Methods: A cross-sectional study was conducted in five health centers of East Wollega Zone of Oromia Region, Ethiopia between November 2015 and January 2016. Pregnant women were selected consecutively using proportional stratified sampling. Stool specimens were collected and processed using direct wet mount and formol-ether concentration techniques to detect intestinal helminths. Sensitivity, specificity, positive predictive value, negative predictive value, test efficiency and kappa agreement of direct wet mount microscopy was determined using formol-ether concentration (FEC) method as a gold standard. Data were entered and analyzed by SPSS version 20 software.

Results: The total prevalence of intestinal helminths was 18.8% (70/372) by direct wet mount microscopy and 24.7% (92/372) by FEC technique ($P < 0.001$). The sensitivity, negative predictive value (NPV) and test efficiency (TE) of direct wet mount microscopy in diagnosing intestinal helminths was 76%, 92.7%, and 94%, respectively. The sensitivity of direct wet mount microscopy was very low in detecting ova of *Hymenolepis nana*. The two methods showed excellent agreement in detecting ova of Hookworm and *Ascaris lumbricoides* (Kappa > 0.81) but they fairly agreed in detecting ova of *Hymenolepis nana* (Kappa = 0.39).

Conclusion: Intestinal helminths were underdiagnosed and the total diagnostic performance of direct wet mount microscopy was significantly poor in detecting intestinal helminths as compared to FEC technique. Routine use of FEC method is recommended for the diagnosis of intestinal helminths in pregnant women.

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Tuberculosis Treatment Response and the Efficacy of Anti-tuberculosis Chemotherapy can be Effectively Monitored and Evaluated by the Interferon Gamma Release Assays

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Tuberculosis (TB) is a leading cause of death and become one of the major threats to the world. The emergence of drug-resistant strains of *Mycobacterium tuberculosis* (Mtb) exacerbates the public health impact. Monitoring and Evaluation (M&E) of chemotherapeutic responses would contribute to the control of drug resistance. This study used Interferon-gamma release assay (IGRA) to evaluate TB treatment response and the efficacy of anti-TB chemotherapy. Institutional based prospective longitudinal cohort study design was used. Patients either positive for Acid Fast Bacilli Stain (AFB), culture and/or GeneXpert MTB/RIF assay were recruited for the study and evaluated by IGRA. The recruited 21 patients had the mean age of 35.5, median 33 and range of 23-56 years. All patients were cured after treatment. The mean concentration of the IFN- γ response showed decreasing trends from baseline (mean+SD, 2.09+1.09) to the end of the treatment (mean+SD, 0.23+0.20). The individual baseline IFN- γ value had wider differences and at the end of their treatment it showed lower with a narrowed difference. Repeated measurements of the IFN- γ had been evaluated for each time points shown statistical significance only between two pairs ($P < 0.001$). In this study, IFN- γ response to TB chemotherapy was not affected by any of the socio-demographic factors of the participants ($P > 0.05$).

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Cryptococcal antigenemia among HIV infected patients at a Referral Hospital, Northwest Ethiopia

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Background: Cryptococcosis remains as one of a common opportunistic fungal infection among HIV infected patients living in Sub-Saharan Africa, including Ethiopia. The magnitude of the disease at Felege Hiwot Referral Hospital (FHRH) in particular and in Ethiopia at large is not well explored.

Methods: A retrospective document review was done on records of 137 HIV infected patients at who visited the FHRH ART clinic from 1 Sep to 30 Dec 2016 and had registered data on their sex, age, CD4 count and cryptococcal antigen screening result were included in the study. The cryptococcal antigen (CrAg) detection was done by the IMMY CrAg[®] LFA (Cryptococcal Antigen Lateral Flow Assay) kit from patient serum as per the manufacturer instruction. All data were entered, cleared, and analyzed using the SPSS v20. Descriptive data analysis and chi square was calculated to assess factors associated with cryptococcal antigen. Statistical significance was set at p-value less than or equal to 0.05.

Results: Most of HIV patients were females at 75 (54.7%). The median age of the participants was at 32.0 years (ranged: 8-52 years). The mean CD4 count was at 51.8 with SD of 26.3 (range 3-98). All the patients were HIV stage IV. The proportion of positive cryptococcal antigen from serum test was at 11.7% (95% CI: 7.3-18.1%). The IMMY CrAg[®] LFA result was found statically associated with patient sex ($p = 0.045$). However, it was not associated with patient age group and the CD4 count ($P > 0.05$).

Conclusions: This study provided baseline data on the magnitude of cryptococcal antigenemia among HIV positive patients that is not touched before in the studied area. The results of the study showed this opportunistic fungal infection is an important health concern among HIV patients. Further studies with sound design employing adequate sample size should be considered.

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Seroprevalence and Molecular Detection of Hepatitis E Virus (HEV) Among Pregnant Women in Port Sudan State, Sudan

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Background: The hepatitis E virus, which occur in epidemic and sporadic form, It is one of the major public health problems encountered in developing countries Most outbreak are associated with poor personal hygiene and water borne infections. HEV infection in pregnant women is more common and more often fatal in third trimester.

Objective: This cross sectional study aimed to determine the seroreactivity, and molecular HEV RNA positively among pregnant women in Port Sudan city, Sudan ,during the period November December 2015.

Methods: Ninety serum samples were collected from pregnant women in obstetric clinics of Port Sudan. Samples were tested for IgG and IgM antibodies using Enzyme Linked Immunosorbent assay (ELISA) and HEV RNA using Real-time PCR.

Results: The results showed that 95.6 % (86/90) of the samples had HEV IgG and 3.3% (3/90) had HEV IgM. HEV RNA was detected in 4.4% (4/90) by using Real time RT-PCR.

Conclusion: The high prevalence of HEV pregnant women in Port Sudan state was documented through detection of HEV-specific antibodies and viral RNA.

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Leprosy case detection campaign in Islands of Lakshadweep, India

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Leprosy Case Detection Campaign (LCDC) was a good initiative by the government of India for bringing the hidden case from the society and early intervention for the cure. It was implemented by Central Leprosy Division with following objectives to detect the hidden leprosy cases and detect them early so as to stop the community transmission of disease, need to involve the Stake holder.

The campaign was based on house to house visit by ASHA and male volunteer, examination of house hold members and detects the suspect. The suspects detected by team confirmed by Medical Officers. The team member has enquired about signs and symptoms and physical examination of family member, followed by recording in tally sheet and house marking on door of house. If all members are available for examination that house will marked as L/Date and if some family member are not available or house was locked, this house will be marked as X/Date. The team members will revisit 'X' house and do examination of remaining family members, convert that house to 'L' house to get maximum examination. The suspected cases during campaign were listed and confirmed by trained Medical Officers.

As a part of these campaigns of October- November 2017, populations of 16,907 were screened and 402 suspects were noticed. Out of these 402 suspects, 8 cases were confirmed in two island kadamath and Andrott. Out of 8 cases, MB cases and PB cases were 3 and 5 respectively.

This shows that active screening by these campaigns helps in bringing the hidden cases in the community and helps in earlier treatment and prevention of disability and checks the transmission of the infectious agent by treating as per the WHO guidelines.

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Chronic Hepatitis C Virus infection in young adult injecting drug in south - west Nigeria

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Background: Hepatitis C Virus (HCV) infection, clearance, and re-infection are best studied in injection drug users (IDUS), who have the highest incidence of HCV and are likely to represent most infections.

Methods: A prospective cohort of HCV-negative young IDUS was followed up from march 2012 to December 2016 in south-west Nigeria to identify acute and incident HCV and prospectively study infection outcomes.

