

**2<sup>nd</sup> International Conference on  
(Re-)Emerging Infections  
Diseases**

**Oral Presentations  
Abstracts**



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## Risk Communication and Risk Perception in the 2014-2015 Ebola Outbreak in Sierra Leone

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**Background:** Sierra Leone had the highest number of Ebola virus disease (EVD) cases and deaths during the 2014-2015 outbreak in West Africa. Risk communication efforts aimed to provide the population with life-saving information and encourage adoption of protective behaviors. Perceived susceptibility to a disease threat (risk perception) has shown to be associated with uptake of protective behaviors and avoidance of risky behaviors. During the Ebola outbreak in Sierra Leone, the association between risk perception and Ebola-specific knowledge and behavior has not been examined.

samples obtained by district and time in the outbreak. Mediation analysis was carried out to understand whether risk perception functioned as a mediator between information sources and behavior.

**Results:** New media (Adjusted Odds Ratio (AOR) 1.6, 95% CI 1.4-1.9) and community sources (AOR 1.3, 95% CI 1.1-1.4) were significantly associated with perceiving some Ebola risk. A dose-response association was also observed, showing that the more sources one was exposed to, the higher the likelihood to perceive some risk.

Risk perception was further associated with knowledge (AOR 1.4, 95% CI 1.2-1.5) and protective behavior (AOR 1.2, 95% CI 1.1-1.4), but not with risk behavior (AOR 1.0, 95% CI 0.9-1.1). It had an inverse association with misconceptions (AOR 0.7, 95% CI 0.6-0.8). Ebola risk perceptions mediated the associations between new media, community and protective behavior.

**Discussion:** New media and community sources (such as religious and traditional leaders) were associated with risk perception. Compared to information sources such as radio and print media,

**Aim:** To better understand the relationship between exposure to outbreak information sources and perceiving some Ebola acquisition risk, and to further examine how such risk perceptions might have been associated with Ebola-specific knowledge, misconceptions, and behaviors.

**Methods:** The study is based on three cross-sectional, national surveys that measured Ebola-related knowledge, attitudes, and practices in Sierra Leone during the 2014-2015 outbreak. The first survey was conducted in the August 2014, n=1413, the second shortly before the peak (October, n=2086) and third shortly after the peak (December, n= 3540). Data were pooled, and composite variables were created for knowledge, misconceptions, protective and risk behavior. Risk perception was captured by asking 'what level of risk do you think you have in getting Ebola in the next 6 months?', with answering options 'no, small, medium or great risk'. This was dichotomized to 'no risk perception' vs 'some risk perception'. Information sources (electronic media, print media, new media (internet, mobile phones), government, community) were dichotomized to exposed and unexposed. A variable was created for the sum of information sources exposed to (0-1, 2, 3, 4-5 sources). Multilevel logistic regression models were fitted to account for the clustering of

these sources can be seen as more personal, with the possibility to engage in dialogue. Having at least some risk perception seems to be beneficial for EVD knowledge and for engaging in protective behavior. Results should be interpreted with caution, as reverse causality cannot be ruled out when using cross-sectional data. These results can inform risk communication strategies in health emergency preparedness

2A

## Effect of Oral Cholera Vaccine on Geographical Spread of Cholera Epidemic in Borno State, Northeastern Nigeria, 2017-2018

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**Background:** Oral Cholera Vaccine (OCV) has been known to play an important role as a preventive and control measure in epidemics especially amongst Internally Displaced Persons (IDP) and areas facing complex emergencies. The ongoing humanitarian crises in North-eastern Nigeria disrupted social services and displaced thousands into overcrowded IDPs camps with the scarcity of water, sanitation and hygiene. Borno State is the epicentre of the humanitarian crises where epidemics likely occur. We confirmed and characterized three cholera epidemics. We mounted an emergency response with Shancol Cholera Vaccine the first ever use of oral cholera vaccine in Nigeria. We also determined the effect of OCV on the geographical spread of the cholera epidemic in Borno State to guide targeted intervention and future epidemic control strategies.

**Methods:** We investigated three cholera epidemics between 16th August, 2017-24th November 2018 in Borno State. We defined a case-patient as any person  $\geq 2$  years presenting with acute watery diarrhoea with or without vomiting and severe dehydration or died as a result. We launched a reactive two-dose OCV campaign during the first epidemic. The first dose was between 18th-22nd September 2017 while the second dose between 8th-18th November 2017. We targeted all persons  $\geq 1$  year of age (target population=855,492). We vaccinated eligible persons in selected hot-spot wards of Jere (3 wards), Maiduguri (3 wards), Konduga (3 wards), Mafa (2 wards), Monguno (1 ward) and Dikwa (1 ward) Local Government Areas (LGAs). We conducted a descriptive and analytic

study of the epidemic using the R software and Epi Info Version 7.2.2.2

**Results:** We identified 13,595 case-patients; 140 died (Overall case fatality rate [CFR]=1.03%) First epidemic occurred between 16th August-21st December, 2017 with 6,430 case-patients and 61 deaths (CFR=0.95%); 6,109(95.00%) were IDP and lived in official and unofficial camps in Jere: 3,512(54.62%), Monguno: 1,870(29.08%), Dikwa: 845(13.14%), Guzamala: 115(1.79%), Maiduguri: 63(0.98%), Mafa: 23(0.36%) and Gubio: 2(0.03%) LGAs.

Overall, 896,919 people were vaccinated (coverage rate=105%) using 914,565 OCV doses (wastage rate=0.4%)

Second epidemic occurred between 13th February-16th July, 2018 with 935 case-patients and 6 deaths (CFR=0.64%) in Kukawa: 785(83.96%), Askira-Uba: 111(11.87%), Bama: 31(3.32%), Jere: 6(0.64%) and Damboa: 2(0.21%) LGAs.

Third epidemic occurred between 5th September-24th November, 2018 with 6,230 case-patients who did not receive OCV and 73 deaths (CFR=1.17%) in Jere: 2,388(38.33%), Maiduguri: 1,520(24.40%), Ngala: 1,052(16.89%), Magumeri: 340(5.46%), Konduga: 166(2.66%), Kwaya-Kusar: 161(2.58%), Chibok: 136(2.18%), Kala-Balge: 106(1.70%), Askira-Uba: 91(1.46%), Guzamala: 70(1.12%), Dikwa: 57(0.91%), Bama: 56(0.90%), Damboa: 42(0.67%), Kaga: 34(0.55%) and Shani: 11(0.18%) LGAs.

**Conclusion:** With a high reactive OCV coverage, we controlled the protracted cholera epidemic which increased in magnitude and strength affecting mostly IDPs in camps and spreading to host communities despite combining several control measures. The second epidemic occurred in an entirely different geographical location while the third epidemic was in wards not previously vaccinated with OCV. We recommend preventive OCV campaigns in high-risk areas to boost herd-immunity and prevent the geographical spread of cholera epidemic.

2B

## Cholera Outbreak Response in a Complex Emergency: The Importance of Oral Cholera Vaccine in Borno State, Northeastern Nigeria, 14th August–21st December, 2017

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**Background:** Cholera Outbreak is a global health problem amongst Internally Displaced Persons (IDPs) and areas facing complex emergencies. The insurgency in North Eastern Nigeria caused disruption in social services, and displacement of thousands into IDP camps which are overcrowded with sub-optimal Water, Sanitation and Hygiene. We confirmed, characterise the outbreak and instituted control measures which include the first-ever use of Oral Cholera Vaccine (OCV) Shanchol Cholera vaccine was licenced for use in Nigeria.

**Methods:** We defined a suspected Cholera case as any person  $\geq$  2years in Borno State presenting with acute watery diarrhoea with or without vomiting and severe dehydration or died as a result, between 14th August to 21st December 2017. We did a descriptive and analytic study. Using the Polio vaccination structure, we conducted an OCV campaign in two phases targeting all people above one year of age in the affected communities and IDP camps.

**Results:** We line-listed 6,430 suspected cholera cases. Of these, total deaths were 61 (CFR: 1.1%) 3512 (54.6%) cases were reported from Jere, 1870(29.1%) Monguno, 845 (13.3%) Dikwa, 115 (1.8%) Guzamala, 63 (1.0%) Maiduguri, 23 (0.4%) Mafa and 2 (0.03%) from Gubio LGAs. 6109 (95%) of the cases were seen in IDP camps. Median age was 9 years (range: 2-80) and 2780 (52%) were females. 914,565 doses of OCV was used. A total of 855,492 were targeted, 896,919 people were vaccinated giving the coverage rate of 105%. Wastage rate was 0.4% No Adverse Events Following Immunization were reported. The highest number of daily cases was 122 recorded on the fourth day of vaccination since then, cases begin to decline until the end of the outbreak.

**Conclusion:** There was a Protracted cholera outbreak that increased in magnitude and strength affecting mostly children in IDP camps. Rapid detection and response were a possible reason for low CFR. Reactive OCV might have influenced the ending of the outbreak. Despite the complex and challenging context, the outbreak was contained within four months with a case fatality (CFR) of 0.95%

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## Upsurge of Lassa Fever Cases in Nigeria, January to March 2018: What Has Changed?

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**Introduction:** Lassa fever is an acute viral haemorrhagic illness with high morbidity and mortality rates. It is endemic in Nigeria with high transmission season occurring from December through March yearly. The 2018 massive wave of laboratory confirmed cases of Lassa fever in Nigeria raised the important question, whether the “outbreak” was due to a new virus variant, increased high-season incidence, improved case recognition, availability of laboratory diagnostics and therapy - or a combination of these factors. We therefore elucidated the likely major drivers of the unprecedented high Lassa fever cases reported in Nigeria from January to March 2018 .

**Methods:** The national LF 2017 and 2018 data was extracted from the VHF case-investigation-form database and analysed using microsoft excel. Viral genome sequencing was carried out on positive Lassa fever samples to describe changes in the viral genome or transmission patterns by Nigeria Centre for Disease Control collaborating partner institutions. Key informant interviews were conducted with pillar leads of national Lassa fever technical working group stakeholders.

**Results:** In the first 12 weeks of the years 2017 and 2018, 107 and 394 laboratory confirmed cases, were recorded respectively with a decline in case fatality rate among confirmed and probable cases from 43.9% in 2017 to 25.8% in 2018. In the same period, respectively 45.0% and 66.0 % of all confirmed cases were reported from neighboring Edo and Ondo states with 15% originating from a non-adjacent Ebonyi state. Although Edo and Ondo States comprise 4.6% of Nigeria’s population, they accounted for 74.6% of the increase in confirmed cases from 2017 to 2018 (first 12 weeks of the respective year). Evidence from viral sequencing yielded no indication that the circulating viruses are different from those in previous years. Phylogeny points to multiple zoonotic infections instead of

extended person-to-person transmission. Key informant interview results indicated increase in number of Lassa fever testing laboratories from two to four in addition to a provision of free national sample transport logistics framework which all led to an improved result turnaround time. Other factors include, designation of additional treatment centers supported by the federal government and its partners, improved surveillance activities at the States due to capacity building by rapid response teams deployed to support affected states in the 2017 outbreak. There was also increased Lassa fever awareness in early January 2018 following the cluster of healthcare worker affectation and associated with high mortality rates.

**Conclusion:** There is currently no evidence for the high number of Lassa fever cases reported in Nigeria in early 2018 due to new virus strains. But the addition of new and growing capacity in the laboratories, an overall intensified response, increased awareness, and an improved surveillance sensitivity are likely major drivers of the very high Lassa fever case numbers reported in Nigeria early in 2018.

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## The Global Point Prevalence Survey (Global-PPS) of Antimicrobial Consumption and Resistance: Results of Antimicrobial Prescribing at the University College Hospital (UCH), Ibadan

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**Background:** Antimicrobial resistance is a global health challenge. There is inadequate information on antimicrobial prescription practices in many sub-Saharan African countries including Nigeria. A standardized method for surveillance of antimicrobial use in hospitals was employed to assess the antimicrobial prescribing practices in UCH, Ibadan, Nigeria.

**Methods:** Point Prevalence Survey (PPS) was conducted in December, 2017 at the UCH Ibadan. The survey included all in-patients receiving an antimicrobial on the day of PPS. Data collected included details on the antimicrobial agents, reasons and indications for treatment as well as a set of quality indicators. A web-based application was used for data-entry, validation and reporting as designed by the University of Antwerp ([www.global-pps.be](http://www.global-pps.be)).

**Results:** This survey included a total number of 451 patients from 38 different wards of which 59.6% received at least one antimicrobial. The adult surgical wards contributed for the highest number of patients, (n= 221; 49.0%), of which 115 (52.0%), received antibiotics. A total number of 172 therapeutic antibiotic prescriptions were issued, mainly for Community-Acquired Infections (n=119; 69.2%). Most prescriptions for Health care Associated Infections (n=53) were intervention related (47.2%).

Frequently used antibiotics include third generation cephalosporins (23.9%; mainly ceftriaxone); followed by combination of penicillin's (17.4%; mainly amoxicillin with enzyme inhibitor) and

fluoroquinolones (16.6%). Majority, 312(69.9%) of the patients had parenteral antibiotics and only 95 (21.3%) of all antibiotic prescriptions had a documented stop or review date. Although the reason for antibiotic prescription was indicated for 413 (92.4%) prescriptions, targeted therapy was the basis for only 17 (3.8%) of these prescriptions. Out of all antibiotics for surgical prophylaxis, 98.7% were given for more than one day. Compliance to guidelines was non-existent.

**Conclusions:** Our findings showed high broad spectrum prescribing, high number of intervention related health care infections, high use of prolonged surgical prophylaxis, inexistence of local guidelines; and low utilization of laboratory facilities. There is need for antibiotic policy to ensure rational prescription of antimicrobial agents. Additionally, well established surveillance is important to prevent prolonged surgical prophylaxis in Nigerian hospitals..

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## Can We Track Antimicrobial Resistance Using Pharmacovigilance Intelligence?

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**Background:** VigiBase contains over 10 million Adverse Drug Reaction (ADR) reports from 134 countries (in 2018) participating in the WHO Programme for International Drug Monitoring (PIDM). Based on the opinion expressed by experts stating that antimicrobial resistance (AMR) is an overlooked adverse event that should be reported as part of events around drug ineffectiveness, we undertook this study, to investigate the potential role of pharmacovigilance databases in the track of AMR.

**Methods:** To establish a list of antimicrobials to be targeted by the search in pharmacovigilance databases, we first conducted a review of drugs on the AWaRe (Access, Watch and Reserve) list of antimicrobials in the WHO Essential Medicines List (EML), and reviewed the drugs used to manage diseases on the Priority Pathogens List (PPL) established by the WHO to inform the discovery and development of new antimicrobials. We then carried out an extensive search in VigiBase, looking for Adverse Drug Reactions (ADRs) recorded using Preferred Terms (PTs) that refer to events of resistance. The Medical Dictionary for Regulatory Activities (MedDRA) was used to identify international codes linked to the PTs and used to share relevant information on ADRs.

**Results:** Based on the AWaRe and PPL lists, we established a list of 109 drugs in the following classes of antimicrobials: Carbapenems, Vancomycins, Methicillins, Clarithromycins, Fluoroquinolones, Cephalosporins, Penicillins and Ampicillins. The retrieved reports from VigiBase were recorded between 1968 and 2018. Events of interests were found in 3 System Organ Classes(SOCs): 1) infections and infestations, 2) general disorders and administration site conditions, and 3) injury, poisons and procedure complications. The initial search focused on the PT

“Pathogen Resistance” with MedDRA code: 10034133, but the extended search under the 3 SOCs led to a total of 17 Preferred Terms (PTs) suggesting cases of suspected resistance or events likely to lead to resistance following antimicrobial administration. PTs such Pathogen Resistance (code: 10034133), Drug Ineffective (code:100313709) or Drug Ineffective (code:10059866) are found in ADRs on Amoxicillin, Ciprofloxacin or Daptomycin.

**Conclusion:** Our findings suggest that among the ADR reports in PV databases, a significant number contain important information on existing or rising AMR cases. We further plan to look into how PTs with internationally agreed codes can be used in pharmacovigilance intelligence systems to capture geo-tagged signals of resistance to specific antimicrobials. Such systems would be an important tool in AMR tracking, especially in settings where laboratory capacity for causality confirmation is still in its development stages.



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## Antimicrobial Usage by Traditional Livestock Farmers in Lactating Cows in Northcentral Nigeria: Risk Perceptions, Drivers for Antimicrobial Misuse and Public Health Implications

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**Background:** Milk is an important source of nutrients to humans and animals. Antimicrobials are used by pastoralists for treatment and prevention of mastitis, as well as maintain good health and production for higher milk yields. Improper antimicrobial usage in food animals contributes to development of antimicrobial resistance, now a global health threat. Pastoralists in Nigeria herd about 90% of cattle populations under extensive husbandry system in rural areas. Exploration of pastoralists' local knowledge and practices regarding antimicrobial usage in lactating cows is crucial for the development of antimicrobials surveillance on local milk production and control of antimicrobial resistance. Study objectives were to: 1) assess pastoralists' local knowledge and practices regarding antimicrobial usage in lactating cows; and 2) explore perceived risk pathways for antimicrobial resistant pathogens emergence and dissemination to humans through cow milk. We hypothesized that pastoralists' socio-economic activities cannot influence antimicrobials misuse in lactating cows.

**Methods:** Interview structured questionnaire-based cross-sectional study was conducted on systematic randomly selected households in pastoral settlements of North-central Nigeria, between October 2016 and April 2017. Descriptive, bivariate and multivariable logistic regressions analyses were performed at 95% confidence level.

**Results:** All 384 recruited pastoralists (175 agro-pastoralists and 209 nomadic pastoralists) participated in the study. Majority (65.2%) of them had no formal education. Only 10.9% of

participants knew antimicrobials misuse to be when given under-dose, 10.2% indicated when given over-dose and 58.9% had no idea of what misuse entailed. Majority (51.6%) of respondents did not know about effects of improper antimicrobial usage in lactating cows. More than half (61.7%) reported self prescription of antimicrobials used in lactating cows. Regarding antimicrobials dosage determination before use, 65.4% of pastoralists reported arbitrary applications. More than half (53.4%) of respondents used antimicrobials for therapeutic purposes, 24.2% of them used antimicrobials for preventive purposes, and 15.4% of them to increase milk yield. Frequently used antimicrobials by pastoralists were tetracycline (98.7%), neomycin (96.6%), sulfonamides (95.8%), penicillin (95.3%), streptomycin (94.3%), and gentamicin (86.2%). Significant perceived risk pathways for dissemination of antimicrobial resistant pathogens through lactating cows were: consumption of contaminated raw milk ( $p < 0.001$ ); handling of contaminated udder and milk ( $p < 0.001$ ); and discarded contaminated milk in the environment ( $p = 0.010$ ). Socio-economic factors that significantly influenced antimicrobials misuse were: improper antimicrobial usage (OR=26.2; CI: 13.79–49.59), non-enforcement of laws regulating antimicrobial usage (OR=4.8; CI: 3.05–7.46), weak financial status of pastoralists (OR=4.5; CI: 2.88–7.07), pastoralists' low education and expertise (OR=5.4; CI: 3.43–8.57), and extensive husbandry system (OR=9.2; CI: 5.77–14.62).

**Conclusions:** This study highlighted overall low levels of knowledge and practices towards antimicrobial usage in lactating cows among surveyed pastoralists. To effectively combat menace of antimicrobial resistance in lactating cows, it is imperative to promote prudent antimicrobial usage through registered veterinary services, and raise pastoralists' knowledge/awareness about consequences of resistance in humans and animals. Antimicrobials misuse in lactating cows is influenced by pastoralists' socio-economic activities. Gradual reform of these activities through multifaceted public-animal-environmental health strategies is recommended, as these would assured food safety, food security, public and environmental health.

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## Inappropriate Use of Antimicrobials and the Determinants Among Patients Hospitalized in Three Hospitals (Mizan, Bonga and Tepi) in Southwest Ethiopia

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**Background:** World Health Organization (WHO) estimated that 80% of antibiotics is used in the community, of which about 20-50% is used inappropriately. Inappropriate use of antimicrobials leads to produce drug resistance which is one of the major issues. The spread of antimicrobial resistance in developing countries is associated with complex and interconnected factors. Accordingly, there is poor controlling system in use of all the available antimicrobials in the hospital. This facilitates for the spread of inappropriateness of prescribing ending up with emergence and spread of antimicrobial resistance. The study aimed to assess the inappropriateness of the use of antimicrobials and the associated factors among patients admitted in 3 hospitals in southwest Ethiopia.

**Materials & Methods:** The study was conducted in Bonga, Tepi and Mizan general hospitals of Keffa, Sheka and Benchi Maji zones, South west Ethiopia from March 1-30, 2015. A prospective observational study design was employed at medical wards of the hospitals. The antimicrobial therapy was reviewed to assure compliance with the recommendations of the national guidelines or/and evidence based clinical guidelines. The charts of all hospitalized patients who received an antimicrobial agent were reviewed, and the pertinent data on patient, disease and drugs used was recorded anonymously in a patient specific protocol using the pre-prepared data abstraction format. Each patient was then asked for compliance related problems and the responses filled to the same checklist. Data was analyzed using SPSS, version 16.0. The logistic regression model was fit to determine the association between the patient specific factors and the occurrence of the different types of DTPs. Comparison of factors contributing for drug therapy problems at patient level was

shown using odd ratios. Statistical significance was considered at p-value <0.05.

**Results:** A total of 348 antimicrobial containing orders were prescribed for the 291 patients during the 2525 person-days of follow up. At least one antimicrobial use problem was identified among most (80.1%) of the patients. Moreover, the use of antimicrobials for non-infectious diseases such as, asthma exacerbation, heart failure, cor-pulmonale and noninfectious diarrhea in the absence any laboratory test suggesting the infection was found to be rampant. This practice significantly contributes for antimicrobial resistance. The multivariate logistic regression showed that the use of social drug [AOR=2.549(1.279-5.080) at 95% C.I.; p value=0.008], the use of antimicrobial in the previous 3 months [AOR=4.095(1.855-9.040) at 95% C.I.; p value=0.000] and the total number of drugs used [AOR=2.997(1.413-6.356); p value=0.004 for 3-4 drugs and AOR=4.653(1.985-10.906); p value=0.000 for  $\geq 5$  drugs at 95% C.I.] were independently associated with antimicrobial use problems.

**Conclusion:** At least one antimicrobial use problem was identified among most of the hospitalized patients. The independent determinants of antimicrobial use problems were the total number of drugs used, use of social drugs and the previous use of antimicrobials. The hospitals and the stakeholders should closely monitor the use of antimicrobials and provide the necessary trainings.

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## Propagation of Drug Resistance by Clinicians Through Concurrent Treatment of Malaria and Typhoid Fever Among Patients Presenting with Febrile Illnesses in a Municipal Hospital in Ghana 2017

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**Introduction:** Malaria and typhoid fever are well known undifferentiated febrile illnesses which may be responsible for varying degrees of morbidity and mortality in developing countries. In Ga West Municipal Hospital (GWMH), malaria cases increased from 3934 in 2015 to 4603 in 2016. Typhoid fever also increased from 1369 to 2033 during the same period. People in endemic areas are at risk of contracting both infections concurrently due to insanitary conditions. Due to similar clinical presentation, clinicians treat concurrently which may lead to drug resistance and exposure of patients to side effects of antibiotic. These study was conducted to determine the proportion of malaria and typhoid fever co-infection and susceptibility patterns of the Salmonella isolates to antimicrobial agents.

**Methods:** A hospital based analytical cross sectional study was conducted to collect both qualitative and quantitative data on patients reporting with temperature  $\geq 37.5^{\circ}\text{C}$  at the out-patient department of the GWMH between Februarys to May, 2017. Blood samples were collected for blood culture, Widal test, and blood film preparation for microscopy. Data were analyzed using Stata version 13 statistical software.

**Results:** Total of 157 patients aged 2-37years with a mean temperature of  $38.7\text{ }^{\circ}\text{C} \pm 0.7$ . The median age of participants was 6years (IQR=3-11years). Out of the 157 febrile patients, 57/157(36.31%) had malaria, 23/157 (14.64%) had typhoid fever using Widal test and 10/157 (6.37) by blood culture. Other bacteria isolates are Staphylococcus aureus 18 (11.5%), Escherichia coli 8 (5.1%), Klebsiella spp.

5 (3.2%) and Citrobacter 1 (0.6%). Comparing patients with only malaria, the geometric mean parasite density was 174485 (45782-665000) for those with co-infection (p-value=0.009). Malaria for male 31/57(54.4%) and typhoid 6/10(60%). With age  $\leq 10$ ; malaria 42/57 (73.7%) and typhoid 8/10 (80%). The co-infection of malaria and typhoid fever using Widal test and blood culture was 5.73% and 1.91% respectively. The isolates exhibited high resistance ranging from 60%- 100% against ampicillin, tetracycline, co-cotrimoxazole, gentamicin, cefuroxime, chloramphenicol, and meropenem. The sensitivity also ranged from 66.7% - 100% against cefotaxime, ceftriaxone, ciprofloxacin and amikacin. No isolate of Salmonella typhi was susceptible to gentamicin, cefuroxime and co-trimoxazole. Other species of Salmonella were also not susceptible to tetracycline, ampicillin, co-trimoxazole and cefuroxime. All of the Salmonella isolates were susceptible to ciprofloxacin and amikacin.