Results: Among 1,481 young IDUS screened, 931 (61.4%) were HCV negative, and 550 (71.1%) of the 76 were enrolled into follow-up. Cumulative HCV incidence was 23.7/100 person-years of observation (95% confidence interval [ci], 21.5–31.6). Of 135 acute/incident HCV infections, 95 (70.4%) were followed; 20 (21.1%) of the 95 infections cleared. Women had a significantly higher incidence of viral clearance than men did (age-adjusted hazard ratio, 2.91 [95% ci, 1.68–5.03]) and also showed a faster rate of early HCV viremia decline ($p < .01$). The estimated re-infection rate was 24.6/100 person-years of observation (95% ci, 11.7–51.6). Among 7 individuals, multiple episodes of HCV re-infection and re-clearance were observed.

Conclusions: Females show demonstrative differences in the rates of viral clearance and kinetics of early viral decline in the large sample of young IDUS. Recurring infection and re-clearance suggest possible protection against persistent infection in young adults injecting drug in south-west Nigeria.

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A training curriculum for conducting clinical research during outbreaks

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Background: Patients are at the heart of every infectious disease outbreak and patient-centred research is essential to generate evidence to improve the care of individual patients and to guide the public health response to the outbreak. The challenges of clinical research during outbreaks cannot be adequately met by current approaches, which usually require long lead-times, predictable epidemiology and fixed research assets. The Clinical REsearch During Outbreaks (CREDO) is a training curriculum developed to strengthen the capacity of research teams in low- and middle-income countries to conduct clinical research on emerging and epidemic-prone infectious diseases. The programme is being developed by TDR, the International Severe Acute Respiratory and Emerging Infection Consortium (ISARIC), the University of Oxford and the UK Public Health Rapid Support team, funded by the UK Government. The primary target users of CREDO are multidisciplinary research teams (clinicians, nurses, biomedical scientists, data and study managers) in Low and Middle Income Countries that are susceptible to outbreaks. A pilot of the CREDO training was conducted between March and August of 2017.

Methods: CREDO uses a learning approach that blends face-to-face teaching and on-line training tools. The training modules cover: 'evidence-based' medicine for epidemic infections; rapid 'evidence-needs' appraisal; research study planning; study design; logistics and operational planning; data management; ethics; communications and engagement; special groups (children, pregnant women, mother/child); and good clinical practices. Eighteen participants from four multi-disciplinary teams from Côte d'Ivoire, Ethiopia, Ghana and Uganda were selected for the CREDO pilot. The training began with an initial two-day workshop held in March 2017 in Entebbe, Uganda. Participants completed the online training modules

between March and August. At the final workshop, held in July in Addis Ababa, Ethiopia, the teams participated in two outbreak research scenarios, where they developed and presented their design for a theoretical observational clinical study and a theoretical clinical trial. Course and workshop evaluations were done in a semi-structured format to give participants the opportunity to give ample feedback. All course evaluations were done anonymously to encourage candid responses.

Results: The workshops were well received but many participants felt that two days did not allow enough time to thoroughly cover all of the material. Participants were asked to rate their level of confidence with the 19 CREDO learning objectives. Before the training, only 20% of participants considered themselves to be 'confident' or 'very confident', this increased to 91% following the CREDO training. Overall, participants were satisfied with the CREDO training and comments were largely positive.

Conclusions: The 2015 Ebola virus outbreak in western Africa exposed a major gap in research capacity. The CREDO curriculum was well received and the training materials received good evaluations from the pilot participants. The CREDO training curriculum will contribute to developing a strong, sustainable capacity in the countries that are the most vulnerable to outbreaks.

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Prevalence and Risk Factors for Catastrophic Health Expenditure Due to Tuberculosis in Kaduna State, North-Western Nigeria, 2016

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Background: Despite providing free tuberculosis (TB) diagnosis and treatment, TB patients and their households still incur financial hardship while seeking for care. Such expenditure at times may become catastrophic. The World Health

Organization (WHO) through the End TB Strategy has set a target of eliminating catastrophic health expenditure (CHE) due to TB by 2020. However, there is a dearth of information on the prevalence of CHE due to TB in Nigeria. We therefore assessed the prevalence and risk factors for CHE due to TB in Kaduna State, North-Western Nigeria.

Methods: We conducted a cross-sectional study in 2016 recruiting 274 pulmonary TB patients using a multi-stage sampling technique. Data was collected using a pre-tested semi-structured interviewer administered questionnaire adapted from a tool developed by United State Agency for International Development USAID and analyzed using SPSS version 23.0 software. CHE was measured using a threshold of out of pocket health expenditure > 40% of non-food expenditure. Bi-variate analysis and multi-variate analysis were used to identify risk factors by estimating the adjusted odds ratio (AOR) and 95% confidence interval (CI).

Results: Of the 274 TB patients, 171 (62.4%) were males, 41 (15.0%) were unemployed and 218 (79.6%) were within the first and second wealth quintiles. The prevalence of CHE due to TB in Kaduna State was 17.2%. TB patients were at a higher risk of incurring CHE when they are unemployed (AOR = 2.31; 95% CI, 1.02-5.23), had TB diagnosed more than two weeks after first time treatment was sought (AOR = 2.56; 95% CI, 1.19-5.53), collected drugs more frequently (AOR = 2.82; 95% CI, 1.36-5.84) and had sputum smear negative TB (AOR = 2.70; 95% CI, 1.03-7.08).

Conclusion: The prevalence of CHE due to TB in Kaduna State was above the target set by WHO and is associated with unemployment, delay in diagnosis of TB, frequent collection of TB drugs and having sputum smear negative TB. We recommend that the National TB Control Programme increase efforts such as reducing frequency of drug collection and diagnosing TB early to reduce CHE due to TB.

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The response to the plague epidemic in Mahajanga Madagascar, good practices

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Plague has been discovered in several regions of Madagascar for decades within endemic form. Every year, 2 districts of the Boeny Region are declared plague areas, Mahajanga 1 and Mahajanga 2. Epidemic cases and sporadic cases have occurred for years, then appears the epidemic of urban pneumonic plague of this year 2017.

After the alert at the national level, the response to the epidemic in Mahajanga 1 took off after the declaration of cases of pneumonic plague of Antananarivo and Tamatave. The Regional Crisis Cell coordinated all the activities of prevention, surveillance, care, communication, the establishment of sanitary control at the airport, port, entrance of the city.

Sixteen cases of bubonic plague and or suspected bubonic plague have been reported. The last case admitted to the hospital was on October 21st, 2017. No case of pneumonic plague was detected. There was an appropriation of the media team, and of all stakeholders, the effectiveness of the technical and financial support from the partners, the efficiency and speed of the decisions taken by the Regional Crisis Cell Staff. Interventions by using Kartman's Box have yielded results on the occurrence of new cases of bubonic plague.

A strong and permanent vigilance deserves to be instituted because the major risk for the city of Mahajanga 1 is the importation of pneumonic plague.

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Vaccination as a Means of Control of Parasitic Diseases

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Parasitic infections are responsible for the etiology of many pathological conditions in both humans and animals globally. The human productivity and animal production losses incurred as a result of these varied disease conditions are hard to adequately quantify; and this is despite the use of the traditional approaches at controlling and mitigating the effects of parasitic agents. The use of vaccine as a one-step approach in the control of parasitic infections is very economical and highly sustainable, and it's also very efficient and highly viable. Many animal vaccines are already in use, and many more are still being researched. However, researches and clinical trials are still ongoing towards the successful development of a viable human parasite vaccine. Also, many emerging and novel approaches are being explored towards the successful development of both human and animal vaccines. This review identifies the use of vaccines as a one-step solution to the emerging inadequacies of the traditional methods of parasite control; and the potential possibilities provided through molecular advances in vaccine development.