**Conclusion:** Due to the low prevalence of malaria and typhoid fever co-infection, Clinicians should investigate febrile cases to identify the causes of their illness prior to treatment

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## A Situation Analysis of Antibiotic Consumption and Its Potential Contribution to Antimicrobial Resistance in Nigeria

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**Introduction:** Globally, human antibiotic consumption rate grew by >30% between 2000 and 2015 with significant increases recorded in low to middle-income countries. A Technical Working Group was set up to conduct a situation analysis on antibiotic consumption in Nigeria. The objectives were to describe antibiotic use in humans and animals, define its potential impact on the occurrence of antimicrobial resistance (AMR).

**Methods:** The assessment took place between January and April 2017. We reviewed online literature, reports, programmatic data and documents and key informant interviews with stakeholders in human and animal health sector. A systematic review of observational studies on antibiotic use in humans was conducted and primary data on antibiotic consumption in animals was reviewed. For numeric data, frequencies and proportions were calculated and qualitative responses were analysed using a thematic approach.

**Results:** Five regulatory bodies and 22 laws and policies exist to define and regulate medicine distribution and use in Nigeria. However, the medicine distribution system was described as chaotic and the ratio of licensed pharmacies to unlicensed premises was 1:5. Antibiotics account for 15% of locally produced medicines market share and 24% of registered medicines in Nigeria. Up to 16 billion grams and litres of antibiotic tablets and

syrup are manufactured locally, but large quantities are also imported. The systematic review put the median prevalence of persons using antibiotics without prescription in Nigeria at 46.8%. The proportion of antibiotics used in animal health rose from 8% in 35 % between 2014 and 2015, with a 2000% increase in tetracycline use.

**Conclusion:** Potential drivers of antibiotic consumption and AMR include an over-reliance on imported pharmaceuticals, shortage of licensed prescribers leading to unregulated antibiotic sales. We recommend that the government enforce regulations on access to antibiotics in humans and animals. The identified gaps were used to determine priorities for AMR surveillance in the National Action Plan.

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## Implementation of the Epidemiological Telephone Conference (EpiTec) in Tunisia, 2016-2018

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**Background:** Indicator-based surveillance is no longer sufficient to respond in a quick, flexible, and adequate manner to public health challenges. Therefore, event-based surveillance (EBS) becomes necessary to respond to urgent public health threats. In Tunisia, the weekly epidemiological teleconference (EpiTec), which is an innovative surveillance method providing a structured scientific platform for regular exchange about current events related to infectious diseases, was implemented in March 2016 in collaboration with Robert Koch Institute (RKI). Our aim is to share the Tunisian EpiTec experience, to cite the most frequently reported events and to assess challenges for sustainability.

**Methods:** Surveillance experts from the Strategic Health operations Center (Shocroom), National Observatory for New and Emerging Diseases (ONMNE), Primary Healthcare Direction (DSSB), Pasteur Institute of Tunis (IPT) and focal points from 24 governorates jointly developed a standardized operating procedure (SOP) for EpiTec implementation during workshops from 2015 to 2016. In April 2016, a simulation exercise was conducted to refine the procedures and to share a real operational EpiTec experience. Participant satisfaction was evaluated using an online survey in August 2017 and the EpiTec SOP was adapted accordingly during workshops in September and October 2017.

**Findings:** The first EpiTec was held on March 13, 2016. Since then, the median number of participants per conference was  $10 \pm 0.73$  (range 4-16). The highest participation rate per governorate was 86.4%, followed 77.3%). . Out of 24 regions, 22

participated at least once and the average number of events reported per EpiTec was  $3.5 \pm 0.45$  (range 1-7). The main reported events were hepatitis A, SARI/ILI, human rabies, tuberculosis and brucellosis. The evaluation in 2017 showed that the majority of the participants felt well prepared to actively participate in the teleconferences and that they found the required amount of time adequate. The continued participation of all stakeholders and an agreement regarding the kind of events that should be reported via EpiTec was recommended.

**Conclusion:** EpiTec is a new surveillance method in Tunisia, commitment of all stakeholders and implementation of the recommendations from the evaluation are required to improve it. A training curriculum targeted at local, regional and national level is currently being developed to reinforce its implementation.

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## The Development of Smartphone-Connected Point-of-Care Tests for the Diagnosis of Ebola Virus Disease

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**Background:** Ebola virus disease (EVD) causes widespread and highly fatal epidemics in human populations. Most of the cases occur in rural areas with a limited access to an equipped laboratory, trained personnel and a poor ability to transport the samples for evaluation. Today, there is still a great need for point-of-care tests for diagnosis, patient management and surveillance, both during and post-outbreaks. Here, we present the development of point-of-care tests comprising an immunochromatographic strip and a smartphone reader, which detects and semi-quantifies Ebola-specific antibodies in human survivors.

**Materials and Methods:** We designed and produced a lateral flow-based assay with specifically-engineered recombinant Ebola viral proteins and combined this with a custom smartphone application for semi-quantitative detection of EVD immunoglobulin G (IgG) antibodies in human serum. We utilised serum samples obtained from EVD survivors to validate the performance of our assay.

**Results:** Our monoplex platform and validated it using sera from 90 human survivors and 31 local non-infected controls. The performance of the glycoprotein monoplex was 100% sensitivity and 98% specificity compared to standard whole antigen enzyme-linked immunosorbent assay (ELISA) and it was validated with freshly collected patient samples in Africa. Moreover, we constructed a multiplex test for simultaneous detection of antibodies against three recombinant

viral proteins. A pilot study comprising 15 survivors and 5 non-infected controls demonstrated sensitivity and specificity of 100% compared to standard ELISA. Finally, we developed a second multiplex subtype assay for the identification of exposure to three related EVD species: Sudan virus, Bundibugyo virus and Ebola virus (formerly Zaire) using recombinant viral glycoprotein. This multiplex could distinguish between the host's immunity to specific viral species and identify cross-reactive immunity. These developed serological platforms consisted of capture ligands with high specificity and sensitivity, in-house developed strips and a compatible smartphone application. Moreover, early-stage research towards a smartphone connected test for the diagnosis of the acute stage of EVD via direct antigens detection will also be presented. These platforms enabled rapid and portable testing, data storage and sharing as well as geographical tagging of the tested individuals in Uganda. This platform holds great potential as a field tool for diagnosis, vaccine development, and therapeutic evaluation.

**Conclusion:** The platform combines lateral flow strip technology with a custom-designed smartphone app, providing a rapid, robust, simple, and portable device for the specific and sensitive detection of IgG antibodies in EVD human survivors. Our system shows great potential for use as a point-of-care test for the surveillance

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## Recent Outbreak of Monkeypox in Nigeria a Major Threat to Global Health Security: An Urgent Call for Rapid Action

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**Background:** Monkeypox virus remains the most pathogenic poxvirus of this present time, being mainly restricted to Central Africa, with some few foci in West Africa. Before 1970, there were no reports of human monkeypox in Nigeria while three cases were reported between 1971 and 1978. In September 2017, a case of contagious skin rash syndrome typical of monkeypox was observed in an 11-year old boy from the southern part of the country and confirmed to be associated with the monkeypox virus. So far, this has been the largest outbreak in the whole West African region. Similarly, the report of the imported cases to the US and UK suggests that Monkeypox is now a major threat to global health security requiring an urgent multidisciplinary approach to fast track the development of diagnostic assays, vaccines, antivirals and other control strategies.

**Materials and Methods:** Relevant literature search for articles published in English and in peer reviewed journals was conducted to retrieve the most updated, comprehensive and timely information about monkeypox including the most recent and the largest outbreak ever documented in Nigeria.

**Results:** Between September 2017 to October 15 2018, two-hundred and sixty-two suspected and 115 confirmed cases of human monkeypox including seven mortalities were reported in Nigeria. Similarly, two cases were separately imported to the UK for the first time in Europe and were travel associated in September 2018. A third health care worker related case was reported in the UK while treating the second imported case.

**Conclusion:** The recent apparent increase of monkeypox across a wide geographic area suggested the potential for its further spread and

thus calls for an improved level of concern and action. The limited specific experience, surveillance capacity, laboratory capacities, disease treatment, infection control, and knowledge about the disease require further concerted global efforts to contain the disease. Although the development and license of tecovirimat as an antipoxvirus agent is an achievement in antipoxvirus therapy and the vaccinia virus vaccine can protect humans against monkeypox virus infection, symptomatic management and adequate environmental public health measures provide the foremost line of care, with reduced mortality and morbidity.

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## Yellow Fever Laboratory Capacity On-Site Assessments in Africa: Preliminary Findings

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**Background:** The global strategy to Eliminate Yellow fever Epidemics (EYE) was launched in February 2017 following two yellow fever (YF) outbreaks in Angola and Democratic Republic of Congo. This strategy aims at containing outbreaks rapidly, and preventing international spread. Due to the limited vaccine supply, one of the primary pillars of the EYE Strategy is to prioritize public health interventions based on risks. Given the current limitations in YF diagnosis capacity, particularly in Africa, a strong YF laboratory network is crucial to ensure rapid and reliable case confirmation and outbreak characterization. The objective of these assessments was to examine factors that can affect YF laboratory capacity, to inform investment decisions by the Global Alliance for Vaccines and Immunisation (GAVI) that recently agreed to a YF diagnostic strengthening initiative.

**Methods:** On-site assessments of the current and potential YF diagnostic capacity of the national public health laboratories in the Global Yellow Fever Laboratory Network (GYFLN) were conducted by four independent consultants in coordination with the World Health Organization (WHO) in African countries that are both eligible for GAVI support and at high risk of YF. Based on a standardized questionnaire, we examined procurement of reagents, supplies and equipment for YF laboratory tests, technical assistance to improve YF laboratory capacity and training, quality assurance/quality control (QA/QC) for YF testing, and transportation of samples from YF patients.

**Results:** A total of 23 national-, regional-, and proposed regional reference laboratories (RRL) were assessed, of which 17 (74%) do YF testing by IgM-Antibody Capture Enzyme Linked Immuno-

Sorbent Assay (MAC-ELISA). Twelve (71%) laboratories had stockouts of reagents in 2017; 11 out of 23 (48%) laboratories have incorporated molecular testing into their YF testing algorithm and 21 out of 23 (91%) laboratories have molecular testing platform, equipment, and trained staff. 16 of 23 (70%) laboratories including the RRLs use biosafety cabinets for handling clinical specimens. There is no routine program for YF serologic or molecular proficiency testing. The YF staff are generally well trained and experienced. Data management and results reporting systems are good, and the coordination and cooperation between laboratories and WHO is appreciable.

There is a strong coordination between the national surveillance program and laboratory with a good domestic sample transport system. However, international sample transport for confirmation of initial test findings to the RRL is not efficient due to lack of funds and/or collaboration of transporters, leading to delays in confirmation ranging from one to three months.

**Conclusion:** These baseline data are essential for the improvement of YF laboratory diagnostic capacity, both at national and regional levels. Priority should therefore be given to: management of MAC-ELISA reagents and supplies procurement and distribution; production/distribution of validated YF MAC-ELISA kits; procurement of molecular testing equipment, supplies, YFV laboratory diagnostics and management training workshops, QA/QC programs, and accreditation. In addition, we recommend contracting courier services; and technical training for preventive maintenance and calibration of equipment. An overall willingness of governments to sustain the laboratory activities at the end of GAVI support was noted.



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## Drug Resistance Among HIV-Affected Pregnant Women in Rural Hospitals 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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## Multi-Drug Resistance Profile of Bacteria Isolated from Blood Stream Infection at Tikur Anbessa Specialized Hospital, Addis Ababa, Ethiopia

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**Background:** Hospital acquired bloodstream infections are major cause of mortality and morbidity.

**Objective:** To assess bacteria implicated in causing blood stream infections and their multi-drug resistance profile.

**Method:** A single institutional cross-sectional study was conducted at Tikur Anbessa Specialized Hospital from September 1/2016 to October 30/2017. A total of 422 blood samples were collected and cultured on blood agar bottles and bacteria were isolated and characterized by conventional methods. Antibiotic susceptibility testing was carried by Kirby Bauer disc diffusion technique.

**Results:** Out of a total of 422 samples processed, bacterial pathogens were isolated from 64 (15.2%) samples. Among the isolates, 29 were Gram-positive and 35 were Gram negative bacteria. Staphylococcus aureus and Klebsiella pneumoniae were the dominant isolates. Penicillin (86.7%) was the least effective antibiotic against Gram-positive bacteria while ampicillin (85.7%) and amoxicillin clavulanic acid (77.14%)

were the least effective antibiotic against Gram-negative bacteria. Clindamycin (80%) and amikacin (97.1%) were the most effective antibiotic against Gram positive and Gram-negative bacteria, respectively. Out of 29 isolate of Gram-positive bacteria, 16 (55.2%) were multi-drug resistant of which 11 (35.9.3%) were extensively drug resistant and 2 (6.9%) were pan-drug resistant. Out of 35 isolates of Gram- negative bacteria, 26 (74.3%) were multi-drug resistant of which 18 (54.4%) were extensively drug resistant.

**Conclusions:** The magnitude of blood stream bacterial infection and the prevalence rate of multi-drug resistant bacterial strains causing blood stream infections were high. These findings warranted the need for continuous investigations of bacteria implicated in causing blood stream infection and evaluation of their antibiotic susceptibility profile in health institution large scale.

**Aberrations:**

MDR: Multidrug-Resistant; XDR: Extensively Drug Resistant; PDR: Pandrug Resistant; CONS: Coagulase Negative Staphylococci; BSI: Blood Stream Infection

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## Antiretroviral Therapy Response Among HIV-1 Patients With Opportunistic Infections in Sudan

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**Introduction:** Human Immunodeficiency Virus-1 (HIV-1) becomes a threat concern recently, many subtypes developed resistance against most common antiretroviral therapies especially in co-infections such as rifampicin.

**Objectives:** to determine Antiretroviral Resistance and patterns of opportunistic infection among HIV patients.

**Methods:** Samples were implemented using routine surveillance to utilize among 200 positive HIV patients tested by ELISA and (RT-PCR) sequencing for resistance using dried plasma spot. Virus load was used to monitor the course of disease and the response to antiretroviral therapy. T-cell count test gives an indication of CD4 cells in a person's bloodstream. The HIV-1 pol region from the viral clones of index patients, source patients in the same geographical area and wild-type HIV-1 subtype's strains were aligned to confirm the linkage between sources and index viruses, the sequence alignments were generated using Clustal W 1.6. The intra-variability percentage of each viral population, pairwise evolutionary distances were estimated using Kimura's two-parameter and maximum likelihood methods. The trees were then constructed using the neighbor-joining method.

**Results:** Around 90.9% cases were found to be HIV-1 positive and 9.1% were negative. The distribution of HIV-1 subtypes in North Sudan (A and C) (1.0%), in East Sudan (A, C and D) (8%, 9% and 3%), in West Sudan (3%, 7% and 2%) and in Center Sudan (19%, 6% and 3%). In South Sudan State (A, C and D) (15%, 10% and 13%) respectively. Patients responding to antiretroviral therapy was 71% and those non-responding was 29%. The opportunistic infection found among patients' were (36%) Fungal infection, Viral infection, Tuberculosis, other Bacterial infections (32%). HIV- 1 subtypes among intravenous drug users was (2%) subtype (A), (3%) subtype (C) and Non IDU subtype was (44%) subtype (A), (30%). HIV-1 subtype and Opportunistic infection were viral infection (12%) subtype (A), (8%) were subtype (C) subtype (D). Tuberculosis (12%) subtype (A), (16%) subtype (C) and (4%) subtype (D). Other bacterial infections (1%) subtype (A). According to our results, we found that, there was no significant association between HIV-1 subtypes and opportunistic infection,  $P > 0.05$ , The different clinic with subtypes were dermatology, surgery and psychiatry clinic the common subtypes found on the patients were subtype (A), (C), and (D), we found that the most common subtype was subtype (A). The study showed no significant association between HIV-1 subtypes and patient's attending different clinics  $P > 0.05$ , Moreover association between Blood transfusion as mode of transmission – and HIV-1 subtypes  $P > 0.05$ . The confirmed HIV-1 positive patients given the antiretroviral drugs named triomune after three months of treatment, the CD4 count was re-estimated as indication and monitoring for Antiretroviral drugs response and resistance.

**Conclusion:** Determining the antiretroviral therapy resistance and opportunistic infection with HIV characterization is very important for clinical decision to obtain more facts about the virus polymorphisms, mutation, ARVs resistance and to determine the circulatory recombinant Forms(CRFs). Determination of the association between HIV Tuberculosis patients treated with ARV and Rifampicin is a key role in building our policy and strategy for HIV treatment and vaccination.

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## Methicillin Resistant Staphylococcus Aureus (MRSA) in Africa—Prevalence and Associated Factors: A Systematic Review

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**Background:** MRSA have been included in the list of high priority WHO, which requires urgent intervention, which is paradoxical for sub-Saharan Africa, where diagnostic means are lacking. The purpose of this systematic review is to highlight the prevalence and associated factors among studies that have been conducted in sub-Saharan Africa.

**Methods:** We searched the PubMed database in August 2018 using the search term 'prevalence AND methicillin-resistant Staphylococcus aureus AND Africa' to find articles published from 2017 onwards.

**Results:** Our search strategy allowed us to select 77 publications, of which 26 corresponded to our criteria. Most studies come from East and South Africa (Malawi=1, Tanzania=3, South Africa=4, Kenya=1, Ethiopia=2, Botswana=2, Uganda=2, Zambia=1) and few studies from West and Central Africa (Angola and São Tomé and Príncipe =1, Democratic Republic of the Congo=1, Ghana=3, Mauritania=1, Nigeria=1, multi-country (Benin, Congo, Togo, Madagascar) =1, and the other two were systematic reviews. Prevalence of MRSA in

ranged between 2.8% to 50% of *S. aureus* Isolates. There are two sources of transmission, community acquired (CA) and Hospital-acquired (HA) MRSA. CA-MRSA and HA-MRSA infection represent respectively 2.3% and 26.8% of all Staphylococcus aureus bacteraemia (SAB). CA-MRSA rate in suppuration was 25 and 26%. Even if MRSA nasal carriage rate is high in Tanzania, nasal swabs were collected from pre-school children in Ethiopia and showed no MRSA, the same result has been reported in Zambia. MRSA is common among HIV-infected individuals with asthma and eczema. The risk of complicated infection is high with non-optimal definitive antibiotic therapy. In Africa the distribution of CA-MRSA clones is unclear. The most prevalent spa types were t037, t084, and t064 in Africa.

**Conclusion:** Data on MRSA are becoming increasingly available in sub-Saharan Africa with high prevalence, which implies the provision of an adequate technical platform for molecular characterization to better investigate during epidemics.

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## Bacterial Isolates and Their Current Drug Susceptibility Profile from Urine Among Asymptomatic Pregnant Women Attending at the Felege Hiwot Referral Hospital Antenatal Clinic, Northwest Ethiopia

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**Background:** Asymptomatic bacteriurias (ASB) are common during pregnancies that have potentially serious consequences for maternal and fetal health. The rapid emergence of antimicrobial resistance necessitates continuous monitoring of the

susceptibility patterns of pathogens in the urinary tract of pregnant women. The purpose of this study was to identify bacterial pathogens from asymptomatic pregnant women and by extension to determine the antimicrobial susceptibility profile of these isolates.

**Methods:** A prospective cross-sectional bacteriological study was conducted at Felege Hiwot Referral Hospital (FHRH) from 1 Feb to 30 May 2016. Freshly voided clean catch midstream urine samples were collected and processed using conventional culture and biochemical tests as per the standard protocol. A concentration of >105 cfu/ml in urine sample was considered culture positive for asymptomatic bacteruria (ASB). Isolates were tested against the commonly used antibiotics by Kirby-Bauer disc diffusion methods. The degree of susceptibility pattern was determined based on the Clinical Laboratory Standards Institute. Descriptive and Chi-square test was done using SPSS version 22,  $p < 0.05$  was considered to be significant.

**Results:** Out of the 234 pregnant women attending the antenatal clinic in the study site, 11.5 % (27/234) were positive for ASB. The mean age of participants was at 26.8 years (ranged 18–41 years). The majority, 139 (59.4%) and 134 (57.3%) were primigravida and at the 3rd trimester, respectively. Similarly, among the study subjects, 20 (8.5%) were HIV sero-positive. A total of 27 bacterial uropathogens were identified. Out of these, Gram positives consisted at 20 (74.1%). The predominant isolates were *S. saprophyticus* at 48.2% (13/27) followed by *S. aureus* at 22.2% (6/27) and *E. coli* at 11.1% (3/27). Eleven (84.6%), 10 (76.9%) and 9 (69.2%) of 13 isolates of *S. saprophyticus* were found to be resistant for co-trimoxazole, oxacilin and tetracycline respectively. No resistance was documented for amoxicillin-clavulanic acid and ciprofloxacin among gram positives. History of diabetes was found significantly associated with ASB ( $p=0.019$ ).

**Conclusions:** The observed prevalence of ASB and drug resistance profile of the isolates call stakeholders to strength the infection prevention practices in the study area.

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## Surfaces and Air Bacteriology of Selected Wards at a Referral Hospital, Northwest Ethiopia

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**Background:** The Hospital environment is a reservoir for medically important pathogens that are mostly multidrug resistant (MDR) thus posing a major therapeutic challenge. The aim of this study was to assess the surface and air bacterial profile and their current antimicrobial resistance report of selected wards at Felege Hiwot Referral Hospital (FHRH), Northwest Ethiopia.

**Methods:** A hospital based cross-sectional study was carried out from 15th February to 30th April 2017. A total of 356 surface and air samples were collected from selected wards using 5% sheep blood agar (Oxoid, UK) as per the standard protocol. The samples were processed following standard bacteriological procedures at FHRH microbiology laboratory. Pure isolates were tested against nationally recommended antibiotics using Kirby-Bauer disc diffusion methods and the susceptibility pattern was determined based on Clinical Laboratory Standards Institute (CLSI). Data were entered and analyzed using SPSS version 23 for Windows.

**Results:** Of the total 356 samples processed, 274 were from surfaces and 82 were from air. Among these, 141 (39.6%) showed bacterial growth, some with mixed growth in which a total of 190 isolates were identified. Gram positive isolates were predominant at 81.6% ( $n= 155$ ) while the gram negatives were at 18.4 % ( $n= 35$ ). The main isolates were Coagulase negative staphylococci (CoNs), 44%, followed by *S. aureus* ,37.4%, and *Klebsiella* species at 11.6%. The bacterial load on surfaces and air were found beyond the standard limits. Besides, the antimicrobial susceptibility profile of the isolates showed that the overall sensitivity for Norfloxacin was at 76.7% and 79.8% for gram positive and negatives, respectively. About 75% of the identified isolates were found resistant for two and more antimicrobial agents tested.

**Conclusions:** This study showed high degree of bacterial load that is beyond the standard limits on both surfaces and air samples of the hospital. Further, some 75% of the isolates were found multi drug resistant. Therefore, it is important to evaluate and strengthen the infection prevention practice of the hospital. Moreover, stakeholders should also reinforce actions to decrease the pressure of antimicrobial resistance in the studied area.

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## Mechanism of Pseudomonas Aeruginosa Resistance to Carbapenems in Kinshasa

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### Summary:

P.Mampasi;o.Lunguya;jj.Muyembe;P.Mbaya;M.F.P.hoba;E.Bonebe;2015

**Background:** Pseudomonas aeruginosa (P. aeruginosa), an opportunistic pathogen is a major responsible for frequent and serious nosocomial infections such as pneumonia, skin infections secondary to burns, urinary tract infections, joint infections and bacteraemia. Recent global trends show an increase in the prevalence of nosocomial infections caused by Pseudomonas aeruginosa with documented resistance to  $\beta$ -lactams, carbapenems, aminoglycosides and fluoroquinolones.

**Objective:** The main objective of our study was to identify Pseudomonas aeruginosa resistance to carbapenems mechanisms in Kinshasa in order to contribute to the improvement of the management of infections caused by Pseudomonas aeruginosa.

**Methods:** This was a descriptive cross-sectional study, conducted from 31 July 2014 to 31 May 2015 in six different medical facilities. The synergy tests were performed to distinguish strains resistant to ceftazidime overproducing the natural cephalosporinase AmpC those producing  $\beta$ lactamase broad spectrum type ESBL, MBL or ES-

OXA. All hospitalized patients or not having an infection with Pseudomonas aeruginosa resistant to imipenem and meropenem were included in the study. Data analysis was made by SPSS 21. The chi square tests software for meaning.

**Results:** The prevalence of Pseudomonas aeruginosa infection with class B carbapenemase was 42.2%, it concerned mostly aged 30-42 years, 35.6% followed by the age group between 17 -29 years and 56-68 years, 20.0% and urinary tract infection was in first position, followed so it 46,7% of musculoskeletal infection, or 24.4%. The different mechanisms detected were mostly Class B carbapenemases 42.2% penicillinases 8.9%, or 6.7% cephalosporinase and ESBL, or 2.2%.

**Conclusion:** The study of Pseudomonas aeruginosa resistance to antibiotics, especially shows a resistance to carbapenems multi followed penicillinase, cephalosporinase well as ESBL, which must be considered by implementing an active prevention strategy.

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## Etiologies of Diarrhea and Drug Susceptibility Patterns of Bacterial Isolates Among Under-Five Year Children in Refugee Camps in Gambella Region, Ethiopia: A Case Control Study

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**Background:** Despite substantial global effort and updated clinical management guidelines, diarrhea continues to be among leading worldwide causes of morbidity and mortality in children. Infectious diarrhea, the most common form of diarrhea causes substantial morbidity and mortality among children in developing countries, and the muddled

use of antibiotics needs caution due to potential problems of drug-resistance, side-effects and cost of treatment. The aim of this study is to identify etiologies of diarrhea and drug susceptibility patterns of bacterial isolates in under-five children in refugee camps in Gambella Region, Ethiopia.

**Methods:** An institution- based matched case control study was conducted using a questionnaire-based interview from June to December 2017 in Pugnido and Teirkidi refugee camps. Stool samples were collected and diarrhea etiologies identified by wet mount microscopy and conventional culture supplemented with API 20E identification kit. Antibiotic susceptibility of bacterial isolates was investigated by using the disk diffusion method. Pathogenicity was analyzed using McNemar test or Fisher exact test with a level of significance of P 0.05.

**Results:** The overall prevalence of enteric pathogens were 55 (41.0 %) in diarrhea cases and 18 (13.4 %) in healthy controls. The detected etiologies include *Giardia lamblia* (28), *Shigella* spp. (16), *E. histolytica/dispari* (13), *Ascaris lumbricoides* (10), *Salmonella* spp (6), *Cryptosporidium parvum* (6), *Hymenolepis nana* (4) and *Isospora belli* (3). All isolates were sensitive to kanamycine and ceftazidime. The high resistance rate was observed against ampicillin (100%), amoxicillin (100 %), erythromycin (52%), chloramphenicol (47.5 %), tetracycline (40.5 %), cotrimoxazole (34.8 %) and amoxicillin-clavulanic acid (33 %). The majorities of the isolates had a low rate of resistance to ciprofloxacin (8.7 %), nalidixic acid (8.7 %) and amikacin (13 %).

**Conclusions:** *Giardia lamblia*, *E. histolytica/dispari*, and *Shigella* spp are the major etiologies of diarrhea in children in the studied refugee camps. The study also showed that significant numbers of bacterial isolates resist the commonly used antimicrobial drugs. Therefore, improving clinical laboratory services and promoting evidence-based drug prescription may reinforce proper use of antibiotics and reduce the emergence of microbial resistance.

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## Factors Associated with Multidrug-Resistant Tuberculosis During an Outbreak: Arua District, Uganda, 2013-2017

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**Background:** Multidrug-resistant tuberculosis (MDR-TB) causes higher mortality and requires more expensive, prolonged treatment than non-resistant TB. In 2015, 68% of TB treatment in Uganda was directly observed. In mid-August 2017, Arua District, Uganda reported increased MDR-TB cases to Ministry of Health. We investigated to evaluate the extent of the problem, identify risk factors for MDR-TB, and recommend control measures.

**Methods:** We defined a confirmed MDR-TB case-person as a resident of Arua District from 2013-2017 with a clinical sample yielding rifampicin- and isoniazid-resistant TB, confirmed by a drug susceptibility test. We conducted hospital record reviews and visitations of case-patients. In a case-control study, we compared risk factors for MDR-TB between case-patients and community-matched controls, selected among registered TB patients with isolates susceptible to rifampicin, confirmed by Xpert MTB/RIF assay. We used a checklist to assess infection prevention and control (IPC) practices in 10 treatment facilities for ambulatory MDR-TB patients and in community.

**Results:** We identified 33 cases. Mean monthly reported MDR-TB cases in 2017 (1.4) was nearly three times as high as during 2013-2016 (0.48) ( $p=0.02$ ). Cumulative incidence of MDR-TB was four times as high in men (2.1/100,000) as in women (0.48/100,000) ( $p=0.0001$ ). Of 33 case-person and 99 controls, 12 (48%) case-persons and 6 (6.1%) controls had interrupted treatment for  $\geq 3$  weeks (ORM-H=14, 95%CI=4.6-45); 17 (52%) case-persons and 30 (30%) controls had HIV co-infection (ORM-H=2.4, 95%CI=1.1-5.5). All facilities reported experiencing stockouts of anti-TB supplies. MDR-TB patients were not wearing masks in the communities during home visits.

**Conclusion:** Reported MDR-TB cases increased substantially in 2017 compared with previous four years. MDR-TB was associated with poor treatment adherence and HIV co-infection. Poor adherence may be linked to drug stockouts. We recommended training health workers to improve MDR-TB patients' adherence to IPC practices, and strengthening home visits by health workers.

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## Leishmania donovani: An In-Vitro Study of Antimony-Resistant Amphotericin B-Sensitive Isolates

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**Introduction:** Visceral leishmaniasis (VL) is a major health problem in the Sudan where control measures, that include case detection, treatment with antimonial drug and vector control, have been insufficient or practically difficult. The first line drug (antimonials) are expensive and beyond the reach of those who need it most, require long term daily injections, are associated with toxicity and are becoming useless due to increasing resistance in Sudan. This study was initiated in an attempt to determine the in vitro sensitivity of *Leishmania donovani* isolates from Sudanese VL patients with diverse clinical drug responsiveness to standard leishmanicidal drugs.

**Materials and Methods:** Eight isolates, six from antimony-resistant and two from clinically responsive patients were included in the study. Parasites were tested as promastigotes and four of them were selected to be tested as amastigotes using a murine macrophage-like cell line. The results indicated that the conventional promastigotes and amastigotes-screening assays did not correlate with the clinical picture of patients. In vivo unresponsiveness does not necessarily mean primary parasite resistance.

**Results:** The results indicated that the conventional promastigotes and amastigotes-screening assays did not correlate with the clinical picture of patients. Increasing concentrations of SSG diminished the incorporation of the [3H]thymidine in a linear fashion compared to the control values in both sensitive and resistant isolates. [3H]thymidine uptake was inhibited in all isolates in a linear fashion with increased concentrations of amphotericin B. In the macrophage assays, the four parasites tested were highly infective to the cells (80–99%) and exhibited moderate to high intracellular replication potentials.

**Conclusions:** Amphotericin B could be a suitable second line drug in patients unresponsive to pentostam and without concomitant diseases, if close hospital monitoring is available. Promastigotes sensitivity testing concentrations are virtually incomparable with the in vivo clinically curable doses and the amastigotes/macrophage test concentrations.

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## The Risk of Cross-Infection and Factors Influencing the Decision of Healthcare Workers in Rural Clinics in Ghana

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**Background:** Clinical gloves are routinely used in the delivery of patient care but unless integrated with the '5 moments of hand hygiene' have the potential to increase the risk of HCAI transmission. To examine glove use in an acute care setting, the extent to which they are associated with a risk of cross contamination, and factors that influence healthcare workers (HCW) decision to wear them.

**Method:** Observation of the use of clinical gloves was conducted in 6 wards by two trained observers. Independent observations were compared for inter-rater reliability. Glove use was considered appropriate if the episode involved potential contact with blood/body fluid (BBF). Risk of cross

contamination was defined as violation of one or more of the 'moments of hand hygiene' during the glove-use episode. Semi-structured interviews were conducted with a purposive sample of 25 HCW from audited wards to explore attitudes towards the use of gloves.

**Result:** 164 glove use episodes were observed over 13 hours. Glove use was appropriate in 58% (95/164) of episodes, but gloves were commonly used for procedures with minimal risk of exposure to BBF. In 39% of glove-use episodes there was a risk of cross contamination, this was significantly more likely to occur where gloves were used inappropriately (58.4% vs 28.4%; Chi2 p <0.01). In 24% (39) episodes more than 5 objects were touched by a gloved hand before the procedure was performed. In one third of episodes, hand hygiene was not performed after glove removal. The key themes from qualitative interviews with HCW indicated that the decision to wear gloves was influenced by multidimensional socialization and emotion. Key emotions were disgust and fear, but assumptions about patients and their preferences regards glove use, confusion about when to wear them and peer pressure, were also important influences.

**Conclusion:** Glove use in acute clinical settings is associated with a significant risk of cross contamination and needs to be more explicitly integrated into hand hygiene policy. An understanding of drivers of glove use behaviour is required to design interventions to reduce their misuse and overuse.

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## Antimicrobial Resistance Surveillance Among Gram Negative Bacterial Isolates from Patients in Khartoum State Hospitals

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**Background:** Antimicrobial resistance (AMR) among Gram-negative bacilli is a global health

problem. Surveillance of AMR is required to advise on empirical antimicrobial therapy. This study aimed at evaluating the frequency and the AMR patterns of Gram-negative isolates from patients treated in eight hospitals in Khartoum State, Sudan.

**Methods:** Across-sectional laboratory based study was conducted over six months period at the microbiology department, Soba University Hospital, Khartoum State, Sudan. All Gram-negative isolates from blood, urine, wound, and sputum during the period of study were included.

**Results:** A total of 734 Gram-negative bacilli were isolated. *Klebsiella* spp.249 (34%) was the most frequently encountered one, followed by *Pseudomonas* spp.153(21%), *E.coli* 123(17%),*Acinetobacter* spp.75 (10%), *Burkholderia cepacia* 42(6%),*Proteus* spp. 28(4%) *Enterobacter* spp. 28(4%),*Stenotrophomonas maltophilia* 21(2.8%), and others gram-negative bacilli 15(2.2%) The analysis of the antimicrobial susceptibility patterns showed that 134 (22.3%) isolates were multidrug resistant to three or more classes of antibiotics including cephalosporins,  $\beta$ -lactam- $\beta$ -lactamase inhibitor group, quinolones, aminoglycosides and carbapenems.

**Conclusion:** This high level of resistance among Gram-negative bacilli in Khartoum state hospitals is alarming. The local health authorities are prompted to step up infection control program and introduce the concept of antimicrobial stewardship in Khartoum State hospitals.

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## Characterisation of *Vibrio cholerae* Isolates Associated with Diarrhoea Outbreaks in Ghana

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**Background:** Ghana is regularly affected by Cholera outbreaks with an annual average of over 3,000



cases in two decades. In 2014, Ghana experienced an exceptionally large outbreak with over 20,000 cases. We therefore investigated and compared clinical *Vibrio cholerae* (VC) strains from outbreaks in Ghana with special reference to strain diversity and virulence factors acquired by these bacteria over time.

**Methodology:** A total of 219 stool samples were collected within 2012- 2015 from 9 health facilities in Ghana. Samples were cultured and obtained isolates characterised by biochemical assays, serotyping, drug susceptibility testing, phenotypic determination of extended-spectrum  $\beta$ -lactamases (ESBLs) activity, detection of distinct virulence genetic markers and multi-locus variable number tandem repeat analysis (MLVA).

**Results:** Among the 219 samples cultured, 110 (50.2%) yielded *Vibrio cholerae* O1 isolates and 109 (49.8%) were characterized as other bacteria (*A. sobria* :14 (12.8%), *V. parahaemolyticus* :2 (1.8%), *P. aeruginosa* :7 (6.4%), *E. Cloacae* :16 (14.8%), *E. faecalis* :31 (28.4%), *E. coli* :26 (23.9%), *K. pneumoniae* :6 (5.5%), *P. mirabilis* :7 (6.4%)) respectively. Out of the 110 VC, 4 (3.6%) were isolated in 2012, 92 (83.6%) in 2014 and 14 (12.7%) in 2015. This study identified 75% mono-resistance to cotrimoxazole in 2012 but close to 100% MDR to cotrimoxazole, nalidixic acid and ampicillin with reduced susceptibility to tetracycline, doxycycline and ciprofloxacin in both 2014 and 2015 isolates. Serotyping identified 97 (88.2%) Ogawa, 3 (2.7%) Inaba and 10 (9.1%) non-reactive. Genotypic analysis differentiated the isolates into 3 clones. MLVA is still in progress.

**Conclusion:** Microbiological analysis of three cholera outbreak years illustrate emerging Inaba serogroup and 3 clonal complexes, which might hint to an endemic reservoir of *V. cholerae* in Ghana. Considering the rapidly emerging MDRs among *V. cholerae* isolates, laboratories are encouraged to monitor antimicrobial susceptibility closely.

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## Prevalence of Extended Spectrum Beta-Lactamase Producing Enterobacteriaceae at Adama Hospital Medical College, Adama, Ethiopia

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**Background:** The beta-lactam groups of antibiotics are the largest group of antibacterial agents used in clinical

practice and they are the most frequently prescribed by physicians. The wide use of these antibiotics leads to the emergence and spread of resistant bacterial pathogens that produce the extended-spectrum  $\beta$ -lactamases (ESBL). In the present time ESBLs producer bacteria are commonly encountered in clinical practice and their prevalence varies from place to place. This group of bacteria poses the most serious threat to public health in the entire world. The aim of this study is to determine the prevalence of ESBL producing bacterial pathogens among Enterobacteriaceae isolates at Adama Hospital Medical College (AHMC), Adama, Ethiopia.

**Methods:** Across sectional study was conducted from May 1, 2013-June 1, 2014 at Adama Teaching Hospital. A total of 384 consecutive non-repeat culture isolates were obtained from different clinical specimens from patients visiting the hospital. Bacterial strains were isolated following standard bacteriological procedures. Antimicrobial susceptibility test was determined using Kirby-Bauer disk diffusion method and ESBL production was detected by modified double disc synergy test as.

**Results:** A total of 133 bacterial strains were isolated of which Enterobacteriaceae account for 68/133(51.1%). Twenty one isolates from the Enterobacteriaceae were suspected for ESBL production and 17/21 (80.95%) of them were confirmed to produce the extended spectrum beta-lactamase. The overall prevalence of ESBL producers within the Enterobacteriaceae is 17/68 (25%). *E. coli* with the prevalence of 10/35 (28.57%) is the leading ESBL producer while *Proteus* species, *Klebsiella* species, *E. cloacae* and *Citrobacter* species

accounted for 3/9 (33.3%), 2/8 (25%), 1/3 (33.3%) and 1/3 (33.3%) respectively.

**Conclusion:** The prevalence of ESBL producing Enterobacteriaceae was high among the clinical isolates of AHMC. The routine screening of ESBL producing microorganisms from clinical samples should be considered wherever and whenever it is found to be applicable. The factors contributing to the wide spread of ESBL must be controlled in order to prevent the emerging and re-emerging of these pathogens.

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## Faecal Carriage of ESBL-Producing E.coli Among Children in Ghana

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**Background:** Antimicrobial Resistance (AMR) is a phenomenon in which a bacterium survives the lethal effects of an antimicrobial that was originally effective for treatment of infection due to that bacterium. Developing countries most especially the African continent is most at risk of suffering the worse consequences of AMR because of poor prescription and dispensing practices, poor adherence to antibiotic treatment by patients, use of substandard antibiotics for treatment of microbial infections and general lack of policy directions on AMR.

**Aim/Objectives:** We conducted a cross-sectional study among children visiting antennal services in Tafo and Asokwa Government Hospital in the Ashanti regional of Ghana. The study was carried out in 2017 with the objective of determining the proportion of children and their mothers as carriers of Extended Broad Spectrum Beta-Lactamase producing E.coli (ESBL- E.coli).

**Methods:** Rectal swabs were collected from subjects and their mothers and transported to the laboratory via transport medium. The samples were

cultured on differential media and screened for ESBL- E.coli using the double disc synergy method. Bacterial isolates that were positive for the ESBL were further subjected to conventional PCR using primers specific for CTX, TEM and SHV genes. **Results:** Ninety (96) children were screened for ESBL producing E.coli out of which 69 (71.9%) were positive. Similarly, 57 (59%) of the parents of these children were also carrying ESBL E.coli. All positive isolates were further confirmed using conventional PCR and all yielded the genes CTX, TEM and SHV with CTX resistant gene being the most common.

**Conclusion:** The proportion of children carrying resistance microbes harbouring extended beta lactamase enzymes is high in Ghana. Resistance to cephalosporins family of antibiotics is particularly more predominant. Active surveillance is needed to understand the mechanisms for shedding these bacterial strains in the environment.

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## Identify Factors Contributing to MDR TB in Nyamira

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Multi Drug Resistance Tuberculosis (MDR TB) is one of the emerging diseases in the world. MDR is TB resistant to Rifampicin and isoniazid which are two of the first line drugs of ant tuberculosis drugs. Kenya is one of the countries that is affected by MDR TB with 326 cases identified in 2017. The First case of MDR TB was identified in Nyamira in the year 2013 and since then up to October 2018 a total of 28 cases had been identified.

A longitudinal cohort study was conducted between 2017 August and 2018 October with a broad objective of identifying factors contributing to MDR TB in Nyamira county. The study was done in four health facilities of Nyamira County. 14 MDR TB patients were purposefully selected and were observed over their treatment period, the data was analysed quantitatively and the results are as follows; 9 = 64% of the 14 patients were male aged 24-60 years, 4 = 29% were female aged 23-58 years and 1=7% of them was a male child aged 11 years.

7 out of 14 =50% were co infected with HIV and 7=50% were not infected with HIV. 7 out of the 9 men =78% abused alcohol and 3 out of the 4 =75% female also used alcohol. 10 out of the 14 patients=71% were casual laborers, 2 out of 14=14.5% were local brewers, 1 out of the 14=7% a maid and 1% a child of a casual worker. 10 out of 14 =71% had defaulted on first line anti TB treatment prior to being diagnosed with MDR TB, 2 out of 14=14.5% were newly diagnosed whereby out of the two was the 11 year old boy who was co infected and the mother who had since passed on due to TB and 2 out of the 14 =14.5% had TB relapse. Out of the 14 patients 1=7% female who was co infected with HIV died in the 3rd month of treatment, 1 out of the 14 =7% was lost to follow 1=7% has lost hearing, two have completed treatment while 11 are doing well on treatment though still 5 of the nine men are still abusing alcohol.

Conclusion made was that males are at risk of MDR TB than female, those who abuse alcohol are prone to MDR TB, HIV is a contributing factor to MDR TB, non adherence and defaulting of first line anti TB drugs led to MDR TB and low financial background is a contributing factor to MDR TB.

Recommendations made were; create awareness on tuberculosis, give health education to the public on prevention measures of tuberculosis and the importance of adhering to TB treatment and any other treatment to reduce chances of Anti Microbial Resistance (AMR), contact tracing through intensified case finding and embrace infection prevention and control in work place.

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## High Burden of Nosocomial Infections Caused by Multi-Drug Resistant Pathogen in Pediatric Patients at Hawassa University Comprehensive Specialized Hospital

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**Background:** Pediatric patients are at increased risk of nosocomial infections (NIs) with multi-drug resistant (MDR) pathogens, which are more prevalent in the hospital environment. The aim of this study was to determine the prevalence of NIs, antibiotic resistance pattern of bacterial isolates and associated factors in pediatric patients at Hawassa University Comprehensive Specialized Hospital.

**Methods:** A cross-sectional study was conducted from March to August 2016. Socio-demographic and clinical data were collected among patients clinically suspected of developing NI using a structured questionnaire. Bacterial identification and antimicrobial susceptibility test were done with standard microbiological methods. Data were analyzed with SPSS version 20 and p-value < 0.05 was considered to be statistically significant.

**Results:** Out of 939 children admitted to the hospital, 384 patients (40.9%) were clinically suspected for 462 NIs. Bloodstream infection was the most common site of NIs. Culture confirmed NI was reported in 82 patients (21.4%; 95% CI, 17.2-25.8%) with 88 isolates. Among the most frequently isolated bacteria, 21 (23.9%) were *Klebsiella* spp. and 16 (18.2%) were *S. aureus* (62.5% of these were methicillin resistant (MRSA)) were reported. About 88.9% of all bacterial pathogens were MDR and extremely high (97.9%) MDR were observed in Gram-negative bacteria. Among these, all isolates except *E. coli* were 100% MDR. Long hospital stay and malnutrition were significantly associated with NIs.

**Conclusion:** The high prevalence of NIs with MDR bacteria suggests the need for proper implementation of the NI prevention and control measures.

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## The Burden of Antimicrobial Resistance at Tertiary Care Hospital, Southern Ethiopia: A Three Years' Retrospective Study

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**Background:** Antibiotic resistance is a worldwide problem that can cross international boundaries and spread between continents with ease. Hence, information on the occurrence of the causative microorganisms and their susceptibility to commonly used antibiotics are essential for enhanced therapeutic outcome.

**Method:** A cross-sectional study was conducted retrospectively at Hawassa University Comprehensive Specialized Hospital. The culture and antibiotic sensitivity data of the isolates were collected from the records book of Microbiology unit for the study period after official permission obtained from the institutional review board. The data entered and analyzed using statistical package for social science software version 20 and the result presented in tables and figure.

**Result:** A total of 693 bacteria were retrieved, of these 435(62.77%) were gram-negative and the rest 258(37.23 %) were gram-positive. Most of the isolates were from urine. Among the isolates, *S. aureus* was recurrent from gram positives and *Klebsiella* spp from gram negatives. Almost a high-level resistance was observed to most of the antibiotics mainly, penicillin G (81.8%) and cotrimoxazole (81.1%), for gram-positive bacteria. The gram-negative bacteria also show resistance to ampicillin (92.5%), tetracycline (85%) and cotrimoxazole (93.1%).

**Conclusions:** We can say nearly all the isolated bacteria revealed a substantial level of resistance to most of the antibiotic that is frequently used in the study area. Therefore, continuous monitoring of drug susceptibility should be performed to help the empirical treatment of bacterial agents to a health professional in the region. In addition, it helps antibiotic policymakers nationally.

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## Susceptibility Profile of Bacteria Isolated from HIV-Infected Pregnant Women to Cotrimoxazole from Jos, Nigeria

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The susceptibility of bacteria isolated from the gastrointestinal and respiratory tracts of HIV-infected pregnant women in Jos was studied against Cotrimoxazole.

The study population consisted of 235 HIV-infected pregnant women who were on Sulfamethoxazole-Trimethoprim (SXT) and Sulfadoxine Pyrimethamine (SP) for prophylaxis. They were divided into groups A (SXT) and B (SP). Bacteria were isolated from stool and sputum using cultural methods and biochemical tests. Antibiotic susceptibility testing of bacterial isolates was conducted using the Kirby-Bauer Disk diffusion methods with SXT (25 mcg) as antibiotic. The 0.5 McFarland standards was used to standardize bacterial isolate for susceptibility testing. Prevalence of Enteric bacteria was (82.55%) and (76.60%) while that of respiratory tract bacteria was 60.43% and 51.06% among groups A and B respectively. *Escherichia coli* (39.69% & 41.11%) and *Staphylococcus aureus* (34.51% and 39.17%) among A and B, were the most frequently isolated enteric and respiratory tract bacteria respectively. Other enteric bacteria isolated include *Salmonella* sp, *Shigella* sp, *Proteus* sp, *Enterobacter* sp, *Klebsiella* sp, *Citrobacter* sp while respiratory tract bacteria include *Klebsiella pneumoniae*, *Streptococcus pyogenes*, *Haemophilus influenzae*, *Streptococcus pneumoniae* and *Proteus* species. The most susceptible bacteria were *Enterobacter* and *Proteus* sp (77.78% & 100% in A&B respectively) among enterics, *Staph. aureus* (42.86%) and *Streptococcus pyogenes* (90.91%) from the respiratory tract. All the *Salmonella* and *Shigella* sp, were completely resistant to SXT. Whereas all *Haemophilus influenzae* from group A were resistant, 50% of them from group B were susceptible to the drug. Bacteria isolated from group A were significantly ( $P < 0.05$ ) less susceptible

(33.51% & 32.4% of enteric & respiratory tracts respectively) to SXT compared to those of group B (53.33 % & 68.33% for enteric and respiratory tracts respectively).

The need to review the policy on the use of SXT and search for alternative drugs for prophylaxis in HIV has been advocated.

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Abstract 33 was withdrawn.

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## Antibacterial Resistance and Plasmid Profiles of Non-Typhoidal Salmonella SP from HIV-Infected Individuals Attending Some Hospitals in Jos, Nigeria

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This research was conducted to determine the antibacterial resistance and plasmid profile of non-Typhoidal Salmonella sp from HIV-infected individuals attending some hospitals in Jos.

Six hundred and fifty (650) patients including 325 HIV-infected and 325 Hiv-noninfected individuals were involved in the study. Bacteria were isolated using cultural methods and confirmed using Microbact™ Gram-Negative Identification System (24E) kits. Antibiotic resistance was determined using the disc diffusion method while 0.5 McFarland standard was used for the susceptibility testing. Tests were standardized using E. coli 25922 from the American Type Culture Collection (ATCC) as reference strain. Plasmids DNA were extracted using the Zippy plasmid Miniprep kit and characterized using agarose gel electrophoresis with DNA-Hind 111 Digest as DNA ladder.

Prevalence of non-Typhoidal Salmonella was 3.39%. The age-group ≤ 18years were the most infected [5 (22.7%)], while those of age group ≥54years were the least [1(4.5%)]. Salmonella subsp.3B was the most frequently isolated [18(81.82%) among both populations. Each of S. arizonae and S. subsp.1 was isolated from 9.09% of HIV-infected and noninfected respectively. None of the isolates showed resistance to Ciprofloxacin. Only 2 (16.75%) and 1(10%) of the isolates from HIV-infected and HIV-noninfected respectively, were resistant to Imipenem. All the isolates were resistant to Cotrimoxazole. Whereas all the isolates (100%) from HIV-infected individuals were completely resistant to Augmentin and Nalidixic acid, about 20% of isolates from HIV-noninfected were sensitive to the drugs. Although resistance was higher among the HIV-infected individuals, there was no significant difference (P>0.05) between the two groups. Plasmids were isolated from 6 (27.27%) of the isolates. The plasmid copies ranged between 1-7 with no significant difference (P>0.05) between the two groups. The molecular weight of plasmids vary from 2.673 - 23.49Kbp, with 0.51-5.50Kbp and 10.51-15.50Kbp being the most frequent plasmids encountered among HIV-infected and non-infected respectively. There were heavier plasmids among the HIV-noninfected than the HIV-infected population. All the isolates were multidrug resistant and Ciprofloxacin was the most effective of the drugs tested.