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Management of people living with HIV at the Tivaouane Hospital (Senegal) from 2008 to 2016 and evaluation of HIV early warning indicators.

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Objectives: To describe the epidemiological, clinical and evolutionary paraclinical aspects of Living with HIV (PLHIV) followed at Tiva-oune Hospital and to evaluate HIV early warning indicators in this district.

Methods: Retrospective cross-sectional and descriptive study on PLHIV followed at the Tivaouane hospital from January 2008 to December 2016.

Results: We collected 360 positive HIV patients who came mainly from Tivaouane-ville. A female predominance (71%) is a sex ratio (F / M) of 2.39 was noted. The mean age was 42.10 ± 12.8 years. Digestive candidiasis (33.8%) and tuberculosis (23%) were the most common opportunistic infections.

The mean CD4 count was 341.089 ± 295.223 / mm³. The patients were on tritherapy combining two nucleotide analogues of reverse transcriptase associated with a non-nucleoside analogue of reverse transcriptase in 53.6% of cases or associated with a protease inhibitor in 17.1%. During our study period, 95 patients were lost to follow-up (26.4%) and 71 died (19.7%).

Regarding IPA, only the years 2010 and 2012 recorded prescribing rates of 100%. The percentage of patients lost to follow-up was less than 20% throughout the study period. Virtually all patients were retained on first-line ART at 12 months of treatment. All patients (100%) withdrew their ARV drugs on time. No stock-outs of different classes of ARVs were noted during the study period.

Conclusion: At the end of this study, we recommend improving the quality of care for people living with HIV at the Tivaouane hospital and establishing a regular follow-up of the IPA to minimize the occurrence of resistance which is at the origin of therapeutic failures.

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Infection Prevention and Control Practices in a Treatment Centre during a Lassa Fever Outbreak in Southwestern Nigeria, June - 2017

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Background: Lassa fever (LF) is an acute, highly communicable viral haemorrhagic disease. Person-to-person spread occurs by inhalation or direct contact with blood, vomitus, urine, saliva, and other body fluids of an infected patient. Infection Prevention and Control (IPC) is a quality essential in healthcare facilities for the wellbeing and safety of patients, staff, visitors and all who come within the scope of activities. Federal Medical Centre, Owo is the designated LF treatment center in Ondo State. We assessed IPC practices in this facility following report of increased LF cases.

Methods: We selected participants by simple random sampling and assessed their knowledge of LF and IPC by administering a pre-tested semi-

structured questionnaire. We employed purposive sampling technique to assess basic IPC requirements in key units in the facility. Correct answer was awarded one mark and wrong answer zero. Score was considered as good: $\geq 75\%$, fair: 50-74% and poor: $< 50\%$. We calculated odds ratio and confidence intervals to determine predictors of knowledge scores.

Results: Mean age of the 50 healthcare-workers interviewed was 38.9 ± 7.2 years. Thirty two (64.0%) were males. Prevalence of good knowledge on IPC precautionary measures was 82% among respondents while 76% and 58% had good knowledge on LF clinical features and LF epidemiology respectively. Age ≥ 40 years (OR: 4.4 95%CI: 1.0-18.3) and previous IPC training (OR: 4.7 95%CI: 1.0-22.9) were both significantly associated with good knowledge of IPC precautionary measures. The hospital had a central incinerator and every unit had a waste bin. However, color-coded waste bins were inadequate in quantity, red, 4 (13.8%); yellow, 6 (20.7%); black, 9 (31.0%) and wastes were not segregated.

Conclusion: Significant number of staff had good knowledge on IPC. However, knowledge of LF epidemiology skewed towards those whose roles were related to management of LF cases. We recommended more awareness on IPC practices and improved waste management.

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Xpert MTB/RIF Assay for Detection of Rifampicin-Resistant M. tuberculosis from Presumptive Drug Resistance Tuberculosis Patients in Ethiopia

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Background: Rifampicin is a potent first line drug for treatment of M. tuberculosis and acts by inhibiting bacterial DNA-dependent RNA polymerase, encoded by the RNA polymerase gene (rpoB). Resistance to rifampicin has mainly been associated with mutations in the rpoB gene. Xpert[®] MTB/RIF (Cepheid, Sunnyvale, CA, USA) is real-time PCR technology that uses molecular beacons to detect

rifampicin resistance in the *rpoB* gene. In the current study, we aimed to assess the accuracy of Xpert MTB/RIF for detection of rifampicin-resistance *M. tuberculosis* in pulmonary tuberculosis (TB) patients in Ethiopia.

Methods: A cross-sectional study was carried out at Mycobacteriology Research Center of Jimma University in Southwest Ethiopia. A total of 67 smear-positive sputum specimens collected from pulmonary TB patients with increased suspicion of drug resistance were tested by GenoType MTBDRplus line probe assay and Xpert MTB/RIF tests.

Results: Of 67 pulmonary TB patients, 21 (31.3%) were multidrug resistant TB (MDR-TB) (resistant to both rifampicin and isoniazide). Xpert MTB/RIF detected rifampicin-resistance in 23 (34.3%) pulmonary TB patients, of these 22 were also confirmed to be rifampicin-resistant by line probe assay. In addition, 21 (91%) Xpert MTB/RIF-rifampicin-resistant cases were confirmed as MDR-TB cases, making rifampicin-resistance a good surrogate marker of MDR-TB in Southwest Ethiopia. Probe E related mutations (codon 447-452) was the most common *rpoB* genetic mutation observed in 87% of rifampicin-resistant strains, suggesting successful transmission of these strains in Ethiopia. Compared to line probe assay, Xpert MTB/RIF detected all rifampicin-resistance cases correctly with 100% sensitivity and 97.8% specificity.

Conclusions: The high sensitivity and specificity of Xpert MTB/RIF for rifampicin-resistance detection support its use as an initial diagnostic test for drug resistance TB. Implementation of Xpert MTB/RIF for direct diagnosis of rifampicin-resistance would be of great benefit in adapting treatment regimens and limiting transmission of drug resistant strains.

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Detection of Rifampicine resistance mutations on *rpoB* gene in *Mycobacterium tuberculosis* usinf Xpert MTB/Rif : A retrospective Study in Kinshasa,DRC

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Background: The DRC is one of the 30 countries that pays the heavy tribute of the TB with 120 508 cases notified in 2015; and currently, the MDR-TB represents a major challenge with an impact of 13 cases for 100 000 inhabitants according to the report of the WHO (2015). Since OMS have recommended the GeneXpert® MTB/RIF(Xpert) like initial test of diagnosis of the TB and the precocious detection of the RR-TB, several studies have determined the variable prevalence of rifampicin resistance mutations in MTB strains.

This survey aims to value frequency of MDR-TB among presumed patients RR-TB and to determine the frequency of the probes implied in the detection of the mutations on the gene *rpoB* in Kinshasa.

Methods: It is about a retrospective survey led within the National Laboratory of Reference of the Mycobacteria (NLR) of Kinshasa, in DRC. The data of the Xpert tests done from January 01, 2016 to July 31, 2017 have been collected then exported on Microsoft Excel 2010, treated and analyzed.

Results: Of 2172 Xpert test done, 800 (36.8%) were MTB detected with 114 (14.2%) RR-TB. The probes associated to the detection of mutations on *rpoB* Gene presented themselves as follows : E (80/114), B (18/114), D (14/114), A (2/114) and no resistance to the rifampicin was associated to the C probe. Any sample had presented a combination of probe in the detection of the resistance to the rifampicin. Of 114 RR-TB, 64 have been put in culture and 13 were confirmed MDR-TB in DST, with a frequency of 0.6%.