The need to review the use of Cotrimoxazole as prophylaxis for opportunistic infection has been advocated.

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## Retrospective Drug Resistance Mutations Among HIV-1 Infected Gabonese Patients Failing Antiretroviral Therapy

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**Background:** The antiretroviral drugs combinations using has proven remarkably effective in controlling

the progression of AIDS and prolonging survival. Unfortunately, the benefit of this treatment could be compromised by emergence of drug resistance mutations. In Gabon, the monitoring of patients living with HIV is challenging. Thus, the risk of drug resistance development could be high and studies about drug resistance are lacking.

**Objective:** This study aimed to investigate the prevalence of ARV drug resistance mutations among HIV-1 patients suspected to be in therapeutic failure in Libreville, Gabon.

**Material and Methods:** Serum samples from 44 patients suspected to be in therapeutic failure were collected from 2002 to 2009. RNA was extracted using QIAmp RNA extraction mini Kit. After retro-transcription and DNA amplification, protease and reverse transcriptase genes sequencing were performed using TruGene HIV-1 genotyping assay (Bayer Diagnostics, Siemens).

**Results:** Of the 44 patients, they were 68.2% females and 31.8% males. Age median was 38.5±4 years old, 85.6% were irregular in follow-up consultations and 64.3% were at B stage of CDC. The 70.5% of patients had a deep immunosuppression (CD4<200 cells/mm<sup>3</sup>). Among them, 26 (59.3%) received two nucleoside reverse transcriptase inhibitors (NRTIs) associated with one non-nucleoside reverse transcriptase inhibitors (NNRTI) and 18 (40.7%) received two NRTIs with one protease inhibitor (PI).

Protease and reverse transcriptase genes sequencing showed that all the patients was infected with HIV-1 belonging to group M non-B subtype. Mutations was found in 18 patients, including 17 conferring resistance NRTI. TAMs mutations was the most prevalent in 14 cases (77.8%) with 9 cases of M41L, 8 cases of T215Y/F, 6 cases of K70R and 6 cases of D67N mutations. The main non-TAMs mutation found was M184V in 9 cases (50%).

Viruses containing NNRTI mutations was found in 10 of the 18 patients (55.6%) including 5 cases of G190A/S, 4 of L100I, 4 of K101E, 4 of K103N and 4 of Y181C mutations. Mutations associated with PI were found in 8 patients, mainly represented by M46I/L (7 cases), I54L (4 cases), and L90M (4 cases) mutations.

Multi-drugs resistance to 2 or 3 antiretroviral classes was found in 11 of the 18 patients. Eight (8) patients (44.4%) had a virus resistant to 3 antiretroviral therapy. Most of patients with NRTI resistance (7/8) received therapy including 3TC. For those with NNRTI resistance (5), 4 having 190A/S mutations received EFV.

Additionally, Multi-Resistance profiles of patients receiving IDV included cross resistance to the entire IP class. The profiles mutations M46I/L-I54L and L90M conferring PI resistance were found in 6 patients. Four (4) patients exhibited resistance mutations to molecules that they were unexposed.

**Discussion and Conclusion:** According this study, several mutations conferring resistance to antiretroviral drugs exist in Gabon. These mutations may affect the effectiveness of the treatment by decreasing the sensitivity to one or more antiretroviral used. There is a need to improve patients follow-up by detecting resistance as early as possible to adjust ART and enhance its patient adherence. Further studies must be conducted to continue the ARVs resistance surveillance in Gabon.

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## Urinary Tract Infections in Outpatients of a Teaching Hospital in Ethiopia: Microbiological Surveillance of Pathogens and Antimicrobial Resistances

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**Background:** Urinary tract infection is the most common infection worldwide with around 150 million episodes reported every year. Furthermore, it is the most common indication to prescribe antibiotics. Subsequently it is a major driver of developing antimicrobial resistance in Enterobacteriaceae. The geographical distribution of underlying causative agents and antibiotic resistance differs greatly globally.

The Objectives of the study were to determine the prevalence of Urinary tract infections and the microbiological pattern including antimicrobial resistances at Asella Teaching Hospital, Ethiopia to obtain information for the treating physicians and to provide surveillance data on hospital level and to national or international bodies and networks (such as the Ministries of Health (MoH), the Global

Antimicrobial Resistance Surveillance System (GLASS), or the ESTHER network).

**Materials and Methods:** As part of a multicenter study of the ESTHER Antimicrobial Resistance network a cross sectional study was conducted among outpatients with clinical signs of Urinary tract infection who attended the outpatient clinic of Asella Teaching Hospitals from July 16, 2018 to December 15, 2018. A total of 392 participants were included in the study. Demographic Data was collected by a standardized questionnaire. Urine samples were collected and examined at Hirsch Institute of Tropical Medicine with Urine dipstick. Fulfilling the inclusion criteria, bacterial culture was done to identify the causative agent. In case of bacterial growth of gram-negative bacteria antibiotic susceptibility test was performed. Bacterial isolates were stored at -80°C for further investigations. Collected Data was entered and analyzed using SPSS version 21.

**Results:** A total of 392 UTI suspected samples were dipstick positive and included in the study. In 156 cases bacterial growth was found. From those, 89 % were gram-negative and 11% were gram-positive respectively. Concerning the gram-negative bacteria 58.3% *E. coli*, 36.8% *Klebsiella* species, 2.1% *Acinetobacter*, 1.4 % *Pseudomonas* were found. Regarding the antibiotic susceptibility among the gram-negative bacteria 11.1% were resistant to Meropenem even though this medication is not frequently used in the hospital. For Amoxicillin/Clavulanic acid and Piperacillin resistance rate of 41.7 % and 50.7% respectively was found. For 3rd Class Cephalosporines the resistance rate among gram-negative bacteria was around 55%. Ciprofloxacin showed a resistance rate of 66.7%. The highest susceptibility was found for Nitrofurantoin with 25.7 %, most likely due to the rare use of this antibiotic.

**Conclusions:** In 156 suspected Urinary Tract Infections a causative agent could be identified. Among those, *E. coli* and *Klebsiella* were most prevalent. Antibiotic resistance rate was very high among all antibiotics currently used in the country.

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## Validaton of the GenoType® MTBDRplus Ver 2.0 Assay for Detection of Rifampicin and Isoniazid Resistance in Mycobacterium tuberculosis Complex Isolates at UZCHS-CTRC TB Research Laboratory

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**Background:** Multidrug-resistant tuberculosis (MDR-TB) is a public health concern globally. MDR-TB is defined as resistance to rifampicin (RIF) and isoniazid (INH), the two-major anti tuberculosis first-line TB treatment drugs. Rapid identification of MDR-TB can contribute significantly to the control of TB. The GenoType® MTBDRplus Ver 2.0 assay is a molecular assay used to detect genetic mutations that result in RIF and INH resistance. The aim of this study was to validate the performance of the GenoType® MTBDRplus Ver 2.0 assay for the detection of INH and RIF resistance in stored isolates against Mycobacterial Growth Indicator Tube for Antimycobacterial Susceptibility Testing (MGIT AST).

**Methods:** Fifty-five stored *M. tuberculosis* isolates were tested using both the MGIT AST and the GenoType® MTBDRplus ver 2.0 assay. The MGIT AST was done according to the BBL MGIT AST SIRE system with RIF and INH final critical concentrations of 1.0 µg/ml and 0.1 µg/ml respectively. The GenoType® MTBDRplus assay (Hain Lifescience, Germany) was performed following the manufacturer's instructions.

**Results:** The GenoType® MTBDRplus ver 2.0 assay had a sensitivity, specificity, PPV, and NPV of 100% for INH and RIF resistance. The intra-assay precision for the assay was 100%.

**Conclusion:** The GenoType® MTBDRplus ver 2.0 assay's sensitivity and specificity show that the assay is highly accurate for the detection of RIF and INH resistance and thus can be used as an alternate platform due to its shorter results turnaround time.

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## Strain Diversity and Gene Mutations Associated with Clinical Mycobacterium tuberculosis Complex Isolates in Northwest Ethiopia

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**Background:** Mycobacterium tuberculosis complex (MTBc) has been found to be the major cause of infectious disease and a serious public health problem in the world, with an increasing concern for the emergence and spread of antimicrobial-resistant strains particularly in developing countries. This study aimed to analyze the gene mutations and the genetic diversity of the clinical MTBc strains isolated from multidrug resistant tuberculosis (MDR-TB).

**Methods:** In this study we assessed drug resistance and the genotypic distribution of MTBc isolates that had been collected from MDR-TB clinical isolates between 2013 and 2016, and stored in Bahir Dar and Gondar TB culture laboratories at Amhara regional state, Ethiopia. We used a line probe assay (LPA) to analyze the resistance determining genes for the first-and second-line drugs, and spoligotyping to assign isolates to mycobacterial lineages.

**Results:** Among the total 125 MTBc strains tested by LPA, majority of strains (41.5%) harbor the most common S531L mutation in the rpoB gene, while also a substantial number (13%) carry mutations not identifiable by the LPA used. In this analysis, the gene mutations showed that codon 531 of the rpoB gene and codon 315 of the katG gene accounted for 41.5% and 59.3% of rifampicin and isoniazid resistance, respectively. Six isolates were identified as resistant to second-line drugs; three FLQ mono-resistant isolates (D94G), i.e. pre-XDR, two FLQ and KAN/AMK/CAP resistant isolates (XDR), and one FLQ, KAN/AMK/CAP and low-level KAN resistant isolates (XDR). Although FLQ resistance frequency is still relatively low, the detected mutations at codon 94 of the gyrA gene suggest high-level resistance.

Further characterization of isolates from the two sites (n = 108) revealed a total of 33 different spoligotype patterns, 13 “orphan” and 20 shared patterns. We identified the four major MTBc lineages of human relevance, with predominance of the Euro-American lineage. The largest families were the T3-ETH (26.9%), CAS1-Delhi (20.4%) and CAS1-Killi (14.8%) with high proportion, respectively, among the genotypes and that the drug-resistant strains were genetically diverse.

**Conclusion:** In conclusion, our findings provide gene mutations and the genotype diversities associated with the MTBc strains in Northwest Ethiopia, with relevance for public health scientists in tuberculosis control programs.

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Abstract 39 was withdrawn.

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## Resistance Profile of Mycobacterium tuberculosis to First and Second Line Treatment Drugs in Extrapulmonary Samples

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**Introduction:** In the present scenario, extrapulmonary tuberculosis (ETB) forms, although they do not represent risk factors for the transmission of the disease, are becoming increasingly important due to their incidence closely related to the AIDS epidemic, representing 15-20% of all TB cases. Worldwide, the diagnosis and association of resistant strains of Mycobacterium tuberculosis is a cornerstone of ETB. The objective of this study was to describe the



resistance profile of *M. tuberculosis* to first and second line drugs in extra pulmonary samples processed at Mozambique's National TB Reference Laboratory (NTRL) from 2011 to 2017.

**Methodology:** A retrospective cross-sectional study was carried out through the analysis of secondary data from the NTRL to determine the number of ETB cases resistant to 1st and 2nd line drugs detected by drug susceptibility test or Line Probe Assay (LPA).

**Results:** During the study period, there were more cases of resistance related to 1st line drugs, with emphasis on isoniazid 32.1%, rifampicin 21.2%, streptomycin 16.3% and ethambutol 8.7%. In 2012 and 2016, there were 19/52 cases of isoniazid resistance, which are relatively higher than in other years. Of the samples tested for 2nd line drugs 4.3% were resistant to amikacin, kanamycin and capreomycin and 10.1% for ofloxacin. The percentage of Multidrug resistant TB and extensively drug resistant TB were 8.6% and 0.4%, respectively.

**Conclusion:** In this study, there was not much difference in mycobacterial resistance during the period under review except for the period of 2012 to 2016 where the percentage of resistance of isoniazid was high. Most second line drugs were sensitive to the drugs tested. Further studies on mycobacterial drug resistance are recommended to account for the epidemiology and risk factors of *Mycobacterium tuberculosis* drug resistance in extrapulmonary samples.

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## Rate of Transmitted Drug Resistance Mutation in HIV-1 Protease-Reverse Transcriptase to Assess Efficiency of First Line Antiretroviral Therapy in a Region of Long Term Use of Antiretroviral Drugs

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**Background:** Cameroon has adopted the WHO "Test and Treat" approach to reduce HIV incidence and mortality, although an increasing rate of HIV-1 drug resistant variants has been reported. For over fourteen years, first line ARV regimens in Cameroon comprise of two nucleoside or nucleotide reverse transcriptase inhibitors (NRTI) plus one non-nucleoside reverse transcriptase inhibitor (NNRTI). Several indicators and factors have enhanced the emergence of drug resistant HIV-1 although a seroprevalence of HIV of 3.4% was reported in 2018 in Cameroon and 6.4% in the North West Region. The aim of this study was to determine the prevalence of transmitted drug resistance mutations, and predicted antiretroviral drug (ARV) susceptibility among treatment-naïve individuals residing in the North West Region of Cameroon, as a measure of efficiency of the first line ART in Cameroon.

**Materials and Methods:** Eighty one HIV-1-infected, ARV drug naïve patients were recruited in a cross sectional study in urban and rural areas in the North West Region of Cameroon from February 2016 to April 2016. Ethics approval was obtained from the National Ethics Committee of Cameroon and a written informed consent was provided by each study participant. HIV-1 protease-reverse

transcriptase (PR-RT) region was sequenced, and population level transmitted drug resistance (TDR) and patient-specific resistance-associated mutations (RAMs) were identified using the Calibrated Population Resistance (CPR) Tool and the Stanford HIV Drug Resistance Database Interpretation Program, respectively, to predict susceptibility to 28 FDA-approved ARV drugs. The quality of the DNA sequences was checked using the Sequence Scanner software (Applied Biosystems® Genetic Analyzers). The reliability of each TDR mutation was examined if due to APOBEC-mediated hypermutation, artifact, or other factors.

**Results:** The 57 and 81 protease and reverse transcriptase sequences, respectively, were analyzed. Four of the 81 HIV-1 RT sequences (4.9%) had TDR mutations which were K219Q, M184V, D67N, K70R, T215F, M41L of NNRTI, and K103N and Y181C of NRTI. No TDR was identified in the protease region. Further analysis for prediction of drug resistance per patient showed that 9 (11.1%) were infected with ARV drug resistant variants. The resistance-associated mutations (RAM) identified were: K219Q, T215TA, M184MV, I54IFV, D67N, K70R, M41ML (NRTI) and K103N, E138A, A98G, V108I, V179E, Y181C (NNRTI). Only one patient (WHO Clinical Stage 4), was detected with a HIV-1 variant with TDR mutations and other ARV resistance-associated mutations that predict from intermediate to high level of resistance. No minor RAMs were identified. Eight of 9 individuals were infected with HIV-1 CRF02\_AG.

**Conclusions:** These results showed low population level TDR (4.9%) in HIV-1 reverse transcriptase region although 11.1% of resistant variants were estimated. These results although from a small sample size, imply that first line ART regimens currently used in Cameroon are appropriate, overall.

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## Antibiotic Resistance and Identification of Uncommon Gram-Negative Bacteria Isolated from Sputum in Respiratory Tract Infection, Tamale Teaching Hospital, Ghana, 2018

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Globally, Respiratory Tract Infections (RTI's) are a major cause of morbidity and mortality. It is estimated that approximately 4 million deaths occur annually due to RTI's. Sub-Saharan Africa accounts for more than two third of these deaths. Antibiotic resistance has become a serious health problem in the world. Deaths from RTI's due to Antibiotic resistance have become very common in Sub-Saharan Africa. We conducted this study to determine the common bacterial isolates and their antibiotic susceptibility pattern in RTI in the Tamale Teaching Hospital (TTH) of Ghana.

We extracted and reviewed laboratory data from January to December, 2017. This period spans all seasons in the study areas. We analysed the data descriptively into frequencies and proportions in Ms Excel 2013.

A total of 303 sputum culture positive cases were identified. Majority 176(58.10) were females. The three predominant isolates were *Moraxella catarrhalis* 108(35.6%), *Klebsiella* species 52(17.2%) and *Enterobacter* species 36 (11.9%). On the average 26 antibiotics of various classes were used for susceptibility testing for gram-negative bacteria within the period. The antibiotics that showed the highest sensitivity to *Moraxella catarrhalis* were Gentamycin (76.3%), Chloramphenicol (74.2%) and Ceftriazone (70.3%), while those that showed increased resistance were Ampicillin (100%), Clotrimazole (99.0%) and Tetracycline (90.5%). The antibiotics that showed highest sensitivity to *Klebsiella* species were Amikacin (95.8%), ofloxacin (87.9%) and Gentamycin (84.8%), while those that showed increased resistance were Tetracycline (97.1%), Ampicillin (93.5%), and Cefuroxime (76.7%). The antibiotics that showed the highest

sensitivity to *Enterobacter* species were Amikacin (84.2%), Ciprofloxacin (82.4%) and ofloxacin (78.9%) while those that showed increased resistance were Ampicillin (96.8%), Cefuroxime (90.0%) and Tetracycline (88.9%).

We conclude that Amikacin, Gentamycin and Ofloxacin are most suitable in empirical therapy for RTI's in TTH whiles Tetracycline and Ampicillin were not suitable for the treatment of same. We recommend the cautious use of antibiotics based on sputum culture and antibiogram as the best strategy to prevent resistance pattern.

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## A Systematic Review on Antibiotic Use in Humans 2000-2017, Nigeria

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**Introduction:** Antibiotics changed the practice of modern medicine, reduced mortality attributable to infectious diseases. Over 80% antibiotic use often occur within community and it is posited that 20-50% may be unnecessary or sub-optimal. However, this increasing trend in antibiotic consumption is contributory to antibiotic misuse, which is a key driver of the rising antimicrobial resistance (AMR) rates. The objectives of this systematic review are to describe the quantitative indicators of irrational antibiotic use and identify factors influencing use of antibiotics.

**Methods:** We searched for articles published in English from January 2000 to January 2017 from Medline via Pubmed and African Journals Online (AJOL) databases, using the following search terms: "rational use", "antibiotic consumption", "antimicrobials", "Nigeria", "purchase of antibiotics" and "over the counter". This review was done using the preferred reporting system for systematic review and meta-analysis (PRISMA) statement. The two dimensions of irrational antibiotic use were searched for: prescription behavior by health workers and medicine use

behavior by patients. Key indicators were extracted and summarized.

**Results:** A total of 11 articles were included in the final data synthesis of which all were cross-sectional design and for 2 (18%) articles, the study population were prescribers. The proportion of irrational antibiotic use ranged from 31.7% to 71.1% while the percentage of antibiotics prescribed per patient encountered, ranged from 26.8% among persons ≥15 years to 71.1% in children <5 years with a median of 44.7%. The commonest antibiotic used or prescribed were the penicillin group of antibiotics ranging from 25% to 71.2%, with a median of 29.9%. Factors influencing irrational antibiotic use include over the counter (OTC) supply of antibiotics, patients' demand for antibiotics, access to National Health Insurance. Prescribers' characteristics included longer years of practice, lack of specialisation and age.

**Conclusion and Recommendations:** Our findings highlight the need for physician re-training and patient education on rational antibiotic use. National legislation on antibiotic sales based on prescription should be enforced and surveillance of antibiotic prescription per patient encountered at health facilities should also be prioritized. This information was used in the development of the National Action Plan on AMR in the country.

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## Developing a Multisectoral National Action Plan on Antimicrobial Resistance for Nigeria

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**Introduction:** Nigeria lacked an appropriate response to the growing threat of antimicrobial resistance (AMR) partly due to inadequate regulatory policy and data paucity. In November 2016, the Honourable Minister of Health mandated the Nigeria Centre for Disease Control (NCDC) to develop a National Action Plan (NAP) for AMR containment, with support from other stakeholders.

**Methods:** An AMR Technical Working Group inaugurated in January 2017 comprised stakeholders from human health, animal health, and environment sectors. The working group compiled baseline studies, performed gap analysis, and facilitated effective multi-stakeholder participation. Extensive desk review with virtual meetings were followed by two face-face stakeholders' meetings; one to develop a draft of the NAP document in March 2017 and a finalization meeting in April 2017 to validate the document.

**Results:** A situation analysis on AMR was compiled and a 5-year NAP document, with firm commitment to implement coordinated AMR prevention and control activities, were developed. The objectives for the NAP were derived from recommendations made from a Strength-Weakness-Threat-Opportunity (SWOT) analysis of the national AMR situation. Five strategic focus areas were introduced which included increasing awareness on AMR and related topics, creating an AMR surveillance system, strengthening infection prevention and control in the One Health sector, promoting rational access to and use of antibiotics and investing in research to develop new antimicrobials and AMR diagnostics.

**Conclusion:** In 2017, Nigeria was one of two countries in West Africa (15 countries in total), that developed a National AMR action plan approved by government, with an operational plan and monitoring framework. The five-year NAP adopted a One Health approach that leverages existing structures and if fully implemented, it will ensure effective control of AMR.

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## Assessment of Absolute Cluster of Differentiation 4 (CD4) Count in HIV Patients Using Antiretroviral Therapy (ART) in Kosti White Nile State, Sudan

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HIV infection is characterized by a gradual deterioration of immune function. CD4 cell count is used to determine how well the immune system of HIV patients because it is the first cells invaded by HIV virus. HIV patients start ART treatment if CD4 equal or less than 500 cells.

In 2014, across-sectional study conducted in ART center in Kosti , White Nile State in Sudan. The positive HIV individuals were enrolled in this study, their ages range between 19-51 years old. The aim of this study to evaluate the immune system of HIV patient using ART. The test group was compared with control group from normal health persons, a blood samples were collected from both groups. Flow cytometer method were used to measure CD4 cells.

The result of this study we found a significant increasing in CD4 cell in HIV patient when starting ART treatment , also it showed CD4 count increase in males more than females . Result of this study also present insignificant between result and control result due to decrease CD4 in Sudanese. Result of the present study most age suspected to infection with HIV young persons. Also in this study found that the CD4 cells in normal health Sudanese people were low. In Conclusion, the present study indicated that the CD4 count can be used as assessment method of immune system of HIV patients and to evaluate it when HIV patients start ART therapy.

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## Antibiotic Resistance Among Foodstuff in Morocco

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The amount of antibiotics consumed worldwide has increased dramatically in recent years and their use has become completely trivialized.

In recent decades, many studies have shown that the significant increase in the incidence of food-borne illnesses is caused by the contamination of foods by some microorganisms such as *E. coli*. However, by acquisition and combination of genes for virulence and antibiotic resistance, these normally harmless commensal strains can become highly adapted pathogens capable of causing a variety of diseases.

The aim of our work was to contribute to a better understanding of the implication of foodstuffs intended for consumption in the dissemination of antibiotic resistance.

This study involved strains of *E. coli* collected at the level of foodstuffs analysis laboratories where the study of their in vitro sensitivity to antibiotics by the disk method revealed that imipenem, ertapenem and cefepime are the most active antibiotics on strains tested. A high level of resistance was noted for  $\beta$  lactamines, quinolones and tetracycline. The frequency of *E. coli* resistant to third generation cephalosporins is 6%, of which 1.13% are ESBL and 11% were resistant to cefoxitin. The molecular typing of the ESBLs produced shows the presence of the blaCTX-M14 genes for the first time in Moroccan foodstuffs. Cefoxitin resistance is due to the presence of the blaCMY-2 and blaACT21 variants.

The molecular results also show that the quinolone resistance is due to a double chromosomal point mutation of the QRDR region. Plasmid-mediated quinolone resistance is detected in 43% of quinolone-resistant strains with a predominance of aac (6') - Ib-cr (19%), qnrS1 (15%) and qnrB19 (9.3%). Genetic transfer experiments showed that identified genes were carried by high molecular weight plasmid.

Multiplex PCRs of virulence genes revealed that 26% of multidrug resistant strains harbor at least one virulence gene and the phylogenetic group A dominates in *E. coli*. The restriction profile analysis by pulsed field electrophoresis revealed clonal diffusion of these circulating resistance mechanisms in our food. Thus, the optimal use of antibiotics is the cornerstone of the reduction of antimicrobial resistance.

Multidisciplinary collaboration and the establishment of an effective surveillance program for antibiotic use should be integrated to improve the quality of foodstuffs and thus counter the emergence of this resistance.

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## Paromomycin for the Treatment of Visceral Leishmaniasis in Sudan: A Randomized Study

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**Introduction:** The first line drug (antimonials) are expensive and beyond the reach of those who need it most, require long term daily injections, are associated with toxicity and are becoming useless due to increasing resistance in A recent study has shown that treatment of visceral leishmaniasis (VL) with the standard dose of 15 mg/kg/day of paromomycin sulphate (PM) for 21 days was not efficacious in patients in Sudan. We therefore decided to test the efficacy of paromomycin for a longer treatment duration (15 mg/kg/day for 28 days) and at the higher dose of 20 mg/kg/day for 21 days.

**Methods:** This randomized, open-label, dose-finding, phase II study assessed the two above high-dose PM treatment regimens. Patients with clinical features and positive bone-marrow aspirates for VL were enrolled. All patients received their assigned courses of PM intramuscularly and adverse events were monitored. Parasite clearance in bone-marrow aspirates was tested by microscopy at end of treatment (EOT, primary efficacy endpoint), 3

months (in patients who were not clinically well) and 6 months after EOT (secondary efficacy endpoint). Pharmacokinetic data were obtained from a subset of patients weighing over 30 kg.

**Findings:** 42 patients (21 per group) aged between 4 and 60 years were enrolled. At EOT, 85% of patients (95% confidence interval [CI]: 63.7% to 97.0%) in the 20 mg/kg/day group and 90% of patients (95% CI: 69.6% to 98.8%) in the 15 mg/kg/day group had parasite clearance. Six months after treatment, efficacy was 80.0% (95% CI: 56.3% to 94.3%) and 81.0% (95% CI: 58.1% to 94.6%) in the 20 mg/kg/day and 15 mg/kg/day groups, respectively. There were no serious adverse events. Pharmacokinetic profiles suggested a difference between the two doses, although numbers of patients recruited were too few to make it significant ( $n = 3$  and  $n = 6$  in the 20 mg/kg/day and 15 mg/kg/day groups, respectively).

**Conclusion:** Data suggest that both high dose regimens were more efficacious than the standard 15 mg/kg/day PM for 21 days and could be further evaluated in phase III studies in East Africa.

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## New Emerging of Niesseria Meningitidis W135 Among Common Patterns in Sudan with Special Concern of Infected Children

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**Introduction:** This study was conducted to follow-up the frequency of meningitis outbreak or pan-endemic waves and emerging of new patterns, with a special concern of infected children less than five years old since it is very serious condition that might affect the central nervous system (deafness, epilepsy and hemiplegia) and also to evaluate new quadrivalent vaccination for actual application.

**Patients and Methods:** All samples were collected from West, East and Central Sudan and transported to the National Health Central Laboratory in Khartoum with special precautionary measures taken for transportation. Children admitted with clinical diagnosis of meningitis under 5 years old and unvaccinated for meningitis. A pre-coded questionnaire was completed after obtaining informed verbal consent. Thorough clinical examination for each child was conducted. Cerebrospinal fluid (CSF) was withdrawn from cases suspected as meningitis. Serotyping was done using specific antisera for H. influenza type b and quality control was performed using standard control.

**Results:** Out of 196 cases with clinical symptoms and signs of meningitis, conventional culture showed Niesseria meningitidis in 37 (18.9%) cases which also proved positive by PCR. Niesseria meningitidis type A occurred in 29 (78.4%) cases, type C in 3 (8.1%) cases and Niesseria meningitidis W135 in 5(15.5%) cases. The determination patterns of Niesseria meningitidis showed an emergence of new strains of W 135. The emergence of Niesseria meningitidis W135 was from the boarders of Sudan mainly the West (3 cases), and one case from each part of Central and East Sudan, which could be explained by the active movement of pilgrims through the boarders to Hajj season in Saudi Arabia. In children (48.5%) were due to Meningiococcal meningitis, followed by Hemophilus influenza, which account for one-third of the cases (30.3%). Streptococcal pneumoniae is the least common cause which account for only one-fifth of the cases (21.2%). Most of the presentations were fever, convulsion and sign of meningial irritation. Case fatality rate 5 (5.15%), neurological complications account for 12 (12.37%) cases. Vaccination against meningococcal, haemophilus and Streptococcal infection should be considered, because all of the studied cases were unvaccinated, in addition to facilities for investigations should be readily available. Serious consideration may be needed for quadrivalent vaccination to prevent seasonal and Hajj season outbreaks.

**Conclusion:** It was very clear that control measures on boarders and careful investigations with sensitive and specific tools can increase our knowledge towards recognition of Niesseria meningitidis strains which can make our awareness better towards prevention and treatment. In Sudan the adaptation of quadrivalent instead of bivalent vaccine to include W135 and meticulous surveillance performed indicted that no critical infections were recorded clinically up to date.

Preventative measures by vaccines should be strongly considered for all children and reevaluation of the health care budget should be considered to accommodate vaccines .

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## West Nile Virus Neuroinvasive Disease in Northwest Algeria: A First Case Report

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**Background:** West Nile virus, a single-stranded RNA flavivirus was first isolated in 1937 in the West Nile province of Uganda from the blood of a febrile woman. Although one of the most disseminated of all of the arboviruses in the Eastern Hemisphere, West Nile virus first emerged in Algeria in 1994. In Algeria, since the 1994 epidemic, no data on WNV circulation was available until 2012. In September 2012, a fatal human case of WNV neuro-invasive infection occurred in north-east region of Algeria. In 2014, a seroconversion was observed in 2 horses, showing WNV circulation in north-east region of Algeria. In 2018, we report a case of serologically proved West Nile virus encephalitis in north-west of Algeria.

**Case presentation:** 67-year-old man presents presented to our emergency department with a 5-day history of fevers, abdominal pain, nausea, emesis, myalgias, arthralgias, and headache. He travels to Adrar in the south of Algeria and returns to Tlemcen one month later. Temperature is 37°C, blood pressure 135/60, pulse 100, respiratory rate 24. Physical examination was notable for confusion and right hemiparesis. Laboratory values were normal except for WBC 7.1 K/uL. CSF analysis showed total white blood counts of 64/mm<sup>3</sup> with 8% neutrophils, 90% lymphocytes, 1080 mg/dl protein, and 65 mg/dl glucose. CSF Gram staining, acid-fast bacilli staining, bacterial meningitis screen, VDRL, HIV, HSV, were all negative. He was started on acyclovir and Cefotaxim . Serum West Nile IGM 3.49 (Normal <1.0) and CSF West Nile IgM 2.80u (normal <.90u) were both elevated. CT head was unrevealing. MRI brain revealed a bilateral protuberantial ,temporal and thalamic

leptomeningeal inflammation . Supportive care was continued, and the patient progressively improved with partial recovery of motor and language function and was discharged to a rehabilitation center for further management. He continued to improve and was discharged.

**Conclusions:** We report a unique case of WNV encephalitis occurring in the west region of Algeria. The most reliable diagnostic modality for WNV is the serum IgM antibody to WNV in serum and CSF. It is crucial to elicit a good history and diagnostic investigation, including geographic location, recent travels, exposure to mosquitoes, and time of year to establish an early diagnosis and treatment for WNV encephalitis.

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## Health System and Community Readiness to a Lassa Fever Outbreak in Burkina Faso

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**Introduction:** Lassa fever is a hemorrhagic fever that is transmitted to human by rodents through their excretions spread on surfaces or in food. The disease is mainly found in West African Countries including Nigeria, Benin, Ghana, Guinea, Mali, Liberia, Sierra Leone and Togo where it is endemic. In 2018, an outbreak occurred in Nigeria with 1849 suspect cases being reported from 21 states and 413 were confirmed with the Lassa virus. Case fatality of Lassa fever was high and reached 25.4% in Nigeria. Though case fatality is far lower than that of Ebola, the spread of the disease to the neighboring country of Benin has alerted many countries in the region including Burkina Faso. Since the start of the epidemic in the region, no case has been reported in the country until April 25, 2018 when the death of a 56-year-old woman spurred a serious concern in the public health system to respond to it swiftly.

**Objective:** This rare occurring motivated an analysis of the preparedness of the country to an outbreak of Lassa fever should it occur in the country.

**Methods:** A review of existing policies and control plans was performed to assess the institutional readiness, the analysis of the existence of rapid response teams, surveillance set-up in entry-points to the country and their functionality assessed the operational readiness. The specific response to this specific suspect case helped highlight strengths and weaknesses to the readiness. Finally, community readiness was gauged for it is important to preventing human-to-human transmission.

**Results:** Although there is a national plan to preventing hemorrhagic fevers, there is no specific plan to preventing and responding to Lassa fever. There has been no reinforcing of surveillance at the entry-point since the outbreak started and rapid response teams are not ready for such situations. They are not logistically nor procedurally ready to respond due to the lack of meeting and drills. Also, the clinical setting has not reported the case through the formal loop and healthcare providers only used standard precautions. A positive point was the quick reaction of the reference lab for confirmatory test performance. The hospital has no isolating rooms for such cases, no clear procedure for following contacts and keeping them in the territory before the end of the incubation period. Religious and traditional rites and practices in handling dead bodies were not favorable to preventing spread of the infection in the community.

**Conclusion:** A quick overlook to the country's health system has enable the identification of strengths by also weakness should an outbreak of Lassa fever occur. Some strengths that the country could put in contribution in case an outbreak occurs is the existence of a national plan to hemorrhagic fevers and a reference lab that can quickly test specimen. However, the surveillance system and community readiness could be the soft belly of the response system should an outbreak occur in the country.

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## Mathematical Modeling and Analysis of Polio Virus Model Incorporating Immigration and Vaccination

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A new deterministic mathematical model for polio infection dynamics with emphasis on immigration and vaccination was formulated and rigorously analyzed.

We derived the basic reproduction number,  $R_0$  of the model formulated. The effective reproduction number was computed in order to measure the relative impact on individuals or combined intervention for effective disease control. Also, the disease-free equilibrium and endemic equilibrium points were computed.

On inspecting the equilibrium points, we found that the disease-free equilibrium is locally asymptotically stable if  $R_0 < 1$  and the model undergoes a forward bifurcation when  $R_0 = 1$ . More so, by conducting further analysis on the model through bifurcation, we discovered that the model has a negative unstable endemic equilibrium point which is positive asymptotically stable, because one of the control parameters is nonnegative, since  $a < 0$  and  $b > 0$  (where  $a$  and  $b$  are the control parameters).



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## Searching for People with Bacteriologically-Confirmed Pulmonary Tuberculosis: Loss to Follow-Up, Death, and Delay Before Treatment Initiation in Bulawayo, Zimbabwe (2012-2016)

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**Background:** Tuberculosis (TB) is the single most important cause of death from an infectious disease in Zimbabwe, whose eradication is dependent on the identification of all infected patients and commencement on treatment.

**Context and Aim:** Diagnosed patients who do not initiate treatment facilitate onward transmission of the infection. This study quantified and assessed risk factors for loss to follow up (LTFU) and delays before treatment initiation among bacteriologically confirmed pulmonary TB patients.

**Methods:** A cohort study was conducted using programme data from Bulawayo city, Zimbabwe. Diagnosed patients were identified from the laboratory register for 2012-2016, tracked for treatment initiation in the City's TB registers and missing entries ascertained their outcomes in presumptive TB registers at respective clinics. Pre-treatment LTFU referred to diagnosed patients who did not initiate treatment within 90 days and pre-treatment deaths. Multivariable analysis was used to identify risk factors for pre-treatment LTFU and delays.

**Results:** Out of 2,443 identified records, one in five patients (20.8%,n=508) were lost to follow-up, including pre-treatment deaths (10.3%). Above 65 year olds (a RR=2.71,95%CI;2.12,3.47), male gender (aRR=1.21,95%CI;1.04,1.41), HIV positivity (aRR=1.26,95%CI;1.02,1.56) or Unknown HIV status (aRR=4.78,95%CI; 3.80,6.00) were independent risk factors for pre-treatment LTFU. Delay between

testing and dispatch of results by  $\geq 3$  days (aRR=1.42, 95%CI;1.09,1.85), was an independent risk factors for pre-treatment death in addition to the above. Among registered patients, (n=1,935), the mean (SD) delay from diagnosis to treatment initiation was 29.1 (21.6) days. Independent risk factors for treatment delay were new TB type ( $\beta$ =13.5,95%CI;11.5,15.4) and the delay decreased between 2013 ( $\beta$ =-8.8,95%CI;-11.5,-6.1) and 2016 ( $\beta$ =-18.6, 95%CI;-21.7,-15.6).

Innovative contribution to policy, practice and research: High loss to follow-up, deaths and delay of TB treatment initiation observed in this study is cause for concern. Enhancing active case finding, patient tracking from diagnosis to treatment initiation and point of care diagnosis were mitigatory strategies identified for risk factors for pre-treatment LTFU/death and delay.

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## Lassa Fever Infection and Prevention Control Availability and Use at Healthcare Facilities in Western Nigeria

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**Background:** Lassa fever is a zoonotic infection caused by arenavirus contracted primarily through contact with the contaminated excreta of *Mastomys natalensis* rodents. Secondary transmission of the virus between humans occurs through direct contact with infected blood or bodily secretions. The objective of this study was to assess the availability of infection & prevention control measures, consumables & their use in healthcare facilities in Western Nigeria.

**Methods:** This study was a cross sectional study. Data was collected by trained volunteers and supervised by appointed supervisors and investigators, by a face-to-face interview using a pre-tested structured questionnaire on Lassa Fever. Frequency count was generated for all variables and statistical test of significance was performed with Chi-Square test.

**Results:** Eighty five healthcare facilities & workers were surveyed, out of which 80 (94.1%) had wash hand basins but only 48 (56.5%) had running water or any kind of water supply. Most, 55 (64.7%) & 49 (57.6%) of the healthcare workers do not practice hand washing before/after patient contact & had not been trained on infection control while only 48 (56.5%) were regularly using personal protective equipment such as white coat & gloves. There was no association between availability of personal protective equipment & its use ( $\chi^2 = 3.02$ ,  $df = 1$ ,  $P = 0.403$ ).

**Conclusion:** Healthcare facilities do not meet the minimum standard for infection prevention & control measures. It is therefore recommended that government at all levels should immediately prioritize the infection prevention & control programs its health facilities to curb future spread of infectious diseases even in hospital premises among healthcare workers.

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## Outbreak of Human Anthrax Associated with Handling and Eating Meat from a Cow that Died from Unknown Cause: Kween District, Uganda, April 2018

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**Background:** On 20 April 2018, District health officials in Kween District, Uganda reported to the Ministry of Health 7 suspected cases of cutaneous anthrax among persons who had handled and eaten meat from 1 of 4 cows that died of unknown causes in April in one cattle pen. We investigated to determine the scope of and possible exposures for the outbreak, and recommend evidence-based control measures.

**Methods:** We defined a suspected cutaneous anthrax case as acute onset of painless, papulo-vesicular skin lesion, and a suspected

gastrointestinal anthrax case as abdominal pain plus  $\geq 1$  of the following: diarrhea, vomiting, abdominal swelling, pharyngitis, and oropharyngeal lesions, in a Kween District resident during April 2018. A confirmed case was a suspected case with a sample testing positive for *Bacillus anthracis* by polymerase chain reaction (PCR). We reviewed medical records and conducted active community case-finding. We collected lesion swabs and blood samples for PCR testing at Uganda Virus Research Institute. We conducted a retrospective cohort study to identify potential exposures.

**Results:** Among 234 persons who handled or ate the cow's meat, we identified 48 cases (3 confirmed and 45 suspected; 15 cutaneous, 15 gastrointestinal, 18 both) (attack rate=21%), with no deaths. Skinning (RR=4.2, 95%CI=2.6-6.7), cutting (RR=4.9, 95%CI=3.2-7.5) or carrying the meat (RR=4.9, 95%CI=2.7-9.0), and cleaning the processing site (RR=4.2, 95%CI=2.6-6.7) increased the risk of cutaneous infection. Eating the meat increased the risk of gastrointestinal anthrax (RR= $\infty$ , 95%CI=4.3- $\infty$ ). Among persons who ate meat, boiling meat for >60m was protective (RR=0.49, 95%CI=0.26-0.92).

**Conclusion:** This outbreak of mixed cutaneous and gastrointestinal anthrax was caused by handling and eating meat from a cow that died of unknown causes. We recommended treating all cases, vaccinating healthy animals, and conducting community education on avoiding eating meat from, and safe burial of, animals that died of unknown causes.

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## Clinical Profile of Lassa Fever Positive Patients in Abakaliki, Southeast Nigeria, January-March 2018

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**Background:** Lassa fever is an often fatal viral hemorrhagic disease caused by Lassa virus and endemic in west Africa, It is one of the endemic zoonosis in Nigeria with a high rate of nosocomial

infection due to challenges in Health care sector. Early diagnosis is still a major challenge in most Nigerian health care institution We described the clinical profile of positive Lassa fever patients from 1st January – 31st March 2018 in Ebonyi state.

**Methods:** Contacts were traced, monitored and classified by engaging Disease surveillance officers and community informants. Patients were managed at the virology centre, Federal Teaching Hospital Abakaliki. Epidemiological data from the case investigation forms and clinical data from the hospital records were analysed using Epi info version 7.1.4 at 5% level of significance and 95% confidence interval.

**Results:** Sixty cases were positive with mean age of  $35 \pm 16.2$  years. The total case fatality rate was 18%, health worker (31%) and (16%) for patients on ribavirin. The age group mostly affected was 30-39 years and the least 0-9years. Most were females (59.7%), traders (26.2%) with tertiary level of education (42.9%). Fever (78%), headache (62%), cough (38 %), vomiting (32%), diarrhea (32%), and difficulty swallowing (28%) were the most reported symptoms at presentation while common complications included nasal bleeding (14.3%) and jaundice (6%). Having abdominal pain ( $p=0.0039$ ) and diarrhea ( $p=0.0039$ ) were related with mortality while treatment with ribavirin ( $P=0.0334$ ), was associated with survival.

**Conclusion:** Diarrhea and abdominal pain were key symptoms related to mortality. Even with the Ribavirin treatment, there was a high rate of fatalities underscoring the need to develop more effective treatment for Lassa fever.

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

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**Background:** 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  $\mu\text{m}$  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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## Infection Prevention and Control Practices in a Primary Healthcare Setting Following a Nosocomial Outbreak of Lassa Fever in Lagos State, Nigeria, August 2017

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**Background:** Lassa fever an acute viral infection. It poses a risk of nosocomial infection to healthcare workers. There was an outbreak report of Lassa fever in the PHC center, Lagos State, in August 2017. We investigated the outbreak, assess infection prevention and control practices (IPC) and institute control measures.

**Methods:** We conducted a cross-sectional study using a multistage sampling technique to select 240 healthcare workers from 16 PHCs in Surulere and Mushin Local Government Areas. Using a self-administered questionnaire to collect data on socio-demographic characteristics, knowledge, and practices (KAP) on infection prevention and control (IPC), we computed KAP using 11-29 item questions. Each item assigned 1 and 0 for correct and incorrect knowledge. We classified KAP as good if > 80%, fair if > 50%, poor if < 50%. We computed frequencies, proportions and odds ratios (OR) and used chi-square test at a p-value <0.05.

**Results:** All selected participants responded. Eighty-eight (36.7%) were 31-40 years with a mean age of 41.4 ±9.1 years and 172 (71.7%) were females. Seventy-three (30.4%) were community health workers with 124 (51.7%) having 1-10 years working experience. One hundred and forty-four (60.0%) respondents had a poor knowledge of IPC with 123 (51.3%) having poor reported practices [use of alcohol gel 116 (48.3%), face mask and goggles 60 (25.0%), protective gown 68 (28.3%) and protective boots 56 (23.3%)] after contact with a patient. Risk perception of being infected with Ebola virus disease: 185 (77.1%) and Lassa fever: 189 (78.8%). Poor knowledge of IPC was significant, respondents age (p=0.001), profession (p=0.002) and years of practice (p=0.006).

**Conclusion:** Majority of healthcare workers had a poor knowledge and practice of IPC. We recommend training of healthcare workers in Surulere and Mushin LGA on IPC knowledge and practice.

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## Molecular Epidemiology of Hepatitis E Virus, Enteroviruses, and Human Parechoviruses in Osun State

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Hepatitis E virus, Enteroviruses, and Human parechoviruses are transmitted primarily through the fecal-oral route. They present with a variable degree of clinical manifestations of self-limiting infections to sometimes severe and fatal conditions. The study is aimed at investigating the molecular epidemiology of these viruses among different cohorts in Osun state.

This study was a cross-sectional study of 653 human subjects recruited from six selected communities in Osun state and 720 human subjects from HIV, Animal Handlers, Pregnant women, and HBV cohorts. Furthermore, 89 swine and 87 cattle were recruited for the study. MP diagnostic ELISA was used to test for total antibodies and IgM to HEV in 1373 human sera. The ID.VET Hepatitis E indirect ELISA was used to detect IgG antibodies to HEV in the serum of 176 animals. Presence of HEV-RNA was tested for using two different PCR assays one step RT/Nested for the ORF 1 and ORF 2 region of HEV in 724 sera and stool extracts of humans and animals. 5'NCR RT/PCR was used to screen for enteroviruses and HPeV after which VP1 PCR was used for typing in 117 human stool samples. Phylogenetic analysis was carried out using Geneious and Mega 5 software. The statistical analysis was done with the aid of STATA.

The seroprevalence study revealed the HEV total antibody in HIV, Pregnant women, and Animal handlers to be 11.4 %, 6.3%, and 7.9% while IgM antibody 2.2%, 0.6, and 2.2% respectively. HEV total

antibody in Community study Oore, Oke-Osun, Osogbo Ede Esa-Odo and Iperindo were 20.97%, 18.45%, 12.38%, 8.54%, 22%, and 16.67%, while HEV IgM are 3.23%, 1.51%, 2.86%, 1.51%, 11% and 0% respectively. The HEV IgG seroprevalence observed in pigs and cows were 29.47% and 0% respectively. 24.27% HEV RNA positive samples were obtained from pig stool samples and none from cow stool samples using qPCR. One isolate each was obtained from pig stool and HBV human group serum; sequenced to be genotype 3b and untypeable genotype 3 respectively. Location (OR 2.2), age (OR 1.03), and alcohol use (OR 2.2) had a statistically significant association with HEV infection  $P < 0.05$ . Males were more infected with HEV than females ( $p > 0.05$ ). Water consumption also demonstrated a trend; people who consumed river and stream were more susceptible than people who consumed sachet/borehole though weak association exists ( $P > 0.05$ ,  $OR < 2$ ). There were 11 Enterovirus RNA sequences detected in this study; 9 (81.81%) group C and 2 (18.18%) group B enteroviruses. Three positive HPeV RNA were detected at screening however only two were typeable. The two sequences had a 75% homogeneity with HPeV 6.

This study demonstrated the circulation of HEV in swine and human but none in cattle. The prevalence of HEV was age, location, and low sanitation indices dependent. This study reports the first detection of HEV genotype 3 and HPeV in Nigeria human populace. This study further established the circulation of nonpolio enteroviruses in the populace. There is a need to step up sanitation indices in these communities.

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## Outbreak of Wild Strain Chicken Pox Virus Among Naval Personnel Onboard a War Ship, Lagos, Nigeria, 2018

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**Background:** Chickenpox is an acute, highly infectious febrile rash illness caused by varicella-zoster virus (VZV). Secondary infection occurs in about 60%–100% of susceptible household contacts. Unimmunized persons usually do not escape infection when exposed. Person-to-person spread occurs by inhalation of aerosolised respiratory secretions or vesicular fluid of skin lesions and via direct contact with body fluids of an infected patient. On 28 Aug 18, a personnel was reported to have strange rashes onboard a naval warship berthed in Apapa jetty, Lagos State. We investigated to identify the causative agent, its source and to propose recommendations.

**Methods:** We defined a case as any person with sudden onset of influenza-like symptoms, progressing two to three days later to develop characteristic itchy, blister-like rash; first on the face, hands and forearms and then after a few days progressing to the trunk or other parts of the body or anyone whose sample tested positive by polymerase chain reaction for wild strain varicella zoster virus between 28 Aug 18 and 09 Nov 18. We managed cases symptomatically in isolation using barrier nursing techniques. We described the outbreak by time, place and person and conducted a study to identify the source of infection.

**Results:** We identified eight cases among 75 persons (Attack rate: 10.5%) between 24 Aug 18 and 5 Oct 18. Seventy five percent of eight specimens tested positive for Chicken Pox Wild Type. Attack rate was highest among males 7(87.5%) and 26-30 years old 4(50.0%). The first case occurred on 24 Aug 18, peaked in 28 Sep 18 and decreased afterwards. All cases occurred among ratings onboard a naval vessel including one wife of personnel.

**Conclusions:** Wild-strain chicken pox outbreak occurred onboard a Nigerian Naval warship. The index case was a personnel who contracted the virus onboard his former ship in Port Harcourt. We sensitized and quarantined members of the ship company to minimise spread to other vessels and their families. We decontaminated the ship in collaboration with the state public health department. We recommended standard infection prevention and control practices which resulted in the control of the outbreak.

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## Seroprevalence of Yellow Fever Virus and Associated Risk Factors in Selected Health Facilities in Borena District, Southern Ethiopia

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**Background:** Yellow fever is a reemerging public health threat in Ethiopia. Yet, little is known about the epidemiology and risk factors. In this study the seroprevalence and associated risk factors of yellow fever virus infection were assessed in Borena district.

**Methods:** An institution based cross-sectional study was conducted from May to August 2016. A total of 519 consecutive acute febrile patients attending the outpatient departments of Teltelle health Center, Yabelo and Moyale Hospital were enrolled. Data on socio-demographic and environmental risk factors were collected using structured questionnaire. Blood samples were collected from all participants and screened for yellow fever virus exposure using indirect immunofluorescent assay.

**Result:** The overall prevalence of anti-YFV IgG and IgM was 12.5% and 7.3% respectively. A relatively higher IgM titre in females (COR=1.51; 95%CI 0.78-2.95), absence of significant difference by age both with respect to IgG or IgM positivity is indicative of probable peridomestic and active transmission.

**Conclusion:** though EUROIMMUN IIFT was claimed to be highly specific, to our knowledge to data exist to rule-out cross reactivity with other Flaviviruses in endemic setting; thus we recommend further systematic studies to determine the environmental and host factors that determine the extent of exposure to yellow fever virus infection in the district to inform appropriate interventions and validate the result to avoid potential emergence of public health disaster.