Conclusion: The Xpert test executed in NLR in Kinshasa city permitted to detect to 70% the E probe as the one detecting the more of mutations on the gene *rpoB* with at 0.6% frequency of MDR-TB

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Characterization of HIV-1 Genetic Diversity and drug resistance-associated mutations among treatment-naïve individuals newly infected in Morocco

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Background: Human immunodeficiency virus type 1 (HIV-1) is the causative agent of AIDS. The prevalence of HIV-1 in Morocco remains low (<0.14%). However, a program to fight AIDS was established early, when the first AIDS case was identified in 1986 in our country. Despite significant progress in HIV-1 prevention and treatment, the emergence of viral resistant strains is one of the main impediments to antiretroviral therapy. The aim of the present study was the monitoring the evolution of circulating HIV-1 strains in Morocco and to adapt the care of people living with HIV/AIDS by epidemiological surveillance of the emergence of resistance mutations (DRMs) in treatment-naïve HIV-infected during the period 2011-2015.

Methods: The viral protease (Prot) and reverse transcriptase (RT) partial regions were amplified and sequenced to determine subtypes and potential DRMs. HIV-1 subtypes were determined by phylogenetic analysis of Prot region sequences. Drug resistance mutations were defined according to the International AIDS Society mutation lists and the National Agency for AIDS Research (ANRS) algorithm.

Results: Subtype determination revealed that B variants were the most prevalent (44.4%) followed by CRF02_AG (37%). These 2 strains B and CRF02_AG accounted for 81.4% of all circulating viruses in Morocco. Moreover, from 2004 to 2015 a drift of circulating HIV-1 strains with the progressive increasing dissemination of HIV-1 non-B subtypes among Moroccan drug-naïve HIV-infected individuals, mainly CRF02_AG variants was

observed. Analysis of drug-resistance mutations showed that 97.5% of samples harbored at least one PI resistance-associated mutation. High-level resistance associated mutations to the PI drug class were identified at 2.47% prevalence. I54V was detected in one specimen, D30N in one patient and N88D mutation in two specimens. Two transmitted NNRTI major resistance mutations K103N and M230V were found in two patients with prevalence of 2.56%. This data showed also an emerging prevalence of NNRTI major resistance mutations and a significant decrease in the prevalence of protease inhibitors (PIs).

Conclusions: Our results may contribute to the improvement of the treatment strategies and in HIV-1-infected patients in Morocco and also highlight the importance of HIV-1 molecular epidemiology surveillance in Morocco.

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Determination of Human Immunodeficiency Virus Type-1 and allied Subtypes in Sudan

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Background: Human Immunodeficiency Virus-1 (HIV-1) is the causative agent of an unresolved worldwide pandemic that has had enormous social, political and economic impact since its emergence. Transmission of HIV-1 is still rapidly spreading despite identification over 33 years ago and an immense worldwide research effort to counter it.

Objectives: The aim of this study is to determine the HIV-1 genotype and subtypes that cause AIDS in Sudan.

Methods: Samples were investigated and analyzed in three different laboratories; two in Sudan and the third one in Kenya, the Central Lab of Omdurman Military Hospital, Department of Microbiology, Virology Lab of Faculty of Medicine University of Khartoum and Kenya Medical Research Institute (KMRI) -Virus Research Center- Nairobi Kenya.

Results: HIV-1 was detected by RT-PCR at the virology lab and the result revealed (188) samples (90.9 %) positive for HIV-1 (12) samples (9.1%) were negative for HIV-1. Concerning HIV-1 subtypes or

clades one hundred of EDTA samples were processed at Kenya Medical Research Institute (KMERI), Using heteroduplex Mobility Assay Technique (HMA) for env gene. Three subtypes were detected: subtype (A) (46%), Subtype (C) (33%) and subtype (D) (21%). CD4 count was estimated before antiretroviral therapy and three month after treatment, it was found that 71% were responding and 29% were not.

Conclusion: The study concluded that the detected HIV subtypes in Sudan were subtypes (A) (C) and (D). Most of the patients were responding to ARV.

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Five years malaria trend analysis of Woreta Health Center, Northwest Ethiopia

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Background: An estimated 60% of the Ethiopian population, living in 75% of the landmass, is at risk of contracting malaria at any time making it the leading public health problem in the country. The temporal analysis of malaria data on different health care systems could be important to evaluate the performance of malaria prevention programmes. The aim of this study was to determine the trend of malaria at Woreta Health Center (WHC), Northwest Ethiopia over a period of five years.

Methods: We analyzed the records of 8,057 presumptive malaria cases registered at WHC in the period of 2012 to 2016. The following patient data were retrieved for analysis; sex, age, residence, blood film (BF) microscopy result, type of malaria parasite identified, year and month when the patients visited WHC. Patients were suspected for malaria when they presented with fever and related clinical symptoms. Data were retrieved directly from laboratory registration log book using prepared data extraction sheet. Data were entered, cleaned and analyzed using SPSS version 23 for windows. Stepwise logistic regression was employed to assess the association between potential predictors and malaria infection; p value < 0.05 was considered to be significant.

Results: Among the total suspected patients registered, 4447 (55.2%) were females. The median age of the patients was at 25.0 years. Of the participants 5062 (62.8%) and 6176 (76.7%) were from rural settings and in the age group >15 years, respectively. The prevalence of malaria in each year was ranged from 4.1% to 6.7%. The overall prevalence of malaria among suspected cases was at 5.4% (95%CI: 4.9%-5.9%). The two most important species of malaria parasite identified were *P. falciparum* at 233 (53.7%; 95%CI: 49%-58.3%) and *P. vivax* at 184 (42.4%; 95%CI: 37.8%-47.1%). Relatively higher proportions of cases were documented in the month of November, December and June at 11.1%, 8.1% and 7.2%, respectively. Patients who visited the health center in the month of December were >4 times more likely to be infected as compared with those who came to the health center in September [AOR: 4.2, 95%CI (2.374-7.560)]. Females were 1.3 times more likely to be infected than males, [AOR: 1.3, 95%CI (1.101-1.638)]. Similarly, patients in the age group above 15 were 1.9 times more likely to be infected than children < 5, [AOR: 1.9 95%CI (1.498-2.455), p value 0.000].

Conclusions: In the studied area malaria remains as one of important causes of though the country is working towards malaria elimination by 2030. Hence, interventions to decrease the impact of the disease have to be evaluated and strengthened.

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Risk factors for Hepatitis B infection among pregnant women attending antenatal care in Kunene region, a case control study

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Background: The Hepatitis B is a viral infection is caused by Hepatitis B virus (HBV) which is a double stranded DNA virus, a member of the Hepadnavidae family of viruses. World Health Organization estimates that about 257 million people are living with Hepatitis B virus infection. Namibia has a high prevalence (9%) of Hepatitis B infection among

pregnant women and Kunene region prevalence of 8%.

Methods: We conducted an un-matched 2:1 case-control study to determine the associated risk factors for Hepatitis B infection among pregnant women in Kunene region. Cases were study subjects with reactive results for HBsAg or HBeAg and controls were study subjects with negative for both HBV markers. A total of 115 cases and 230 controls were interviewed. Mean age among the cases was 29 years range 16 – 45 (SD = 6.6), controls the mean was 26 years range 13 – 45 years (SD = 6.8). Bi-variate analysis was conducted to determine the odds ratios at 95% confidence level. Significant risk factors at p-value less than 0.05 were retained in multiple logistic regression models to determine significant associations.

Results: The multivariate analysis found that polygamous marriages (AO: 3.45; CI: 1.25 – 9.57; p= 0.02). Body piercing and scarification (AOR: 4.34; CI: 2.30 – 8.17; p= 0.00), body tattoos (AOR: 2.95; CI: 1.09 - 7.99; p= 0.03), history of abortion (AOR: 2.91; CI: 1.38 – 6.16; p= 0.00), STI's (AOR: 3.34; 95%CI: 1.92 – 5.80; p= 0.00) and previous history tooth extraction or any dental procedures (AOR: 2.03; 95% CI: 1.17 – 3.54; p = 0.01) was significantly associated with Hepatitis B infection. Gravidity, parity, HIV positive status and history of blood transfusion were not associated risk factor in multivariate model (p = >0.05).

Conclusions: Ministry of Health and Social Services in Kunene region should implement preventative strategies such as Hepatitis B screening, treatment, health education, infection control and hepatitis B vaccination for the general population.

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Viral load suppression rates among HIV infected adult patients on treatment in rural HIV clinics in South-Western Nigeria

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Background: In sub-Saharan Africa where genotypic drug resistance testing is rarely performed and poor adherence is blamed for the inability to achieve viral

suppression and treatment failure, programmatic approaches to preventing & handling these are thus essential. Hypothesis tested was antiretroviral therapy adherence effect on viral load outcome. This study was aimed at determining and monitoring HIV/AIDS disease progression using viral load to provide prognostic information and evaluate patients for viral suppression using the World Health Organization (WHO) guideline strategies.

Materials & Methods: This study was an observational longitudinal prospective cohort study of subjects living with HIV already initiated on antiretroviral therapy for at least six months, enrolled in health facilities across Ekiti State, Western Nigeria, during a 12-month observation period starting October 2016 till September 2017. Quantitative viral load analysis was done using Polymerase Chain Reaction, Roche Cobas Taqman 96 Analyzer. All data were statistically analyzed, using Statistical Package for the Social Sciences (SPSS), with multiple comparisons done using Post Hoc Bonferonni test.

Results: A total of 3920 (1005 males & 2915 females) subjects eligible for the study were recruited. Most of them are in the age range of 25 – 54 years, with a mean age of 39.35 ± 10.41 years. 3086 (78.7%) & 2363 (60.3%) of the subjects had viral suppression of <1000 RNA copies per ml and <50 RNA copies per ml respectively. The 834 subjects went through intensive adherence counseling optimized health care worker delivery model for three months and viral load test repeated three further months after, which made 3377 (86.1%) & 2578 (65.8%) of the subjects have <1000 RNA copies per ml and <50 RNA copies per ml respectively during the period of observation. ART adherence has significant effect on viral load outcome from the study hypothesis tested.

Conclusion: HIV treatment intensive adherence counseling is key to the achieving viral suppression and determine infection prognosis, thus, routine viral load monitoring will ultimately help in HIV/AIDS disease progression follow up and reduce treatment failure tendencies. This will help more patients stay on first line regimen and prolong their life expectancy, indicating that the UNAIDS last 90 target is achievable.

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Prevalence of *Schistosoma mansoni* infection and the therapeutic efficacy of Praziquantel among school children in Manna District, Jimma Zone, southwest Ethiopia.

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Background: Intestinal schistosomiasis is one of the neglected tropical parasitic disease caused by *Schistosoma mansoni* (*S.mansoni*). Currently, the control measures for the disease is mainly based on mass drug administration (MDA) with praziquantel (PZQ) targeting the school age children. In Ethiopia, the potential foci for schistosomiasis and therapeutic efficacy of PZQ among school age children remain poorly explored. Therefore, we determined both the prevalence and intensity of *S. mansoni* infection and the therapeutic efficacy of PZQ among school children in Manna District (new foci for *S. mansoni*), Jimma Zone, Southwest, Ethiopia.

Methods: A cross sectional study was conducted among the school children aged between 6-18 years in three primary schools in Manna district from March to April 2014. For diagnosis of *S. mansoni*, a single stool sample was obtained from each child and processed using single Kato Katz and examined using light microscope. A questionnaire was used to collect demographic information of the school children participated in the study. Data were analyzed using SPSS."

School children excreting eggs *S. mansoni* were administered with 40 mg/kg of PZQ and re-examined after three weeks of the treatment. The therapeutic efficacy of PZQ against *S.mansoni* was evaluated by cure rate and egg reduction rate.

Results: The overall prevalence of *S. mansoni* among the school children in the three primary school in Manna District was 24.0% (120/500). The higher prevalence was recorded among males 25.6% (61/238) than females 22.5% (59/262).

Majorities (27.5%) of infection intensity were light; among infected children with mean fecal egg count (FEC) 202 egg per gram (EPG). The therapeutic efficacy of PZQ at a dose of 40 mg/kg was highly efficacious (cure rate: 99.1% and egg reduction rate: 99.9%) among the School children in the three primary schools in Manna District.

Conclusion: The school children in the three primary schools of Manna District, Jimma Zone were at moderate risk of the morbidity caused by *S.mansoni* (prevalence > 10% and < 50% according to WHO threshold), and hence a biannual MDA with PZQ is required. PZQ available on the local market revealed efficacious and can be recommended for individual treatment in absence of MDA. PZQ at 40 mg/kg has 99.9% ERR and 99.1% CR. Therefore, the therapeutic efficacy of PZQ at 40mg/kg against *S. mansoni* was high in the study area.

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General Overview on Viral Hepatitis B and C in The Maghreb Region

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Background: Hepatitis B (HBV) and C (HCV) viruses represent important health problems in the five Maghreb countries, Algeria, Libya, Mauritania, Morocco and Tunisia but no detailed synthesis of their epidemiology is available.

Materials and Methods: We systematically searched for data about HBV and HCV in the Maghreb in peer-reviewed databases and included in our analysis works written in English and French, as well as institutional reports and regional conference meeting abstracts. We estimated a national and regional prevalence of chronic infections (patients with anti-HCV antibody or HBs antigen). In addition, we discuss molecular features of the viral strains circulating in the region.

Results: A substantial proportion, 1.2-1.9% of the Maghreb inhabitants (1.24 million persons), has anti-HCV antibodies. Genotype 1b predominates among viral strains in all countries except in Libya, where genotype 4 is dominant as in neighboring Egypt. Chronic hepatitis C infection is the most

important causes of HCC in the Maghreb region. Anti-HCV carriers in the HIV-infected group is ranging between 2.7 and 40%.

Data analysis suggests that in the region HBs antigen carriage concerns 1.8-4.9% of the population for an estimated number of 2.7 million persons. Genotype D, subtype D7, is predominant and mutations in the pre-core region of HBV genome are highly prevalent. In addition, the prevalence of HBsAg in HIV-infected patients was estimated at 6% and anti-hepatitis delta virus seroreactivity is ranging between 1.4% and 33%.

Conclusions: This epidemiological situation requires obviously widespread active interventions for prevention and control. More specifically, the application of state-of-the-art hygiene procedures and rigorous controls in medical domains as hemodialysis, transfusion, endoscopic practices and dentistry is necessary to significantly reduce the number of novel infections in the region. In addition, anti-hepatitis B vaccination program should be applied with the utmost discipline in the five countries. The present synthesis intends to stimulate policies aiming at preventing the spread of HBV and HCV, keeping in mind that eradication of these viruses in Maghrebi populations should be the ultimate objective of Public Health authorities.

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Guillain Barré Syndrome during the Zika outbreak in Mexican southeast

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Background: There is an increase in the incidence of Guillain Barré cases during the Zika outbreak of 2015 to 2017 in Latin America, however the Zika virus is not always identified as the precise causative agent, resulting in disparate percentages in the different series of cases studied.