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## Mycobacterium tuberculosis Genotypes Causing Pulmonary and Extrapulmonary Tuberculosis in Southwest Ethiopia

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**Background:** Ethiopia is a hotspot for tuberculosis infection and ranks 10th in the world in terms of the number of TB. Understanding the genetic diversity and transmission dynamics of the circulating M. tuberculosis strains is very important to propose more effective preventive strategies. However, little is known about Mycobacterium tuberculosis (Mtb) strains responsible for TB in Southwest Ethiopia.

**Objective:** To investigate the overall genetic diversity of M. tuberculosis strains and the role of M. bovis in human TB infection in Southwest Ethiopia.

**Methods:** A total of 304 Mtb complex strains from extrapulmonary and 177 Mtb strains from pulmonary TB 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). Isolates were classified into phylogenetic lineages and families by using the reference strain collections available at [www.miru-vntrplus.org](http://www.miru-vntrplus.org).

**Results:** Of the 481 M. tuberculosis isolates, 394 (81.6%) were belonged to the Euro-American lineage (Lineage 4), with the ill-defined T and Haarlem as largest sub-lineages. The next predominant lineages were the Delhi/CAS (14.5%) followed by Haarlem (14.1%). Interestingly, six isolates (2%) from extrapulmonary TB patients were belonged to the newly defined Ethiopian lineage called lineage 7. Only two M. bovis isolates were identified from extrapulmonary TB cases. Eighty spoligotype patterns from pulmonary TB patients corresponded to orphan that were unique among the strains recorded in the SITVIT2/SPDB4 database. The overall clustering rate was 35%

indicating high rate of recent transmission in Southwest Ethiopia.

**Conclusion:** This study revealed a high diversity of *M. tuberculosis* complex genotypes responsible for TB in Southwest Ethiopia. We reported the presence of a new phylogenetic lineage called Lineage 7 from extrapulmonary TB patients in Southwest Ethiopia. Zoonotic transmission of *M. bovis* infection has been excluded as a major factor in TB in Southwest Ethiopia.

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## Investigation and Management of Two Probable Fatal Cases of Respiratory Diphtheria in Tunisia, 2015

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**Introduction:** Diphtheria is an acute, toxin-mediated disease caused by the *Corynebacterium diphtheriae*. Death occurs up to 20%, among those under 5 years or older than 40. In Tunisia, vaccination was introduced in 1978 and notification became mandatory in 1992 . The detection, management and public health response of two probable cases occurred in 2015, following a 22 year disease free interval, are described here.

**Methods:** Two probable cases of diphtheria, patients A and B, and their close contacts were immediately investigated by the respective epidemiologic surveillance departments.

**Results:** A 5 years-old unvaccinated girl (patient A) and a 49 years-old woman (patient B) were hospitalized for mild fever and sore throat on 20th September 2015 and 1st December 2015 respectively in the region of Nabeul (North East of Tunisia) with no epidemiological link. Both patients had an adherent membrane of the tonsils and negative *C. diphtheriae* cultures (swabbed under antibiotics). A difficult search for equine-derived diphtheria antitoxin (DAT), non-available in Tunisia,

started with patient A, who died with cardiogenic shock due to myocarditis on 24 September 2015, despite appropriate intensive care and administration of DAT received that same day. Patient B, after an initial recovery, was diagnosed with polyradiculoneuritis diphtheria. Her serum antibody level was 5kUI/l and despite of administration of DAT, patient B died on 12 February 2016. For both cases, the close household contacts and the medical staff underwent physical examination and throat swabs, received prophylactic antibiotic, their vaccination statuses were analysed, updated and completed.

**Conclusion:** The lack of first-hand diphtheria experience by clinicians and the shortage of DAT for immediate use when diphtheria is suspected are still challenges for countries with suboptimal vaccination coverage.

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## Real-Time Genomic Assessment of Medical Countermeasures During the 2018 Nord-Kivu and Ituri Provinces Ebola Virus Disease Outbreak

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**Background:** Real Time Genomics has become the “Holy Grail” of outbreak response. Recently established genomic capabilities in the Democratic Republic of the Congo (DRC) allowed us to explore fully the concept after the declaration of the 10th filovirus outbreak in the country.

**Methods:** After an initial report of 20 deaths among 26 suspected cases of acute hemorrhagic fever in

the Nord-Kivu Province, the Institut National de Recherche Biomédicale and several international groups rapidly responded to a possible outbreak of EVD. Using a targeted sequencing approach, we were able to generate near-complete viral genomes confirming a new EBOV variant, "Ituri", as the causative agent.

**Findings:** Sequencing of two positive samples allowed us to deeply characterize the causative agent within 4 days confirming the second EBOV emergence in 2018. The actionable information collected was used to guide the response as the EBOV vaccine was only deployed after confirmation of its "fitting" to the new variant. It also demonstrated a single spillover, distinct from the Équateur outbreak (2018). On a total of 47 near-complete viral genomes, we found primer and probe mismatches in all deployed diagnostic PCR assays, except for the Gene Xpert glycoprotein (GP) assay. Based on the GP mutations observed, the deployed antibody therapeutics (mAb114 and ZMapp) ought to be efficacious against EBOV "Ituri". Additional evolutionary analysis of the Ebola strains revealed DRC as a central point in historical EBOV movement.

**Interpretation:** Real time genomic sequencing conducted in the DRC during a hemorrhagic fever outbreak enabled immediate characterization of the causative agent. Rapid genomic characterization should become included in routine outbreak response procedures to ascertain the efficacy of common and novel medical countermeasures prior and continuously with their use.

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## Knowledge and Practice of Lassa Fever Infection Prevention and Control Among Healthcare Workers in Federal Medical Centre, Asaba, Delta State, Nigeria, October, 2018

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**Background:** Lassa fever is a viral hemorrhagic disease caused by Lassa virus. Healthcare workers (HCWs) are at high risk of being infected. Infection Prevention and Control (IPC) measures can reduce the spread of the virus in hospitals. We investigated the knowledge and practice of Lassa fever IPC among HCWs at the Federal Medical Centre (FMC), Asaba, Delta State, Nigeria.

**Methods:** We conducted a cross sectional study among HCWs at the FMC. We collected primary data using a self-administered questionnaires and a checklist. A sample size of 209 was calculated, univariate, bivariate analysis were done and odd ratio was calculated. knowledge of IPC was graded by assigning a score of "1" for a correct answer and "0" for an incorrect and scores were summed up. A score of 50% and above were graded as good and less than 50% as poor knowledge. Compliance with IPC was also graded by assigning scores of 0–2 on a likert scale and summed up as good for scores of > 75%, poor for scores <50%, and fair for those between 50 and 74%

**Results:** Among the 190 HCWs surveyed, 89 (46.8%) were doctors, 51 (26.8%) were nurses, 24 (12.6%) were laboratory scientists, and 16 (8.4%) were orderlies. Majority were females: 109 (57.4%) and had tertiary education: 173 (91.1%). The median age was 25-34 years and their mean number of years of job experience in the hospital was  $8.5 \pm 6.8$  years. Seven (3.7%) respondents had poor knowledge of IPC of lassa fever while 177 (92.7%) had good knowledge. Similarly, 166 (86.9%) had good practice whereas 1 (0.53%) had poor practice. The overall compliance rate to IPC of Lassa fever in the hospital was fair (62%) with hand washing point and running water and soap scoring the highest (96%). The adult intensive care unit has the highest proportion of compliance: 166 (83%) while female surgical ward has the lowest proportion of compliance 167 (56%). Doctors were 0.9 times less likely to have good practice towards Lassa fever IPC compared to others.

**Conclusion:** The HCW's knowledge and practice toward IPC of lassa fever were good but when observed on different IPC measures, their level of compliance did not translate into observed practice. We recommended to the management of the hospital on the need to retraining HCWs on IPC measures.



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## Yellow Fever Outbreak in a Community with Low Vaccination Coverage and Poor Knowledge, Attitude, and Practices Regarding Yellow Fever, Kebbi State, Northwestern Nigeria - January 2018

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**Introduction:** There is an apparent re-emergence of yellow fever in Nigeria, a disease that was last reported in the country in 1986. In November 2017, a yellow fever outbreak was reported in Kebbi State. We were deployed by the Nigeria Centre for Disease Control to describe the epidemiology; determine the presence of yellow fever vectors; conduct surveys on yellow fever vaccination coverage and community knowledge, attitude and practices regarding yellow fever; and to institute control measures.

**Methods:** We defined a presumptive case as any suspected case that tested positive for yellow fever in a Nigerian laboratory and a confirmed case as any presumptive case who tested positive for yellow fever in the reference laboratory in Dakar, Senegal. We conducted larval surveys and used human landing catch, CDC UV light, biogent-sentinel traps and ovitraps to catch mosquitoes. We calculated a minimum sample size of 384 for the surveys on yellow fever vaccination coverage and yellow fever knowledge, attitude and practices among community members. We gave equal allocation of 12 questionnaires per settlement and randomly selected 12 households per settlement for the surveys. We calculated proportions of vaccinated and unvaccinated children; and computed percentage scores of knowledge, attitude and practices of respondents.

**Results:** Between 30th August, 2017 and 27th January, 2018, there were 151 reported cases, of which five (3.3%) were presumptive cases, one (0.7%) was a confirmed case, 113 (74.8%) were negative and 31 (20.5%) results were pending. The presumptive and confirmed cases were clustered. Ninety-seven (64.2%) were male. Median age was 12 years (inter quartile range = 6-25 years). Out of 39 mosquitoes trapped, 38 (97.4%) were *Culex* spp. Out of 432 eligible children, 130 (30.1%) had their yellow fever immunization cards sighted. Out of 432 caregivers, 311 (72.0%) caregivers have heard about yellow fever, of which 2.3%, 2.6% and 48.2% had good knowledge, attitude and practices regarding yellow fever respectively. There was no significant association between caregivers good knowledge regarding yellow fever (Fisher's exact test,  $p=0.30$ ) and caregivers good attitude regarding yellow fever (Fisher's exact test,  $p=0.09$ ) with vaccination status of their children.

**Conclusion:** There is a potential for future yellow fever cases and other arbovirus infections in Kebbi State. We conducted mass risk communication activities and requested for reactive vaccination from International Coordinating Group on Vaccine Provision. We recommended rapid laboratory turn-around time, intensified surveillance for arbovirus infections, and continuous community engagement and dialogue regarding yellow fever prevention.

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## Sero-Prevalence of Human Papilloma Virus in Pregnant Women at a Teaching Hospital in Nigeria

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Documented studies on HPV infection among pregnant women are limited in Ogbomoso, South-west, Nigeria. The likely consequences of the infection are cervical cancer and vertical transmission of the infection from mother-to-child.

A total of 97 consented pregnant women, between 20-45 years of age, attending the antenatal clinic of BUTH were recruited for the study. Sera were tested serologically for the presence of IgM antibodies against HPV. Data on socio-demographic characteristics and potential risk factors were collected using structured questionnaires. Chi-square test was used to assess the association between the socio-demographic variables and HPV status. Overall seroprevalence of HPV was 5.38 % (5/93). The mean age of the study participants was 30.62±5.03 years. The highest prevalence was recorded among the age group 26-35 years (6.3%, 4/64) while the least was recorded among the age group 20-25 years (6.7%, 1/15). Parity wise, participants in the Primiparous group had a higher prevalence of 7.3% (4/55) than those in the multiparous group with a prevalence of 3.6% (1/28).

Results further underscores need for strict blood screening and public health education to hype awareness; and need to study prevalence of cancer in groups with highest HPV prevalence.

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## Emerging Plasmodium vivax Malaria Infections and Evidence of Duffy Binding Protein Gene Duplication in P.vivax Field Isolates in Sudan

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**Background:** Plasmodium vivax was less common in Sub-Saharan African countries including Sudan. Recently in Sudan the parasite has become widely distributed and witnesses a sharp increase in the number of cases reaching 25% and server cases has been reported. P. vivax Duffy binding protein gene (PvDBP) appears to be essential for red blood cells (RBCs) interacting with erythrocyte Duffy antigen receptor for chemokines(DARC). Until recently, the gene that encodes PvDBP was described as single copy gene. How-ever, whole genome sequences from field isolates from Sudan, Madagascar and

Cambodia provides evidence for duplication of the PvDBP gene. Also in Sudan P. vivax infections are becoming more frequent during the recent years. It is not known whether PvDBP gene duplication has a role in the recent increase Duffy negative transmission. In this study PvDBP gene duplication and it isrelation to Duffy genotype was investigated.

**Methods:** A cross sectional hospital based study was conducted in two P. vivax malaria endemic regions namely Khartoum and River Nile. Ethical clearance was obtained and informed consent was taken prior to study enrolment. A total of sixty-four vivax malaria blood samples were collected. Genomic DNA was extracted and P. vivax mono infection was confirmed by nested PCR. PvDBP gene duplication and Duffy genotyping was performed using PvDBP specific gene primers and allele specific PCR respectively. Data was analyzed using SPSS software.

**Results:** Out of the sixty-four samples Fifty-eight (90.6%) were confirmed to be P. vivax monoinfection. The PvDBP duplication was detected in 26/58 (44.8 %). The two types of PvDBP duplication the Malagasy and the Cambodian were detected in Sudanese isolates. However, the frequency of Cambodian duplication type was higher than the Malagasy type (69% vs 31%). PvDBP duplication was detected in all patients bearing Duffy negative allele (FYES). The frequency of PvDBP duplication was 72% and 28% in heterozygous and homozygous Duffy negative vivax patients respectively.

**Conclusion:** In conclusion this study confirms the DBP gene duplication in Sudanese P. vivax isolates and is first to show the Cambodian duplication type. The present study detected high frequency of gene duplication among Duffy negative individuals. Further studies are needed to investigate functional significance of PvDBP duplication.

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## Outbreak Investigation of Cutaneous Anthrax in the Sharifabad Village, Vakhdat City, Tajikistan, 2016

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**Background:** On July 12, a case of suspected anthrax was reported after the slaughter of a sick cow in the village of Sharifabad. The area has been known to have periodic anthrax cases for several decades. We performed an investigation to confirm the case(s), to determine the epidemiology, and to implement control measures.

**Methods:** We defined a suspected case as an individual who had participated in the slaughter or had contact with products from it and had fever (> 38C) with either a skin lesion, rigors or myalgia. Confirmed cases had characteristic skin ulcers. The Response Team interviewed all cases and reviewed all medical records. One sample of meat and four samples of soil from the slaughter site were tested for forms of *Bacillus anthracis*.

**Results:** 16 suspected cases were identified, of which 10 were confirmed (six men, four women; age range, 16-60, mean 32 years). Seven people participated in the slaughter and all were confirmed cases; nine people bought meat and three were confirmed cases. The incubation period ranged from one to eight days (mean, three days). All 10 cases were hospitalized and received antibiotics; all recovered. The remains of the sick cow were destroyed subsequent to human illness. In the meat, large gram-positive bacilli characteristic of *B. anthracis* were detected; in the sample of soil, spores characteristic of *B. anthracis* were identified. The slaughter site and personal objects were disinfected with calcium hypochlorite. Anthrax vaccine, used haphazardly on small farms in the area, was not used in animals on the farm from which the sick animal originated.

**Conclusion:** This outbreak was caused by a sporadic case of anthrax in a cow, and would have been prevented by either the use of vaccine in cows or the awareness/conduct of advice not to butcher sick animals; both should be improved.

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## Evaluation of Lassa Fever Surveillance System, Edo State, Nigeria, February 2018

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**Background:** Lassa fever (LF) is an acute viral haemorrhagic fever. There was an increase in the number of reported LF cases in LF-endemic Edo State. As cases were increasingly reported, we were deployed from the Nigeria Centre for Disease Control to evaluate the LF surveillance system in the state to guide appropriate intervention.

**Methods:** We used the CDC Updated Guidelines for Evaluating Public Health Surveillance Systems. We interviewed the 18 Local Government Disease Surveillance and Notification Officers (DSNOs) and their assistants using self-administered questionnaires. We reviewed Lassa fever data for 2017. The attributes we evaluated were simplicity, flexibility, data quality, acceptability, sensitivity, representativeness, timeliness, and stability. We analyzed the data using Microsoft excel.

**Results:** Of the 25 retrieved questionnaires 15 (60%) of the respondents were females, mean age was 43+7 years, 12 (42%) were nurses, 18 (72%) correctly stated the case definition for confirmed LF but only 7 (28%) correctly stated the case definition for a suspected LF, and 16 (64%) partially stated the case definition of a suspected LF. Up to 84% had not been trained on LF in the last 1 year, 88% responded that they needed training on LF surveillance, 52% received supportive supervision in the last 6 months, 96% reported not having a computer system to handle data collection, analysis and transmission and only 36% has access to reliable internet, 13 community health practitioners and 12 nurses answered the suspected case or confirmed case definition correctly. Among the respondents, 100%, 96%, 84%, 60% and 56% responded that the system was acceptable, representative, simple, stable and timely respectively. However only 48% responded that the system was flexible.

**Conclusion:** The LF surveillance system was found to be useful and meeting its set objectives, however the DSNOs need refresher training, supportive

supervision, computer systems and internet access. We give DSNOs on the job training and shared our findings with all stakeholders. The system was found to be acceptable, representative, simple, stable and timely. However, the system has gap in data quality and has inadequate funding.

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## Assessment of Timeliness of Commencement of Tuberculosis Treatment Among Patients in Lower Manya Krobo Municipality, Ghana

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Assessment of Timeliness of Commencement of Tuberculosis Treatment Among Patients in Lower Manya Krobo Municipality, Ghana

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**Background:** Delay in commencing TB treatment contributes to the total TB burden of cases as patients remain infectious and spread the disease in the community. It may also result in a more advance state of the condition that can lead to complications, even increasing the risk of death. This study was therefore aimed at assessing the proportion of TB patients who delayed in commencing treatment and the related factors influencing delay in the Lower Manya Krobo Municipality, Ghana.

**Methods:** The study used cross sectional data collected from 71 patients aged at least 15 years in

the Lower Manya Krobo Municipality of Ghana using structured questionnaire. Descriptive statistics and the logistic regression model were the methods of analysis employed.

**Results:** Over 50% of the sampled patients were females and their ages ranged from 15 to 83 years with a mean age of 46.7 years (SD; 17.4 years). Most participants (61.9%) had primary/JHS education. The median patient delay was 56 days, health facility delay was 5 days and total treatment timeliness was 56 days. Patient delay was associated with first place of visit after sickness at the pharmacy shop (P=0.02) and type of treatment facility (P=0.01). Number of health facility visit was also associated with increased delay at the health facility (P=0.026).

**Conclusion:** Delay in diagnosis and treatment of all forms of TB is unacceptably high in the Lower Manya Krobo Municipality of Ghana. Patient delay contributes massively to the total delay as the first place most patients visit prior to visiting a health facility was the pharmacy shop. Increasing awareness of benefits of early visits to health facilities will improve the health seeking behavior of the community to reduce the length of delay.

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## Lassa Fever Outbreak Investigation in Federal Capital Territory Abuja, Nigeria, October 2018

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**Background:** Lassa fever (LF) is an acute viral hemorrhagic illness caused by the LF virus. It is endemic in West Africa. By October 2018, an ongoing outbreak in Nigeria had been reported in 21 states and the Federal Capital Territory (FCT) with 40 health care workers (HCW) affected. We investigated the outbreak in FCT to confirm the diagnosis, describe the epidemiological profile and institute control measures.

**Methods:** We generated a line list from cases reported at health facilities and conducted active case search in affected communities. Socio-demographic data and clinical information were collected. We collected blood samples for testing. We traced contacts among family members of confirmed cases and healthcare workers, line listed and classified them as high or low risk and followed up for 21 days from exposure. Data were analyzed, rates and percentages calculated. Self-administered semi structured questionnaires were used to interview HCWs in selected secondary health facilities through multistage sampling. Knowledge, risk perception, practice and disease reporting scores were computed from 14, 4, 5 and 8 item questions respectively. Scores of '1' were given for correct and '0' for incorrect responses. Knowledge was classified as good if  $\geq 75\%$ , fair if 50-74% and poor if  $< 50\%$ . Practice was scored over 25 marks and classified good for scores  $\geq 20$ . Associations were measured using Chi-square with degree of significance set at 5%.

**Results:** A total of 52 suspected cases with 10 deaths (CFR 20.5%) were reported between January and October 2018. Mean age of suspected cases was  $25.9 \pm 18.7$  years, of which 32 (61.5%) were male. Three (6%) blood specimens tested positive to LF by PCR. CFR among the confirmed cases was 66.7% (2). One hundred and twenty six contacts were line listed, 75 (59.5%) were health care workers.

A total of 424 health care workers were interviewed, 52.4% (218) were female, mean age  $40.8 \pm 9.5$  years. There were 52 (23.7%) doctors. LF case definition was correct for 39.6% (168) of respondents, 109 (37.9%) said it affects only people  $> 5$  yrs of age, 156 (40.8%) believed it can be prevented by vaccination. One hundred and sixty nine (39.8%) had good knowledge scores  $\geq 75\%$ . Three hundred and twenty-nine (83.5%) HCWs consider themselves at risk of nosocomial transmission of LF and 378 (95.9%) agree it is possible to prevent spread of LF among HCWs. LF as a notifiable disease was agreed by 261 (68.7%). Good practice scores were gotten by 73.5% (311) HCWs. Being a nurse and availability of PPE were associated with good practice ( $\chi^2 = 10.5$ ,  $P < 0.0001$ ) and ( $\chi^2 = 5.1$ ,  $P = 0.005$ ) respectively.

**Conclusion:** Outbreak of LF in FCT was confirmed, it was controlled through active case search and effective contact tracing. Sensitization activities were conducted in health facilities and communities, environmental sanitation exercises carried out, trainings on case management and

infection prevention and control were also conducted. Personal protective equipment, IEC materials, Ribavirin® and other supplies were prepositioned in health facilities. We recommend strengthening of LF surveillance, routine environmental sanitation and ensuring strict IPC in health facilities.

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## Containing the Unprecedentedly Large 2018 Lassa Fever Outbreak in Nigeria: The Role of Incident Management System

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**Background:** Lassa fever (LF) is an endemic viral haemorrhagic fever (VHF) in Nigeria associated with high mortality rates. Following geometric increase in number of LF cases in January 2018, the Nigeria Centre for Disease Control LF technical working group immediately transitioned to an Emergency Operation Centre (EOC). The established EOC, involved using an Incident Management System (IMS) to coordinate the outbreak response at national and State levels. This study gives a descriptive epidemiology of the largest LF outbreak in Nigeria and the role of EOC in the containment of the 2018 LF outbreak.

**Methods:** The national LF EOC was activated on the 22nd of January 2018 to coordinate the response via five pillars namely surveillance, case management and infection prevention and control, laboratory, risk communication and logistics. The national LF data from January to April 2018 was extracted from the VHF case-investigation-form database and descriptively analysed.

**Results:** National rapid response teams were deployed to support response in most affected states. The National EOC response was scaled up to level three for effective containment of the outbreak leveraging on strong multisectoral and international collaboration which led to drastic decline in cases. A total of 1892 suspected cases

were reported from 21 States, of which 423(22.3%) were confirmed positive with 106 deaths (case fatality rate: 25.1%) from epidemiologic week 1 to week 18. Age-group 21-40 (44%) were mostly affected with male to female ratio of 2:1. Majority (81%) of the confirmed cases were from the historical hotspot States of Edo (42%), Ondo (23%) and Ebonyi (16%).

**Conclusion:** Nigeria experienced the largest LF outbreak in 2018 with the number of confirmed cases and deaths exceeding cumulative cases reported in the 2017 outbreak. Multisectoral and multidisciplinary tactical EOC IMS coordinated response and consolidated decision making coordination was largely credited led to the containment of the outbreak.

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## Control Strategy for Emerging Diseases: A Case for Monkeypox Surveillance and Control Strategy in Africa

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**Background:** There has been an increase in the incidence of emerging infectious diseases globally. These include the recent increase in human monkeypox cases across a wide geographic area and with potential for further spread. Lack of reliable surveillance and control strategy for this emerging zoonosis remain a challenge.

In September 2017, after 39 years of the last recorded case, Nigeria recorded a resurgence of monkeypox without prior surveillance or response system in place for the disease. This study aims to review the emergence, response and the implication for monkeypox control.

**Materials and Method:** We reviewed the re-emergence of monkeypox in Nigeria, the response strategy to the outbreak as well as lessons learnt from the five decades of monkeypox detection and control and the need for a paradigm shift in the approach to monkeypox control.

**Results:** Nigeria experienced a re-emergence and the largest outbreak of the West African clade monkeypox in history in September 2017. In response to the outbreak, Emergency Operation Centres were established to coordinate the outbreak response. Case-based surveillance system and a nationwide awareness creation about the disease was put in place. A One-Health approach was adopted with the involvement of the animal health sector. Prior to this outbreak, monkeypox was not listed as a priority disease. No surveillance system in human /animal was in place. As at November 2018, a total of 130 confirmed cases with seven deaths were recorded across seventeen states. Circulating viruses were similar to the Nigeria 1971 virus. Three cases were confirmed in the United Kingdom (2) and Israel (1) with travel history from Nigeria. Human to human transmission was demonstrated within households, prison and in health care setting. Animal surveillance could not commence until one year after and results are being awaited.

Sporadic cases continued to occur in the population. There is however a suspicion of a decrease in the sensitivity of the monkeypox surveillance with reports of missed and investigated cases due to inadequate resources at the sub-national level. Smallpox vaccine was not used during the response.