Objective: To determine the incidence of cases and the direct causal relationship between Guillain Barré and Zika virus during 2016 and 2017, in a general hospital in the city of Veracruz, Mexico.

Material and methods: We documented the suspected cases of Zika that had acute flaccid paralysis, and verified Guillain Barré according to Brighton criteria (clinical, cranial tomography,

cerebrospinal fluid analysis, neuroconduction studies) during the 2016 and 2017 seasons. presence of Zika, Dengue and Chikungunya (PCR-RT-serum/urine-, IgM/IgG); extending to HIV, Hepatitis B/C, TORCH, Enterovirus, Campylobacter, Brucella and Salmonella in 2017.

Results: A total of 14 patients were documented (8 in 2016 and 6 in 2017), the male gender was the most affected and the age group was 50-59 years old; September had a higher incidence in 2016 with 7 cases, January with 3 cases in 2017; all were negative to Zika; He highlighted that the cases of 2017 were positive for Campylobacter (only two with acute diarrhea), one case with IgM+ to Dengue and another case with IgM+ Chikungunya; there was a report of IgG+ to Zika and Dengue, however it was considered a cross reaction with other arboviruses. All were treated with immunoglobulin, 13 had good functional prognosis (Hugues initial 4, Hugues final 2), a death was reported. Incidence rate 0.039 individuals/year, cumulative incidence 3.9% during 2016; The 2-year incidence rate was 0.020 individuals/year.

Conclusion: There was an increase in the incidence of Guillain Barré; however, there was no direct causal association with Zika; there was evidence of involvement by Dengue and Chikungunya in two individual cases; in the cases of 2017, the presence of Campylobacter predominates, the asymptomatic carrier state prevailing, this characteristic being able to favor or predispose the appearance of the cases of Guillain Barré together with the presence of viral co-infections.

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Can we achieve the last 90 of the UNAIDS ambitious targets? Evidence for adherence scale up among paediatrics in Western Nigeria

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Background: In resource-limited settings, where genotypic drug resistance testing is rarely performed and poor adherence is blamed for the inability to achieve viral suppression and treatment failure, programmatic approaches to preventing &

handling these are thus essential. Hypothesis tested was antiretroviral therapy adherence effect on viral load outcome. This study was aimed at determining and monitoring HIV/AIDS disease progression using viral load to provide prognostic information and evaluate patients for viral suppression using the World Health Organization (WHO) guideline strategies.

Methods: This study was an observational longitudinal prospective cohort study of subjects living with HIV already initiated on antiretroviral therapy for at least six months, enrolled in health facilities across Ekiti State, Western Nigeria, during a 12-month observation period starting October 2016 till September 2017. Quantitative viral load analysis was done using Polymerase Chain Reaction, Roche Cobas Taqman 96 Analyzer. All data were statistically analyzed, using Statistical Package for the Social Sciences (SPSS), with multiple comparisons done using Post Hoc Bonferonni test.

Results: A total of 126 (64 males & 62 females) subjects eligible for the study were recruited. Most of them are in the age range of 4 – 10 years, with a mean age of 8.59 ± 3.26 years. 73 (57.9%) & 61 (48.4%) of the subjects had viral suppression of <1000 RNA copies per ml and <50 RNA copies per ml respectively. The 53 subjects went through intensive adherence counseling for three months and viral load test repeated three further months after, which made 103 (81.7%) & 82 (65.1%) of the subjects have <1000 RNA copies per ml and <50 RNA copies per ml respectively during the period of observation. ART adherence has significant effect on viral load outcome from the study hypothesis tested.

Conclusion: HIV treatment intensive adherence counseling is key to the achieving viral suppression and determine infection prognosis, thus, routine monitoring of viral load will ultimately help in the monitoring of HIV/AIDS disease progression and reduce treatment failure tendencies. This will help more patients stay on first line regimen and prolong their life expectancy, indicating that the UNAIDS last 90 target is achievable in resource-constrained settings.

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Factors affecting the quality of blood samples for Lassa fever diagnosis at Irrua specialist teaching hospital, Irrua, Edo State, Nigeria

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Background: More than 70% of clinical decisions are based on information derived from laboratory test results. Quality in clinical laboratories cannot be assumed by focusing on analytic aspects only. Studies have shown that laboratory errors occur primarily in the pre-analytic phase. In Nigeria, Irrua Specialist Teaching Hospital (ISTH) is a reference center for diagnosis of Lassa fever. Studies have been done on the analytic phase of Lassa fever diagnosis in Nigeria, but there is limited evidence of studies done on the pre-analytic phase. Pre-analytic errors may affect the test result, increase turnaround time, increase cost of care, and cause death. The aim of this study was to assess the pre-analytic quality of blood samples submitted for Lassa fever diagnosis at ISTH and to assess knowledge and practice of health workers on sample management.

Methods: A cross sectional study was carried out from January to April, 2017. Total sampling method was used for assessment of samples and purposive sampling of health facilities was used to select health facilities for assessment of knowledge and practice of health workers. Four hundred blood samples were assessed using a checklist. Ninety five health workers were administered pre-tested questionnaire out of 167. Independent variables included documentation, volume, packaging, time in transit, temperature and sample container while dependent variable was test result. Dependent variable for health workers was training while independent variables were knowledge and practice of sample management. Performance score was pre-determined for each assessment. Univariate, bivariate and multivariate analysis was carried out 95% confidence level and $p \leq 0.05$.

Results: Of the 400 blood samples, 228 (57%) were from ISTH while 172 (43%) were from other facilities. Mean score of sample quality was 3.74 ± 0.75 . Based on performance score for each

sample, pre-analytic error ranged from 34.8% to 52.3%. Only documentation was not significantly associated with the test result after bivariate analysis (OR 1.46, C.I (0.54-3.93). After multivariate analysis, only volume and packaging had significant effects on sample result. ($P < 0.05$). There was no difference between samples from ISTH and samples from other health facilities. Of the 95 respondents, 44 were males and 43% were doctors. Mean age of respondents was 33.96 ± 8.78 . Eighty nine percent had good knowledge of Lassa fever; 95.8% had good knowledge of sample management and 88.4% had good practice. Mean score of knowledge of Lassa fever, knowledge of sample management and practice of sample management was 10.37 ± 2.67 ; 4.73 ± 1.11 and 4.00 ± 1.29 respectively. Forty nine (53.9%) had been trained and all had good knowledge. Of these, 95.9% ($n=47$) had practice above 50%. Linear correlation between knowledge and practice of Lassa fever and sample management was 0.19 and 0.84 respectively. There was difference between the knowledge and practice of sampling management among trained and untrained health workers.

Conclusion: Pre-analytic errors in Lassa fever samples in this study was 34.8% to 52.3%. Among health workers, good sample management was associated with staff training. It is recommended that ISTH should organize annual trainings for its staff and health workers from other facilities.

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Molecular differentiation of Entamoeba Spp. isolated from Cameroonian human immunodeficiency virus (HIV) infected and uninfected patient

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Background: Entamoeba histolytica is an utmost important cause of dysentery. Entamoeba spp. has been frequently reported in human immunodeficiency virus (HIV) positive individuals. Routine microscopic examination of stool sample is a most widely used technique but microscopy alone has low sensitivity and it is insufficient for differentiation among Entamoeba spp. Molecular

techniques are newer methods which are currently used for the identification of Entamoeba spp.

The present study was planned to differentiate the Entamoeba species by gene sequencing for the confirmation of microscopic findings in stool samples of HIV positive and negative patients of Cameroon.

Out of 265 patients diagnosed microscopically for Entamoeba, 90 positive stool samples (28 from HIV patients) were collected and studied for the differentiation of Entamoeba species. DNA was extracted from infested stool samples and used to amplify a part of the genus Entamoeba small-subunit ribosomal RNA gene (SSU rDNA) as well as the serine rich E. histolytica protein gene and chitinase gene. The SSU rDNA were sequenced to identify the other species that could not be done by polymerase chain reaction (PCR), and for the differentiation of E. histolytica from Entamoeba dispar and Entamoeba moshkovskii. Sequence analysis identified seven different species of Entamoeba which were related to Entamoeba; E. histolytica (28.7%), E. dispar (25%), E. moshkovskii (10%), Entamoeba coli (16.3%), Entamoeba hartmanni (6.2%), Entamoeba polecki (11.3%) and Entamoeba struthionis (7.5%), with the higher prevalence of E. histolytica among HIV infected patients than uninfected individuals.

The phylogenetic analysis within the sequences of E. histolytica isolates suggested two distinguishable variants present among Cameroonian HIV patients. There is a possibility that specific genotypes may be more prevalent among HIV positive patients, and molecular diagnosis is important in establishing the correct diagnosis of amoebic dysentery.

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Characteristics of snail vectors in the transmission of Schistosomiasis in Kumasi, Ghana

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Background and Objectives: Schistosomiasis is the most prevalent waterborne disease in terms of its socioeconomic and public health importance in tropical areas. Different snail species serve as the intermediate host for the transmission of the disease. Rivers create suitable environment for the breeding of these snails therefore, a survey was conducted to determine the particular snail species responsible for the transmission of *Schistosoma haematobium* and *S. mansoni* in four selected endemic communities in Kumasi, Ashanti region of Ghana.

Materials and Methods: From April to July 2017, fresh water snails were collected from rivers in the study communities (Deduako, Emena, Kokoben and Apromase). The different snail species in the study communities were identified by shell morphological characteristics and their infectivity were investigated by shedding or PCR.

Results: Six snail species were collected and 3.2% (21/653) successfully shed cercariae. Out of the 58 *Bulinus globosus* snails that transmit *S. haematobium* collected, one shed 1250 furcocercous cercariae. *Bulinus forskalii* transmitting *S. intercalatum* was also found. *Lymnaea natalensis* responsible for the transmission of *Fasciola* spp. shed *Fasciola* cercariae. Interestingly, *Biomphalaria pfeifferi* known to transmit *S. mansoni* shed rather the *Fasciola* cercariae. Further analysis using PCR to confirm the snails' infectivity status is ongoing.

Discussion/Conclusion: We have established that local transmission of schistosomiasis is ongoing in semi-urban areas of the Ashanti Region of Ghana with the risk of *S. intercalatum* transmission if introduced in the region. Also, further studies

should be carried out on fascioliasis and its impact on cattle, goats and sheep.

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Hepatitis E virus infection among pregnant women in North Kurdofan state, Sudan

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Background: Hepatitis E virus is viral disease infect people through fecal-oral route particularly areas with limited access to clean water and good sanitation. Generally, the virus comes with mild symptoms among patients. Among pregnant women the virus has severe symptoms and may lead to death.

Objective: The aim of this study is to determine the distribution of hepatitis E virus infection among pregnant women in North Kurdofan state, Sudan.

Methods: Pregnant women admitted to the hospital with any of these symptoms jaundice, fever, and headache or vomiting were included in the study. Blood sample was collected from each participant and screened for HEV antibody by ELISA test.

Result: A total number of 232 pregnant women coming from different localities in North Kurdofan state were included in this study. Twenty four women were positive for hepatitis E virus counting for 10.3% of the total participants. 26 (11.3%) of pregnant women were died due to infection with this virus. All patients admitted with fever, 40% had vomiting, 6% had loss of appetite, and 1.7% came with abdominal and joint pain.

Conclusion: Hepatitis E virus representing serious risk for people living in rural area and it is fatal among pregnant women. More effort is needed to provide clean water for people living in remote rural areas. Special care should be provided for pregnant women living in rural areas.

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Health workers Knowledge, Attitude and Practice during Lassa Fever Outbreak, Anambra State, Nigeria, 2016.

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Background: Lassa fever (LF) is an acute viral hemorrhagic fever caused by Lassa fever virus (LVF), Asymptomatic in 80% of cases; Lassa fever is associated with bleeding and multiple organ failure. It's endemic in West Africa and Nigeria has been having severe outbreaks since 2014. On 18th August 2016, a patient was referred to a teaching hospital in the State with bleeding from orifices, hematuria, and bleeding from puncture sites. Lassa fever was confirmed post mortem. This study was conducted to assess knowledge, attitude and practice (KAP) among health workers.

Method: We conducted a cross-sectional study among health workers in Anambra State. We assessed KAP using self-administered questionnaire and multistage sampling technique was employed. KAP score was computed using 12, 10 and 9 item questions respectively. Each item was assigned "+1" for correct Knowledge and "0" for incorrect knowledge. KAP was classified as good if >75%, fair if >50%, poor if <50%. Odds ratio with a significance level set at 5% was used to measure degree of significance of the association.

Results: A total of 128 health workers were interviewed, of which 109 (86.51%) were females, 2% clinicians, 34% nurses, 50% community health extension workers, others 14%. Only 10% were able to give the case definition of LF, 21% were able to mention drug of choice, 10% knew the reservoir for the virus and only 4.7% could properly describe hand washing. 15.6% had good, 32.8% fair and 51.6% poor knowledge. 75.8% had good, 20.3% fair and 4.7% poor attitude. 30.5% had good, 57% fair and 12.5% poor practice. Duration of employment was associated with having good knowledge (OR=3.1(1.4-6.7), p= 0.004), attitude (0.3(0.2-0.8), p=0.009) and practice (3.6(1.4-6.8), p=0.004). Age was associated with good attitude (15.3(5.7-40.9), p=<0.001).

Conclusion: Overall Knowledge and practice was poor but attitude was good. We sensitized health workers in the state.

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Factors associated with Hepatitis B infection among Krachi senior high school students in the Krachi West district of the Volta Region.

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Background: Hepatitis B virus (HBV) occurs globally and is of a great public health importance. According to World Health Organization (WHO), "more than two (2) billion people worldwide have been infected with Hepatitis-B virus and about 350 million people remain chronically infected". Even though Ghana belongs to one of the areas where HBV is highly endemic not much study detailing the burden of the disease among the youth has been conducted.

Objectives: This work was intended to determine the burden of HBV infection and its associated risk factors among students in the Krachi Senior High school in the Krachi West district of the Volta region. **Methods:** Using the 2017 student register as sample frame, 182 students were randomly selected for this cross-sectional sero prevalent survey. Chi-square test or Fisher's exact test was used to compare variables and those variables with p<0.200 were analyzed in a final regression model.

Result: The sero-prevalence of HBV among the 182 study participants was found to be 14.3%. More females than males 14/26 (53.8%) tested positive for the HBsAg. The highest prevalence was recorded in 18-20 age groups 14/87 (16.09%). Place of barbering was found to be statistically significant with HBV (aOR: 0.48 95%CI.0.28-0.84) (p=0.01). Also sharing of same spoon/cutlery among students also significantly influences HBV infection among students (aOR: 0.46, 95%CI.0.26-0.8) (P=0.01)

Conclusion: Hepatitis B virus infection is significantly high among students attending Krachi West Senior High School. Place of barbering and sharing of cutlery among students are factors significantly associated with the virus infection.