**Conclusion:** Control of zoonosis in human cannot be achieved without good understanding of the disease spread in animal and the human-animal interphase. Control of monkeypox must therefore be addressed through coordinated actions between animal and public health authorities through a One-Health approach. This will include a sustainable surveillance and response system in human and the commitment of the animal sector to ensure a surveillance system to detect and report zoonotic diseases in animals.

Further population based surveillance and research programme is required to unravel the risk factors for the re-emergence and the true burden of the disease in the population.

Our findings of human to human transmission in households, closed and health care settings and as reported in other countries show the need to ensure access to smallpox vaccines for use in at-risk group especially healthcare workers.

Furthermore, the factors aforementioned makes the development and review of policies that will enhance early detection of monkeypox and related outbreaks more imperative.

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## Risk Factors for Acute Childhood Diarrhea: A Cross Sectional Study Comparing Refugee Camps and Host Communities in Gambella Region, Ethiopia

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**Introduction:** Refugees are among the most-at-risk population experiencing health problems for a variety of reasons. Diarrhea is one of the most common causes of child morbidity and mortality in refugee camps, aggravated by inadequate Water, sanitation and hygiene service, malnutrition and micronutrient deficiencies, particularly in developing countries. However, there are only a few studies of the epidemiology of diarrhea and WASH services in complex emergencies in sub-Saharan Africa.

**Objective:** This study to assess acute diarrhea and associated risk factors among under-five children in the refugee camps and host communities in Gambella Region, Ethiopia.

**Methods:** A stratified, multi-stage comparative cross-sectional study was conducted from September to December 2016 in refugee and host communities. Data were collected using a structured questionnaire and the Potatest+ water quality testing kit. Descriptive statistics were computed, bivariate and multivariable logistic models and the Mann-Whitney U test was used. Point estimates of odds (ORs) with 95% confidence interval [CI] were determined at statistical significant level P-values < 0.05.

**Results and Discussion:** The overall prevalence of reported acute childhood diarrhea was 36 %. It was 38 % in the refugee camps and 33% in the host communities. Households with children in which the water containers were not covered (P = 0.01), consumed less than 15 liters of water per capita per day (P = 0.021) and lacked hand-washing setups (P = 0.02) were specific predictors of diarrhea in

refugee camps. In the host communities, children from households which did not have a latrine (P = 0.017) and consumed surface water (P = 0.003) had a significantly higher risk of diarrhea than their corresponding households. Moreover, child age (12 – 23 months) and lack of formal education were the most common predictors of childhood diarrhea in both communities. Coliform counts exceeded the moderate risk were also associated with acute childhood diarrhea (P = 0.002).

**Conclusion and Recommendations:** Hygiene related factors and facility problems were the main predictors of diarrhea in the refugee camps and host communities, respectively. Stored water in a lot of households was contaminated in both the refugee and host communities. Therefore, designing and implementing a unique appropriate community education and effective hygiene promotion program is essential in empowering uneducated household heads towards lessening diarrhea. Further collaborations between the government and non-government organizations are required to identify persistent human behavioral, socioeconomic and environmental factors in diarrhea transmission.

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## AFP Surveillance in Cameroon: Reasons for Sub-Optimal Indicators in Selected Health Districts

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**Background:** In 2014 the circulation of poliovirus during the epidemic in Cameroon was interrupted due to efforts made by all levels of the health pyramid. Since August 2016, the country has been on alert due to a polio epidemic in Nigeria. In 2017, several Cameroonian health districts (HDs) remained below the required performance level for epidemiological surveillance. The purpose of this study was thus to evaluate the acute flaccid paralysis (AFP) surveillance system in these poorly performing districts, assess the level of knowledge

of stakeholders and analyze hindrances to AFP surveillance in order to improve the performance.

**Methods:** A cross-sectional study was carried out whereby 28 HDs were conveniently sampled from the 47 poorly performing or silent districts. A silent HD is defined as zero AFP case notified during the last 12 months. A HD is poorly performing when standard AFP surveillance indicators do not reach the target during the same time period. Standardized questionnaires were used to extract data from health registers, reports and key informants; on surveillance organization and functioning, strengths and weaknesses and staff knowledge.

**Results:** Of the 78 surveillance sites visited, 82% had a surveillance focal point. Of 51 respondent sites 48.8% had an operational site visit plan. Thirty-eight percent of the HDs had realized at least 80% of planned high priority site visits. The cold chain was functional in 37 out of 62 (59.4%) surveillance sites. Concerning the knowledge on epidemiological surveillance, of 64 respondent surveillance focal points 95% knew the AFP case definition compared to 48% of 53 clinicians ( $p < 0.00001$ ). Sixty-four percent of these 64 focal points knew what to do with an AFP case. Tradi-practitioners were more involved in surveillance activities than private health facilities.

**Conclusion:** AFP surveillance system in poorly performing HDs was characterized by irregular site visits and low involvement of clinicians in epidemiological surveillance. Regular supervision of those HDs may help reinforce AFP surveillance and prevent outbreaks.

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## An Assessment of Rift Valley Fever Risks in Pastoral Settlements of Northcentral Nigeria: Associated Pathways, Social Drivers for Emergence, and Public Health Significance

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**Background:** Rift Valley fever (RVF) is a vector-borne emerging viral zoonotic disease of threat to animal and human health. Social determinants of health that include socio-economic, cultural and demographic factors have potentials to influence infectious diseases outcomes. In light of unpredictability of RVF outbreaks with consequent public health and socio-economic impacts, there is a need to explore knowledge, perceptions and practices regarding its epidemiology so as to provide basis for surveillance and interventions. Study objectives were: to assess local knowledge, risk pathways and mitigation measures regarding RVF in pastoral settlements. Our Null hypothesis was that pastoralists' social factors cannot influence emergence of RVF in their settlements.

**Methods:** Interview questionnaire-based cross-sectional study was conducted on systematic randomly selected households in pastoral settlements of North-central Nigeria in 2017. Descriptive, bivariate and multivariable logistic regressions analyses were performed at 95% confidence level.

**Results:** All 403 selected pastoralists (201 agro-pastoralists and 202 nomadic pastoralists) participated in the study. Majority (62.8%) of participants had no formal. Only 24.4% of agro-pastoralists and 11.4% of nomadic pastoralists significantly mentioned RVF to be zoonotic disease. Majorities of agro-pastoralists (67.7%) and nomadic pastoralists (92.6%) mentioned high mortality in newborns as RVF signs in animals. Also, 85.1% of agro-pastoralists and 94.6% of nomadic pastoralists reported sudden onset of abortions as signs in animals. About 78.6% of agro-pastoralists and 66.7% of nomadic pastoralists mentioned high



fever as RVF symptoms in humans, while only 23.4% and 26.7% of agro and nomadic pastoralists, respectively knew RVF to be transmissible to humans through mosquito bites. Low proportions of pastoralists significantly perceived bites of infected mosquitoes ( $p < 0.001$ ), drinking contaminated raw milk ( $p < 0.001$ ), contacts with infected aborted fetuses ( $p < 0.001$ ), and co-habitation in same places with animals ( $p < 0.001$ ) as zoonotic risk pathways for RVF in pastoral settlements. Significant mitigation practices against RVF virus were: avoiding ponds and swampy areas during grazing ( $p = 0.001$ ), avoiding contacts of healthy and suspected infected herds ( $p = 0.001$ ), avoiding culture of animal loaning or for dowry ( $p = 0.001$ ), ethno-veterinary practices ( $p = 0.001$ ). Social factors that significantly influenced emergence of RVF in pastoral settlements were: co-habitations of herders with animals (OR=7.8; CI: 4.85–12.37), concentration of animals at grazing and watering points (OR=2.7; CI: 1.78–4.01), introduction of new animal bought at market into herds (OR=4.3; CI: 2.74–6.59), culture of giving out animals as loans or gifts (OR=8.4; CI: 5.36–13.16), culture of giving out animals as dowry (OR=6.1; CI: 3.96–9.43), and extensive husbandry management (OR=2.2; CI: 1.45–3.25).

**Conclusions:** This study found overall low proportions of surveyed pastoralists with significant existing knowledge, perceptions of risks pathways and mitigation measures towards RVF. These challenging gaps call for collaborative efforts of public health and veterinary authorities to support preventive health education on emerging zoonotic diseases among vulnerable human and animal populations in remote areas of developing countries. Social activities were identified as key drivers for RVF emergence in pastoral settlements. Preventive and control programmes that take modification of these factors into consideration, through sensitization, will be beneficial to public health and livestock industry in Africa.

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## Crimean-Congo Hemorrhagic Fever Outbreak in Central Uganda – August 2017

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**Background:** Crimean-Congo Hemorrhagic Fever (CCHF) is a severe, epidemic-prone viral hemorrhagic disease transmitted to humans by ticks that have fed on infected livestock, or by direct contact with infectious livestock or humans. On August 20, 2017, two RT-PCR-confirmed CCHF cases were reported from central Uganda. Both case-persons worked in cattle-rearing districts, Nakaseke and Kyankwanzi, and presented with high-grade fevers, fatigue, and spontaneous bleeding. We investigated to determine the scope of, and risk factors for, the outbreak, and to recommend evidence-based control measures.

**Methods:** We defined a probable case as sudden onset of fever ( $>38^{\circ}\text{C}$ ) for  $\geq 3$  days, with spontaneous bleeding or bruising or laboratory evidence of pancytopenia (all unexplained by other causes) in a resident of the outbreak-affected districts. A confirmed case-person was a probable case-person with confirmation of CCHF by RT-PCR. We reviewed medical records and conducted an active case-search in affected districts. In a case-control study, we compared exposures between case-persons and asymptomatic neighborhood- and age-matched controls. ELISA method was used to test serum samples from 33 cattle and 29 goats from affected farms for CCHF virus infection.

**Results:** In addition to 2 confirmed case-persons, we identified 5 probable case-persons. All case-persons were men. The outbreak affected three cattle-rearing districts: Nakaseke (attack rate[AR]=2.8/100,000), Kyankwanzi (AR=1.8/100,000) and Luwero (AR=0.9/100,000). Of the 7 case-persons and 28 controls, 4 (57%) case-persons and 3 (11%) controls had been bitten by ticks or squashed ticks with bare hands within the incubation period (ORM-H=11, 95%CI Fisher exact=1.1-112). Sero-positivity for CCHF was found in 60% of cattle and 23% of goats.

**Conclusions:** This CCHF outbreak was likely caused by exposure to infected ticks, which transmitted the

virus from infected livestock to humans. We recommended spraying livestock with acaricides to reduce ticks on the livestock in the area, and avoiding human exposures to ticks.

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## A Foodborne Cholera Outbreak in a School Caused by Eating Contaminated Fried Fish – Hoima Municipality, Uganda, February 2018

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**Background:** Cholera is a severe gastrointestinal disease caused by *Vibrio cholera*. It has caused several pandemics. On 26 February 2018, a suspected cholera outbreak, with one death, occurred in School X in Hoima Municipality, western Uganda. We investigated to identify the scope and mode of transmission of the outbreak, and recommend evidence-based control measures.

**Methods:** We defined a suspected case as onset of diarrhea, vomiting, or abdominal pain in a student or staff of School X or their family members during 14 February–10 March. A confirmed case was a suspected case with *V. cholerae* cultured from stool. We reviewed medical records at Hoima Hospital and searched for cases at School X. We conducted descriptive epidemiologic analysis and hypothesis-generating interviews of 15 case-patients. In a retrospective cohort study, we compared attack rates between exposed and unexposed persons.

**Results:** We identified 15 cases among 75 students and staff of School X and their family members (attack rate=20%), with onset from 25–28 February. One patient died (case-fatality rate=6.6%). The epidemic curve indicated a point-source exposure. On 24 February, a student brought fried fish from her home in a fishing village, where a cholera outbreak was ongoing. Of the 21 persons who ate the fish, 57% developed cholera, compared with 5.6% of 54 persons who did not eat (RR=10; 95%

CI=3.2–33). None of 4 persons who recooked the fish before eating, compared with 71% of 17 who did not recook it, developed cholera (RR=0.0, 95%CI Fisher exact=0.0–0.95). Of 12 stool specimens cultured, 6 yielded *V. cholerae*.

**Conclusion:** This cholera outbreak was caused by eating fried fish, which might have been contaminated with *V. cholerae* in a village with an ongoing outbreak. Lack of thorough cooking of the fish might have facilitated the outbreak. We recommended thoroughly cooking fish before consumption.

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## Malaria Outbreak Facilitated by Appearance of Vector-Breeding Sites After Heavy Rainfall and Inadequate Preventive Measures: Nwoya District, Uganda, March–May 2018

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**Background:** Malaria is a leading cause of morbidity and mortality in Uganda. In April 2018, malaria cases surged in Nwoya District, northern Uganda, exceeding the action thresholds. We investigated to assess the outbreak's magnitude, identify transmission risk factors, and recommend evidence-based control measures.

**Methods:** We defined a malaria case as onset of fever in a resident of Nwoya District with a positive Rapid Diagnostic Test or microscopy for malaria *P. falciparum* from 1 February to 22 May 2018. We reviewed medical records in all health facilities of affected sub-counties to find cases. In a case-control study we compared exposure risk factors between 107 case-persons and 107 asymptomatic controls matched by age and village. We conducted entomological assessment on vector-density and behavior.

**Results:** We identified 3,879 case-persons (attack rate [AR]=6.5%) and 2 deaths (case-fatality

rate=5.2/10,000). Females (AR=8.1%) were more affected than males (AR=4.7%). Of all age groups, the 5-18 year age group (AR=8.4%) was most affected. Heavy rain started on 4 March; a propagated outbreak began during the week of 2 April. In the case-control study, 55% (59/107) of case-patients and 18% (19/107) of controls had stagnant water around households for several days following rainfall (ORM-H=5.6, 95%CI=3.0-11); 25% (27/107) of case-patients and 51% (55/107) of controls wore long-sleeve cloths during evening hours (ORM-H=0.30, 95%CI=0.20-0.60); 29% (31/107) of case-patients and 15% (16/107) of controls did not sleep under a long-lasting insecticide-treated net (LLIN) (ORM-H=2.3, 95%CI=1.1-4.9); 37% (40/107) of case-patients and 52% (56/107) of controls had  $\geq 1$  LLIN per 2 household members (ORM-H=0.54, 95%CI=0.30-0.97). Entomological assessment indicated active breeding sites; *Anopheles gambiae* sensu lato species were the predominant vector.

**Conclusion:** Increased vector breeding sites after heavy rainfall, together with inadequate malaria preventive measures caused this outbreak. We recommended increasing coverage for LLINs and larviciding breeding sites.

Key Words: Malaria, *Plasmodium falciparum*, Outbreak, Global Health Security; Uganda.

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## Role of Anti-Leishmania donovani Antibodies in Parasite Internalization into Host Macrophage

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**Introduction:** *Leishmania* promastigotes and amastigotes preferentially infect macrophages, where several host cell surface molecules have been proposed to mediate internalization of *Leishmania* into macrophages. It is generally thought that random attachment of the flagellated promastigotes to mononuclear phagocytes initiates their uptake via circumferential pseudopods. Intracellularly, the promastigotes become located

in phagolysosomes in which they transform to and survive as 'aflagellated' amastigotes that hide their shortened flagellum within the flagella pocket. This study aimed to demonstrate the role of humoral immunity in *Leishmania* parasite internalization into host macrophages.

**Materials and 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  $626 \pm 91$  for antibody-coated *Leishmania donovani*, compared to  $412 \pm 70$  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.

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## Risk Factors Associated with Outbreak of Cerebrospinal Meningitis in Kano State-Nigeria, March-May 2017

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**Introduction:** A multi-state outbreak of Cerebrospinal Meningitis (CSM) from *Neisseria meningitidis* occurred in Nigeria in 2017. As at Week 52 in 2016, 831 suspected cases and 33 deaths (CFR, 4.0%) in 31 States were recorded. Two confirmed cases were reported in Kano on 22nd March, 2017. We investigated to characterize the outbreak, determine risk factors and institute appropriate control measures.

**Method:** We reviewed line list, and conducted active case search in health facilities and neighboring communities. We conducted an unmatched case-control study (1:2). A case was defined as any person with sudden onset of fever (>38.5°C rectal or 38.0°C axillary) and any of neck stiffness, altered consciousness or bulging fontanelle in toddlers, while a control was defined as any apparently healthy person who resides around the case such as family members, caregivers, neighbors, and healthcare personnel. Latex agglutination and bacterial culture were conducted to confirm diagnosis of CSM. We performed descriptive and bivariate analyses, as well as multivariate analysis to determine independent risk factors for CSM.

**Results:** We documented 48 cases with an attack rate of 13.7/100,000 population and case fatality rate of 8%; 34 of 44 local government areas were affected. Median age of cases was 11 years (1 month – 65 years). On multivariate analysis, independent risk factors associated with the outbreak were young age (<14) [AOR =6.58; 95% CI =2.85-15.180, history of vaccination (AOR=0.37; 95% CI=0.13-0.99) and history of travel (AOR=10.16; (1.99-51.85). Laboratory results showed 22 positive cases for *Neisseria meningitidis* types C and A/Y.

**Conclusion:** Major risk factors associated with this outbreak were young age (Children <14years are at risk of CSM), not being vaccinated and history of travel to affected states. We sensitized communities and strengthened case management. We recommended immediate reactive vaccination and enhanced surveillance in bordering communities.

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## Knowledge and Practice of Standard Precautions in Lassa Fever Control Among Healthcare Workers in Two Local Government Areas of Ondo State, Nigeria

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**Introduction:** Health care personnel practice of standard precautions during patient care can reduce Lassa fever-associated morbidity and mortality. We assessed the knowledge and practice of standard precautions in control of Lassa fever (LF) by health care workers in the two affected local government areas (LGA) of Ondo State during an outbreak of LF.

**Methods:** We sampled 190 health care workers from the 59 health facilities (private and public) in the two Lassa fever affected LGAs. We collected data from them using a self-administered questionnaire and a checklist to assess the availability of personal protective equipment (PPE). We computed frequencies, means, and proportions, scored knowledge, tested association using odds ratio at 95% CI and Logistic regression to identify factors predicting practice of standard precautions.

**Results:** We interviewed one hundred and ninety respondents with a mean age (years) 31.7 ± 9.8. More respondents in public health facilities 42(83%) had good knowledge of Lassa fever transmission compared with those in private hospitals. Some of the respondents 87 (45.8%) had

good knowledge of standard precautions while caring for a Lassa fever patient. However, only 57 (30%) had full personal protective equipment (PPE), 114 (60%) had face masks, and 177 (93%) had gloves. There was no association between availability and use of PPE (OR-0.5, 95%CI 0.1-1.9), however, a significant relationship existed between type of health facility (public/private) and practice of standard precautions 3.2 (1.3 – 7.2), having knowledge of standard precautions and its practice (OR-5.2, 95%CI 1.1-23.5). Having a good knowledge, however, determined practice of standard precautions.

**Conclusion:** Good knowledge of standard precautions determined practice. We trained the health care workers on standard precautions and recommended that the state procure more PPEs.

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## Preparedness for Infection Prevention and Control During a Lassa Fever Outbreak in Ogun State, Nigeria, 2017

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**Introduction:** Hospital-acquired infection (HAI) of Lassa fever (LF) during outbreaks often occurs with fatal consequences on healthcare workers (HCWs). In December 2016, Ogun State in southwestern Nigeria experienced LF outbreak in a tertiary health facility with five fatalities including two healthcare workers. We assessed the infrastructural and personnel preparedness (HFIP) of a major tertiary health facility during the outbreak.

**Methods:** We administered a semi-structured questionnaire to all the HCWs to assess their knowledge and practice of infection prevention and control (IPC). We scored and classified knowledge and practice questions as either good or poor using 70% as cut off. We used a standardized checklist to evaluate the infrastructural preparedness. We

calculated frequencies and proportions, with test of associations done using odds ratio.

**Results:** A total of 13 suspected, 3 probable and 2 confirmed LF cases, with 5 deaths (CFR= 100%) were recorded. Good knowledge of IPC was found among 80 (78%) HCW; however only 45 (44%) reported good IPC practices. Of the 101 HCWs interviewed, 59 (58%) had had training on IPC. Good knowledge was found to be a significant determinant of good practice (AOR= 11.1, 95% CI= 3.3-50.0). There was no significant association between having IPC training and adoption of good practices (OR= 1.9, 95% CI= 0.8–4.2). There were no isolation wards, personal protective equipment (PPEs), IPC guidelines or running water.

**Conclusion:** Lack of infrastructure and poor IPC practices probably fueled the health care associated spread of this outbreak. We sensitized all heads of department and other health facility staff, expanded health facility infection control committee, established LF isolation ward and built the capacity of healthcare workers on IPC to curtail the spread of the disease.

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## Ethno-Demographic Correlate and Socio-Cultural Practices Relating to Cholera Infection in Selected Endemic Rural Communities in Zamfara, Nigeria

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**Background:** Cholera is an acute diarrhoeal infection caused by ingestion of food or water contaminated with the bacterium, *Vibrio cholera*. Government efforts at curtailing the ongoing cholera outbreak may not have yielded the desired results as the incidence of the water and food-borne disease continues to soar. Nigeria Centre for Disease Control reports that Zamfara State has shown new number of cases with increasing fatalities and mortality, in 10 Local Council areas. These fatalities and mortality data contain some

variables of demographic importance, which are significant determinants of the socio-environmental conditions leading to new infections and continuing spread among people of similar characteristics.

**Objectives:**

1. To examine the prevalence of Cholera through Data (2013-2018) from selected health facilities within the context of some demographic parameters
2. To determine the influence of some socio-cultural practices of water treatment, food preparations and environmental sanitation on Cholera incidence

**Methods:** A socio-demographic survey of descriptive type relies on quantitative and qualitative data. Data of patients (2013-2018) who tested positive to Cholera were obtained from the medical statistical records of four public health facilities in the two local council areas were obtained to explore their socio-demographic characteristics. The data were collated year by year to give room for basic comparison of basic characteristics. Qualitative interview was conducted among purposively selected 105 members of the family of patients currently hospitals admissions. Data were analysed using SPSS Version 20. Hypotheses were tested with Pearson Product Moment Correlation Coefficient (PPMCC).

**Findings:** On the aggregate, over 68% of all patients cases presented were  $\leq 50$  years, out of which 74% resulted in death, 22% were referred to tertiary health infrastructures. Specifically, the patients were; nursing mothers (24%), Children  $\leq 5$  years (22%), Married (55%), Male (38%), among the married (66% had  $\leq 5$  children), Level of Education (No formal education, 58%, Primary, 31% and Post Primary, 11%). PPMCC analysis confirms a significant relationship between certain socio-cultural practices and rites of passages relating to sources of water for consumption (+0.87), food preparation (+0.57), environmental sanitation (+0.90) and incidences of Cholera, based on some identified sub-ethnic and religious practices.

**Recommendations:** Monitoring people of these significant characteristics, in-depth ethnographic study of these socio-cultural practices relating to water source and food preparation before intake may assist to address the increasing incidence of Cholera among this population.

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## Measles Outbreak Investigation in Rwengiri Hamlet in Misenye District Council, Kagera, Tanzania, 2018

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**Introduction:** Despite the high immunization coverage (administrative) of measles rubella (MR) in the country, on the 30th October, 2018, a five years old boy from Rwengiri hamlet of Bwenkoma village in Kakunyu ward visited Bugango dispensary with onset of rash on 25th October 2018 accompanied with high grade fever, red eyes with no history of MR vaccination. Contact tracing was conducted in the same day in the hamlet, four other suspected measles/rubella cases were found. Blood specimens were collected from each case for serology test at WHO accredited laboratory. On 23rd November 2018 laboratory results showed that four cases had IgM+ for measles and one case was IgM+ for rubella and confirming measles outbreak as there were  $>2$  IgM+ measles cases among the five cases detected within 28 days in the same geographical area. This recent measles outbreak in hard to reach Rwengiri hamlet located within Misenye DC raised questions regarding the effectiveness of immunization program in the area. We investigated the measles outbreak in Rwengiri hamlet in Misenye district council bordering Isingiro district in Uganda.

**Method:** Cross-sectional study design was undertaken from 24th November to 15th December, 2018 to investigate a measles outbreak in Rwengiri hamlet in Misenye district council, Kagera region. Desk review on routine immunization and vaccine preventable diseases (VPD) surveillance in the area was conducted. Also rapid convenient measles rubella vaccination coverage assessment in Rwengiri hamlet was conducted to evaluate vaccine coverage. Vaccine verification was done through reviewing of child vaccination card. Active case search through reviewing of outpatient and inpatient registers in visited health facilities was conducted. Additionally, an intensive door to door search of the measles

cases in Rwengiri hamlet was conducted to identify cases unreported in the community.

**Results:** A total of 24 measles cases line listed were not vaccinated except one case. Both sexes were equally affected. Nineteen probable measles cases were found unreported during an intensive door to door measles case search in Rwengiri hamlet. Attack rate was 0.6% and case fatality was 0%. Only an index case was found during active case search on outpatient and inpatient registers of the eight health facilities visited. Reach every child (REC) strategy not properly implemented as outreaches services in the hamlet began on September, 2018. A total of 143 children in the 45 households were recruited in rapid convenient measles rubella vaccination coverage assessment in Rwengiri hamlet. Of the 143 children, 66 (46.2%) were aged 9 to 59 months and the rest aged 60 -179 months and for each age group 31(47%) and 27 (35.1%) were found to be unvaccinated with MR vaccine respectively. The proportional of unvaccinated children in the hamlet was found to be 40.6% among all recruited children.