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Prevalence of Uterine Cervix Cancer in Kenya, a Major Social economic Challenge on Health Goal

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Background: Uterine cervical cancer is a leading health problem among women. Majority (70%) cases are confined in Sub Saharan Africa (SSA), mainly associated with Human Papiloma Virus (HPV) of genotypes 16 and 18. Generally 85% of uterine cervical cancers are squamous cell cancers while, rest are adenocarcinomas. In Kenya majority of affected women never recognize this cancer for many years because of its silent clinical presentation.

While in developed countries the cancer is detected early due to accessible sustainable screening programs. Prolonged limited access to affordable and quality differential diagnosis, HPV antigen tests, and persistence low coverage screening programs in (SSA) have led to high levels of morbidities and mortalities associated with uterine cervix cancer which has impacted negatively on social economic and health Development in (SSA). It was these reasons that led to determine prevalence of uterine cervix cancer, a major challenge on health goal, using Pap stains in Kenyatta National Hospital, (KNH).

In cross-sectional, 400 respondents were used in saturated sampling. Data was collected and analyzed from Pap slides and mounted in DPX mountant before microscopic differential report concluded. Results, 48% of women seeking healthcare in (KNH) were infected with HPV genotype 16 and 18 that cause cancer of cervix, nevertheless prevalence of other related health risks in uterine and cervix fluctuate gradually. Women cohabiting HPV gene 16 and 18, have greater risk to develop cancer of cervix than to women with physically warts on vulva, with OD (4.9, 0.02) 95% CI (1.5, 0.3). Recommend primary prevention than cure.

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Active Case Search for Avian Influenza among Human Contacts of H5N1 Infected Poultry Birds, Plateau State, Nigeria, March, 2017

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Background: Avian Influenza infected birds shed influenza viruses in their saliva, mucous and feces. Human infections occur when viruses get into a person's eyes, mouth or when inhaled. Plateau State reported the highest number of infected poultries in Nigeria in the 2017 H5N1 virus resurgence. Efforts to stamp out the outbreak were directed at the control of infected poultry population. However, unlike birds which can be controlled by depopulation, man cannot.

Purpose: Conducted active case search in the 14 affected farms and nearby healthcare facilities to detect possible bird-to-human transmission.

Methods: We searched for cases who met the case definition for influenza-like-illness; (Any person having acute respiratory illness with fever ≥ 38.0 C and cough or sore throat with onset within the last 10 days) Or severe acute respiratory illness; (Any person presenting with acute lower respiratory infection with history of fever and Cough or sore throat and shortness of breath, or difficulty breathing with or without clinical or radiographic findings of pneumonia, with onset within the last 10 days and requires hospitalization). Nasopharyngeal and oropharyngeal samples collected were analyzed by reverse transcription polymerase chain reaction at National Influenza Reference Laboratory, Abuja.

Results: Altogether, seven suspected cases were line-listed. The mean age was 33.9 \pm 18.2 years and four (57.1%) were males. Four (57.1%) of the cases presented with sore throat, cough and difficulty in breathing. Two of the suspected influenza patients tested positive for Flu B while none was confirmed positive for Highly Pathogenic Avian Influenza or any other Influenza A sub-type.

Conclusions: Influenza B detected in the suspected patients is a common seasonal flu among humans and was not likely to have come from AI-infected birds. There was probably no human case in this recent outbreak of AI in Plateau State. We sensitized poultry attendants on the need for improvement in infection prevention and control measures.

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Recrudescence de la syphilis et du VIH chez les donneurs de sang a l'hôpital Laquintinie de Douala

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Introduction: la syphilis et le VIH constitue un risque infectieux majeur pour la sécurité transfusionnelle. Face à cette situation, l'OMS recommande un dépistage systématique de ces affections chez les donneurs de sang. L'objectif de cette étude était de déterminer la prévalence des marqueurs du VIH1/2 et l'infection à tréponème pallidum dans la population des donneurs en vue de réduire la transmission de ces infections par transfusion sanguine.

Méthodes: Il s'agit d'une étude rétrospective ayant portée sur 12482 donneurs de la banque de sang de l'hôpital Laquintinie de Douala au cours d'une période de 12 mois allant du 1er Décembre 2016 au 30 novembre 2017. La sélection des donneurs pour l'obtention du sang sécurisé s'est faite en plusieurs étapes : Un pré test à base de questionnaire a été administré à chaque donneur pour l'éligibilité au don, suivi du test de diagnostic rapide (TDR) pour le VIH. Dans la deuxième phase, la recherche des marqueurs virologiques du VIH par méthode ELISA et le test d'hémagglutination pour la syphilis ont été réalisés sur les poches de sang présélectionnées. Les données ont été recueillies à partir des registres et saisies à l'aide du logiciel SPSS.

Résultats: Sur 12482 candidats au don, 2137 (17,12%) ont été exclus lors la présélection des donneurs de sang. Les motifs d'exclusion étaient les raisons cliniques (HTA, partenaires multiples, l'âge > 60 ans, maladie récente...) (49,37%) ; la positivité aux marqueurs sérologiques du VIH était de 11,65%. Au Total 9806 donneurs de sang étaient éligibles dont 95,76% étaient des donneurs familiaux et 4,24% étaient des bénévoles. 9722 (99,94%) poches de sang sélectionnées ont été testées par méthode ELISA. La séroprévalence du VIH était de 3% (294/9722) et celle de la syphilis de 6,2% (608/9722).

Conclusion: La recrudescence de la syphilis chez les candidats au don de sang traduit la tendance à la hausse observée dans la population générale alors que pour le VIH à cause du pré-test est vue à la baisse. La nécessité de développer une meilleure stratégie de dépistage pour la syphilis pourra permettre de contrôler cette pathologie.

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A study of chronic hepatitis C infection and spontaneous recovery in Ghana

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Background: Viral hepatitis is reported to be relatively high in a few countries across the world especially including Africa. Hepatitis C viral infection has however been identified as the second highest cause of liver diseases and liver cirrhosis. Health facilities in Ghana, just as in most developing countries is not well resourced therefore management of hepatitis due to hepatitis C is a great challenge to healthcare givers whilst the cost of management is also expensive for the average Ghanaian. The current study sought to determine the rate of chronic HCV infection and spontaneous recovery among HCV seropositive individuals selected from the Blood Donor Unit of the Komfo Anokye Teaching Hospital, Obuasi and Daboya. So as to have a better understanding of the rate of

spontaneous recovery from HCV infection in an African population and possibly explore it further in the direction of the immune dynamics involved.

Method: A total of 168 HCV sero-positive individuals obtained from the three study populations were analysed. These were screened and further confirmed with ORTHO® HCV Version 3.0 ELISA Test System (100% with specificity of 99.95%). The samples were further processed and quantified the HCV RNA using Abbott m2000sp instrument and Abbott m2000rt instrument respectively. Participants who were screened positive for HCV antibodies but the HCV viral RNA were not detected were classified as being spontaneously recovered from the HCV infection. Persons who were screened positive for HCV antibodies and had detectable HCV RNA were also classified as patients with active or chronic HCV infection.

Results: The rate of chronic HCV infection and spontaneously recovered HCV infection was determined to be 79% (134/168) and 20.2% (34/168) respectively. More than 90% of individuals with chronic HCV infection have their region of origin being either from Upper East, Upper West or the Northern region. The origin of distribution among chronic infected subjects, compared between the spontaneously recovered was statistically significant with a p-value of 0.007. Among the chronic HCV infected subjects, the viremia determined was less than 1.08 Log IU/mL - 6.88 Log IU/mL, with a mean value of 5.32 IU/mL.

Conclusion: The study has demonstrated a high occurrence of chronic HCV infection among HCV infected subjects in Ghana with the Northern, Upper East and Upper West regions being more predominant.

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