**Conclusion:** Failure to vaccinate lead to the current measles outbreak.

**Recommendation:** Emergency quality measles response vaccinations integrated with vitamin A to all under-fives (6 months to 59 months) irrespective of previous vaccination status in the whole Rwengiri hamlet should be conducted. Also VPD surveillance including community surveillance should be intensified.

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## Epidemiological and Microbiological Characteristics of Enteric Fever in an Internally Displaced Persons Camp in Borno State, November 2016

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**Introduction:** Enteric fever otherwise known, as typhoid fever is a potentially fatal multi systemic

bacterial infection caused by Salmonella enterica serovars Typhi and Paratyphi. Globally, 11-20 million cases occur yearly and 161,000 deaths annually. Typhoid fever poses serious health challenge in developing countries like Nigeria due lack of safe drinking water and sanitation, delays in diagnosis and treatment and poor access to health care. The prevalence of enteric fever ranges from 0.071% to 47.1% in Nigeria. We conducted the study to describe the epidemiological pattern of the cases and the microbiological characteristics of the isolates from cases.

**Methods:** We reviewed line list of cases with enteric fever during an outbreak between October to December 2016 and we extracted variables that included age, sex, place of residence, employment status, clinical signs and symptoms. We conducted a descriptive analysis and calculated frequencies and proportions using Epi info version 7.2. We collected stool samples from the suspected cases and used standard microbiological procedures to isolate Salmonella. We conducted antibiotic susceptibility testing by disc diffusion and resistance screening to determine the antibiotic susceptibility and resistance patterns of the isolates respectively. We interpreted using the M 100 Clinical and Laboratory Standards Institute 2017 document.

**Results:** Fifty suspected cases of enteric fever were recorded from October to December 2016. The median age was 10 years (range 1 year to 65 years). Thirty-two (64%) were males. Forty (80%) were unemployed. Thirty-three (66%) were Children aged between 1 to 17 years. Majority 47 (94%) had taken treatment at home before presenting at the health facility while 49 (98%) were managed as outpatients. Salmonella typhi was isolated from 6/10 (60%) of specimens. Isolates were susceptible to ciprofloxacin, amoxicillin/clavulanate, ceftriaxone, and azithromycin. None of the isolates was resistant.

**Conclusion:** The study found Salmonella typhi from majority of the sampled cases. We sensitized the internally displaced Persons on the importance of personal and environmental hygiene. Findings from the study was shared with the internally displaced Persons Camp Co-ordinators and State Ministry of Health. We recommend that Government should provide portable water, hygiene and sanitary facilities in the camps.

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## Suspicion of Yaws-Buruli Ulcer Co-morbidity in Pygmy Children at Lolodorf Health District, South Region Cameroon, December 2017

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**Introduction:** Yaws and Buruli ulcer are two neglected tropical diseases that can cause epidemics in rural communities. The co-morbidity of these two ulcerative diseases is a rare phenomenon. In December 2017, an outbreak of limb ulcers in Pygmy children was reported in Lolodorf Health District. We investigated to describe this outbreak, identify risk factors and implement control measures.

**Methodology:** A standardized questionnaire was used to collect socio-demographic data and risk factors. Swabs from ulcers and blood samples were collected for laboratory analysis. We conducted a case-control study to identify risk factors. Cases were school-age children resident in the said district, with limb ulcers between September 1 and December 20, 2017, controls were matched (age, residence) with cases without ulcers. Odds ratios (OR) were calculated to measure the strength of association between exposure factors and the onset of ulcers.

**Results:** A total of 24 children with ulcers were identified from the same Pygmy community with a median age of 13 years (range 7-13 years) of which 14 (58.33%) were females. The epidemic curve revealed a propagated source of transmission. The absence of a daily bath (OR = 3.08; 95% CI 1.08-8.94) was the main risk factor associated with having an ulcer. No other risk factors studied were significant. Putting on shoes daily was a protective factor (OR = 0.28; 95% CI 0.09-0.84). Laboratory results revealed one (3.57%) out of 28 cases tested positive for Yaws (rapid diagnostic test for *Treponema*), and four (14.81%) positive for Buruli ulcer (PCR). The PCR test for Yaws is awaited.

**Conclusion:** The outbreak of limb ulcers was probably due to a co-morbidity of Yaws and Buruli ulcer. Poor body hygiene was the risk factor associated with these ulcers while putting on shoes daily was protective. Cases and contacts were treated and the population sensitized.

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## Sero-Epidemiological Survey of Infection with Middle East Respiratory Syndrome Coronavirus (MERS-CoV) in Humans, Camels and Other Livestock from Butana Area 2015 -2017– Sudan

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**Background:** Middle East respiratory Syndrome is caused by an emerging virus from the family Coronaviridae, MERS- COV. The first case was reported in Saudi Arabia in 2012. Since September 2012, WHO has been notified of 2,266 laboratory-confirmed cases of infection with MERS-CoV with 804 MERS-CoV associated deaths. Humans are infected with MERS-CoV from direct or indirect contact with dromedary camels. The distribution of MERS-COV in Sudanese Camles and other livestock is not known, but addressing this is important as there is a large stock of camels in Sudan with strong commercial links with the Gulf cooperation countries-GCCs Also there is substantial movement, especially a camels workers, between Sudan and GCCs .

The overall goal of this study was to determine current prevalence of MERS-CoV infection in dromedary camels, other livestock and humans in Sudan.



**Materials & Methods:** The study was a cross-sectional sero-epidemiological study and was carried out during 2016-2018. The study was conducted at the Butana area, Sudan; a total of 73 serum, 73 nasal swabs, 73 nasopharyngeal swabs, 73 rectal swabs and 25 blood samples on filter paper were collected from camels from the market and slaughterhouse in Tambool area (which attracts camel traders from all states of Sudan), and Tambol camel research center (100% close system camel farm) in May 2017. In addition, a total of 80 blood and serum samples were collected from 30 workers in close contact with camels and from 50 students and officials at University Gezira in Sudan-UG (as controls). Finally, a total of 50 blood and serum samples were collected from goats, sheep, cattle, donkeys and horses from the same areas. Detailed background data on animals and humans were gathered by use of the WHO recommended questionnaires for MERS COV investigation. All the specimens were tested for the presence of MERS-CoV DNA by PCR and antibodies by protein microarray. For the samples collected in 2018, the first screening of the samples was done at Blue Nile Institute, Sudan as part of a training on MERS CoV diagnostics, and results were confirmed at Erasmus Medical Centre.

**Result:** One camel nasopharynx sample was positive by PCR for the presence of the MERS-COV, and 100% of the camels tested had serum antibodies, i.e. had been exposed to MERS-COV. All samples from humans were seronegative. Currently, the serological analysis of the samples from other animal species, and the sequencing of the PCR positive sample are underway. After completion, risk factor analysis for MERS COV exposure of the animals will be performed using the questionnaire data.

**Conclusion:** MERS-COV is enzootic in camels in Sudan, although the seroprevalence from these pilot data seems lower than what was observed in the GCC region. In our survey we found no evidence of infection of humans. This baseline data will be used to inform the Sudan government about MERS-CoV at human/animal interface, as basis for strategies for the control and prevention interventions using the one health approach.

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## Epidemiology of Yellow Fever Outbreak in Rivers State, Nigeria - July, 2018

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**Background:** Yellow fever is an acute viral hemorrhagic disease transmitted by mosquitoes and poses serious public health challenge in endemic countries. An estimated 200,000 yellow fever patients with 30,000 deaths annually of which over 90% occur in Africa. In May 2018, a confirmed yellow fever patient was reported in Ikwerre local government area (LGA), Rivers State. We investigated to characterize the outbreak, perform community risk analysis, conduct rapid yellow vaccination coverage in children and determine the presence of Aedes mosquitoes.

**Methods:** We defined a suspected case-patient as any person with acute onset of fever, with jaundice appearing within 14 days of onset of the first symptoms residing in Ikwerre LGA or any of the LGAs sharing boundaries with it from 1st January, 2018 to 24th July, 2018. We reviewed and validated the line list from affected LGAs and searched communities and facilities for those that met the case definition. Purposive sampling using standard structured questionnaire was used for community risk analysis and rapid yellow vaccination coverage. We used ovitraps, larval traps, modified human landing catch and adult collection traps to establish the presence of Aedes species. Frequencies, proportions and odds ratio (OR) were calculated using Epi Info™.

**Results:** We identified 28 suspected yellow fever case-patients. One case-patient (3.6%) was laboratory confirmed at Institut Pasteur Dakar. The index case-patient was a 55-year old male resident of Ikwerre LGA with no yellow fever vaccination or travel history. Twenty (71.4%) of the suspected case-patients were males, median age of 17 years (range 2-58). Among the suspected case-patients, 29% had yellow fever vaccination. Of the 146

community members sampled, 119(81.5%) prefer to go to hospital if they develop fever and jaundice while 24(16.4%) would visit the traditional healer. People who have heard about yellow fever were more likely to go to hospital when they develop yellow fever symptoms OR= 2.7 (95% CI 1.1-6.8) or advise relatives to go to hospital OR= 3.1 (95% CI 1.2-8.0) although others were likely to visit the traditional healers OR= 4.6 (95% CI 1.7-15.6). Out of 104 children sampled, 55(52.9%) were males with mean ( $\pm$ SD) age 4.3( $\pm$ 2.3) years. Those with history of yellow fever vaccination were 69(66.7%) while 43(41%) produced immunization cards. Vector surveillance in affected LGAs yielded various stages of *Aedes albopictus* mosquitoes. The most preferred breeding site was used tires.

**Conclusion:** We concluded that there was no active transmission of yellow fever, however the risk of spread in the state is high due to low vaccination coverage and abundance of *Aedes albopictus* mosquitoes. We sensitized healthcare workers on early detection, reporting of yellow fever disease and routine immunization, and the community on good sanitary and hygiene practices.

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## High Prevalence of Dengue Virus Non-Structural Protein-1 Antigen in People Infected with the Human Immunodeficiency Type-1 Virus in Cameroon

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**Background:** In Sub Saharan Africa regions of high prevalence of infection with the human immunodeficiency virus overlap with areas of high burden of vector borne infections. Dengue virus is endemic in Cameroon but little is known about the extent of dual HIV- Dengue virus infection among people living with HIV. In a six year longitudinal study we have assessed the prevalence of infections with dengue viruses (DENV) in people living with HIV in Cameroon

**Methods:** We enrolled 1986 HIV infected and 1004 negative people from 2012 to 2017. Using RT-PCR together with Dengue virus IgG, IgM and NS1 antigen assay we determined the prevalence of Dengue virus in these samples.

**Results:** Our data revealed a significantly higher prevalence of Dengue virus NS1 antigen in HIV-1 infected people ( $P < 0.0004$ ) relative to their negative counterparts. This high prevalence of NS1 antigens was associated with a significant reduction in Dengue virus specific IgG in both HIV-1 infected children ( $p = 0.0001$ ) and adults ( $P = 0.0001$ )

**Conclusion:** Our findings are critical in assessing vector borne disease burden of HIV infected people in Sub Saharan Africa as persistence of NS1 antigen is an indication of persistent viremia. This calls for a special attention in the long term management of dual HIV-Dengue virus infection within our region.

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## Risk Factors Associated with Cholera Outbreak in Adamawa State, Nigeria, June 2018

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**Introduction:** Cholera poses a global threat to public health and is a key indicator of poor social development. It is endemic in Nigeria where outbreaks occur mostly in the rainy season. In June 2018, a total of 15,167 suspected cholera cases and 168 deaths (case fatality rate (CFR): 1.11) were reported in Nigeria. We investigated the occurrence of a suspected cholera outbreak in Mubi North and South Local Government Areas (LGAs) of Adamawa State to identify risk factors for infection, institute control measures and assess eligibility for reactive vaccination.

**Materials and Methods:** We listed cases at the cholera treatment centre (CTC) and searched for unreported cases in the community. We conducted a 1:2 unmatched case control study. A case was defined as any person aged  $\geq 1$  year presenting with acute watery diarrhea, severe dehydration with or without vomiting. We used systematic random sampling technique to select cases from the CTC. Controls were neighbors without diarrhea. A total of 102 cases and 199 controls were enrolled. We collected data on socio-demographic characteristics and risk factors using interviewer administered semi-structured questionnaires. We calculated frequencies and proportions and used a logistic regression model to calculate adjusted odds ratio (aOR) and 95% confidence interval (CI). Stool and water samples were collected for laboratory investigations. We assessed the knowledge and

practice of health care workers (HCW) in the cholera treatment center, using self-administered questionnaires we interviewed 45 HCWs in the CTC.

**Results:** Total number of cases reported was 1,703 with 27 deaths (CFR: 1.6%), male: female ratio= 1.3:1. Patronizing water vendors, (aOR: 14.0, 95%CI: 7.4-28.2), not treating water (aOR: 3.1, 95% CI: 1.9-5.2), open dumping of refuse (aOR: 3.2, 95% CI 1.3-8.0) and not washing hands after toilet use (aOR: 1.5, 95%CI: 1.4-1.7) were independent risk factors. Thirty-one (74%) out of 42 samples cultured were positive for *Vibrio cholerae*. Fifteen water collection points were heavily contaminated with coliforms.

**Conclusion:** There was a confirmed outbreak of cholera in Adamawa State that was associated with poor sanitary conditions and lack of potable water supply. We supported case management, risk assessment, chlorination at water collection points, household disinfection activities and planning for oral cholera reactive vaccination (OCV). First round of OCV was conducted. We recommend immediate commencement of potable drinking water supply and improved sanitary conditions in the LGAs.

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## Cholera Outbreak in Government Girls College Dala, Kano, Northern Nigeria: The Importance of Handwashing with Soap, May 2018

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**Background:** Cholera remains a public health problem especially in developing countries. Outbreaks are linked to the consumption of unsafe water and food, poor hygiene and sanitation. In May 2018, we were notified of a suspected cholera outbreak in Government Girls' College, Dala (GGCD), Kano through the Integrated Disease Surveillance and Response (IDSR) system. We

investigated the outbreak to identify associated risk factors and institute control measures.

**Materials & Methods:** We conducted a 1:2 unmatched case-control study. We defined a case as any student of GGCD, with acute watery diarrhea with or without vomiting from 4th to 25th May 2018 and a control as any student without acute watery diarrhea. We enrolled 46 cases and 92 controls using random sampling technique. We collected data on socio-demographic characteristics, clinical features and risk factors using interviewer-administered structured questionnaire. We used a logistic regression model to calculate adjusted odds ratios (aOR) and 95% confidence intervals (CI). Laboratory analysis was done on 10 stool samples and one water sample using rapid diagnostic tests to detect antibodies against *V. cholerae* and thiosulphate-citrate-bile salt-sucrose agar to culture *V. cholerae*.

**Results:** Mean age (years) was 14±2 for both cases and controls. The most common presenting symptoms were diarrhea and vomiting in 33 (71.4%) followed by abdominal cramps in 26 (56.5%) of cases. Compared to controls, cases were less likely to have washed hands with soap before eating (aOR= 0.14, 95% CI: 0.05-0.36) and less likely to have washed hands with soap after using the toilet (aOR= 0.08, 95% CI: 0.02-0.31). *V. cholerae* was isolated from seven stool samples, the water sample was negative.

**Conclusion:** Unhygienic hand washing practices was the main risk factor associated with this outbreak among the students. We sensitized the students on good personal hygiene with emphasis on the importance of hand washing with soap and disinfected the hotels and toilets. We shared our findings with the school authority, the local and state governments. We recommended monthly sensitization of students on personal and environmental hygiene, regular inspection of the school by environmental officers and strengthening of the cholera surveillance system.

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## Outbreak Investigation of *Salmonella* Bardo in Kwa-Zulu Natal, South Africa

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**Introduction:** Foodborne outbreaks can result in socioeconomic challenges as a result of hospitalization and associated medications, particularly among the vulnerable groups such as the elderly and immunocompromised individuals. Nontyphoidal *Salmonella* spp. is amongst the top five causes of disability and death globally. *Salmonella* causes salmonellosis, which is characterised by nausea, abdominal pain and sometimes fever. *Salmonella enterica* serotype Bardo (*Salmonella* Bardo) is a zoonotic, uncommon serotype in the South African population that is rarely reported. We investigated three seemingly unrelated Foodborne disease outbreaks in South Africa between July and August 2018.

**Materials and Methods:** Twelve food samples and one human specimen were available for microbiological investigations. Similarities between the isolates were investigated using phenotypic and genotypic techniques. Phenotypic characterization of the isolates was done using automated systems (Vitek Compact 2) and by serotyping using *Salmonella* antisera. Genomic DNA was isolated from the samples using the QIAGEN QIAamp DNA Mini Kit and sequenced using the Illumina MiSeq next generation sequencing technology and raw sequence data was uploaded and analysed using the core genome Multilocus Sequence Typing (cgMLST) tool available on Enterobase interface. Genotypic relatedness was also investigated using pulsed-field gel electrophoresis, using the Pulse net protocol. Epidemiological data was gathered by conducting interviews with the cases from the outbreaks using a standardized questionnaire.

**Results:** All thirteen samples were phenotypically identified as *Salmonella* Bardo, the PFGE pattern from all isolates was indistinguishable, cgMLST showed all isolates to have no more than ten allele differences. Four of the five cases in the first outbreak were interviewed, the four cases reported onset of illness after consuming goat meat. It was also reported from the interviews that according to

their tradition, they use isthebe (a traditional plate) for dishing both raw meat in preparation for cooking and cooked meat for consumption on the same dish. The four cases were hospitalized; however, no clinical samples were collected. Four of the ten cases in the second outbreak were interviewed, these cases reported onset of illness within 24 hours of consuming both sheep and goat meat. The use of isthebe was also practiced in this case. The clinical isolate was from a patient at a local clinic within the same district, the patient consumed beef at a funeral where goat meat was also served before onset of illness. Laboratory and Epidemiological data suggested goat meat as the possible source of the outbreak.

**Conclusions:** The results suggest a foodborne Salmonella Bardo outbreak due to contaminated food. In South Africa, the meat safety Act provides for specific requirements on how meat abattoirs should slaughter cattle. However, in some rural abattoirs meat inspection may not be routinely carried out, which often compromises safe meat handling. This potentially exposes rural communities to various foodborne pathogens. Closer collaboration between agriculture, human health, animal health, is paramount in the One Health approach to tackling Foodborne diseases. Epidemiological investigations are extremely difficult in rural areas in Kwa-Zulu Natal. The analysis showed the first recorded case of human infection due to Salmonella Bardo in South Africa.

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## Trend of Measles Cases and Factors Associated with Laboratory-Confirmed Measles Mortality in Bauchi State – Nigeria, 2013-2017

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**Introduction:** Measles is an acute viral illness caused by the genus Morbillivirus. Its transmitted primarily from person to person via aerosolized droplets or by direct contact with nasal and throat secretions of infected persons. Measles still accounts for considerable childhood morbidity (8.4%-43.95%) and case fatality rate (0.44%-1.43%) in Nigeria despite the availability of an effective vaccine. The WHO/UNICEF regional plan for the reduction of measles morbidity and mortality recommends four strategies including the establishment of measles case-based surveillance. This study describe trends and characteristics of patients with measles infection as well as the determination of risk factors associated with the infection in Bauchi State, Nigeria between 2013 and 2017.

**Methods:** We conducted a secondary data analysis of measles case-based surveillance data for January 2013 to December 2017 obtained from Bauchi State Primary Health Care Development Agency. A suspected case was defined as any person with fever (> 38°C), generalized maculopapular rash, and any one of cough, coryza or conjunctivitis while a confirmed case is a suspected measles case with laboratory confirmation based on measles IgM. We reviewed the data and performed descriptive statistics to determine frequencies, proportions and assessed risk factors by bivariate analysis to determine the odds ratio and 95% confidence interval.

**Results:** A total of 4681 suspected measles cases were reported during the period, with a 70.9% living in rural communities. The number of reported measles cases increased every other year except in 2017, with a peak (1,645 cases) in 2015. Among the 4,681 suspected measles cases, 475 (10.2%) were positive for measles IgM of which 335 (70.5%) occurred in children between 1 and 5 years; 248 (52.2%) in males; 254 (53.5%) zero dose; 434 (91.4%) from rural communities, and 407 (85.7%) were outpatient. Factors associated with mortality among cases were delayed reporting to hospital (OR: 9.1, 95% CI: 3.3-24.8) and delayed notification of epidemiology unit (OR: 8.6, 95% CI: 3.6-20.4).

**Conclusion:** Improved measles surveillance activity will reduce mortality due to delayed reporting to hospital and delayed notification of epidemiology unit. We recommended to the State Ministry of Health that subsequent Supplemental Immunization Activities be intensified targeting children in rural areas in Bauchi State and this recommendation is being implemented.

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## Descriptive Analysis of a Yellow Fever Outbreak in Benue State, Nigeria, 2018

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**Background:** Yellow Fever (YF) is an acute viral hemorrhagic disease caused by Yellow Fever virus, an arthropod-borne virus (arbovirus) of the genus *Flavivirus* (family *Flaviviridae*).

An estimated 200,000 yellow fever cases with 30,000 deaths occurs annually of which over 90% occur in Africa. We received a report of suspected yellow fever outbreak in Vandeikiya LGA, Benue State. We investigated to confirm the outbreak, describe the cases and conduct entomology survey.

**Materials & Methods:** At health facility level, we defined a suspected case as anyone that presented with fever and jaundice appearing within 14 days of onset of first symptoms. We defined a suspected case at community level as any person in Vandeikiya LGA within same period who had unexplained illness with fever and yellowish coloration of the eyes or skin. We reviewed and validated the line list from affected ward and surrounding wards. We also searched for cases from the registers at health facilities but couldn't line list any suspected case that met the case definition. We line listed the suspected yellow fever cases during active case search in the community. Samples were collected and tested for IgM and neutralizing antibodies. We calculated rates and proportions. Various stages (eggs, larvae and adult) of *Aedes* mosquitoes' development was collected from all locations sampled in the state using ovitrap setting, larval sampling, Modified human landing catch (HLC), Adult collection traps.

**Results:** We identified 10 suspected cases and 8 contacts without symptoms. All tested negative using (RT-PCR-positive) except one (1). The case was a female (index case) of 37 years old who had no vaccination history and travel history, presented with fever and vomiting of blood. She is a resident at Vandeikiya LGA. There were no deaths.

A total of 200 children were sampled in Vandeikiya and 3 neighbouring LGAs (i.e Konshisha, Kwande, Ushongo). Sixty seven (50%) were females and 67 (50%) were males Mean (SD) age of children

surveyed was 3.0 (1.9) years. Seventeen (8.5%) were from the affected LGA (Vandeikya). Yellow Fever vaccination status among children in Vandeikya LGA was 16 (8.1%).

A total of 71 mosquitoes were captured using traps (*Aedes albopictus* 7, *Aedes aegypti* 60, *Aedes leutocephalus* 4). Total number of eggs collected were 41 while larva were 37.

**Conclusions:** Early detection and laboratory confirmation of cases may have resulted in no case fatality. YF vaccination coverage is low in Vandeikya. The risk of transmission of the disease in the LGA is high. The presence of yellow fever vector (*Aedes aegypti*) was established in the four local governments where entomology surveys were carried out. The habit and practices of the inhabitants throwing used tyres and empty cans in the environment are factors that can encourage vectors population growth. We carried out Yellow Fever reactive vaccination and community sensitization and social mobilization of the people on yellow fever transmission.

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## Factors Associated with Cholera Outbreak in Kusada, LGA, Katsina State, Nigeria, June, 2018

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**Background:** Cholera remains a public health problem in sub-Saharan Africa despite availability of an effective intervention for prevention and control. On 20th of June, 2018, We investigated a suspected cholera outbreak in Yashe and Bauranya wards, Kusada LGA Katsina State, Nigeria. We investigated to characterize the outbreak, identify the risk factors and institute control measures.

**Methods:** We conducted an unmatched case-control study. A case was defined as any resident of Yashe and Bauranya wards in Kusada LGA two years and above with acute watery diarrhea with or without vomiting from 15th to 27th June,

2018; While a control was any resident of the affected wards of Kusada LGA without acute watery diarrhea and vomiting. Data was collected on socio-demographic characteristics, potential risk factors using structured interviewer administered questionnaire. We calculated frequencies and proportions to characterize the outbreak in time, place and person. Bivariate and Multivariate analysis were done to identify factors associated with the outbreak by using the adjusted odd ratio (AOR) and 95% confidence intervals (CI).

**Result:** A total of 36 cases were line listed of which 23(64%) were male and 21(58%) for control. Median age was 12 (2-70) years for cases and 21(2-70) years for controls; the overall attack rate was 63.6/100,000 and CFR was 8.8%. History of close contact with case (OR=14.0; 95% CI: 2.4-79.7), History of eating vegetable Tafasa (*Senna occidentalis*) (OR=27.76; CI: 5.1-149.3) and unprotected well (OR=5.8; CI: 1.1-29.4) were risks for cholera. *Vibrio cholerae* 01 was isolated in 8/10 (80%) from culture

**Conclusions:** Unhygienic preparations of vegetables, unprotected wells and close contact with a case were the source of the outbreak. Public health education on proper handling of vegetables and Provision of sanitary wells were recommended.

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## Strengthening Biosafety and Biosecurity Capacity Through Promising Model German-Sudanese Partnership Program for Excellence in Biological and Health Security Strengthening Biosafety & Biosecurity

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The Purpose of the presentation to highlight and encourage limited- resource countries to Strengthening Biosafety & Biosecurity through collaboration and partnerships program to handle emerging and re-emerging infections.

German-Sudanese Partnership Program for Excellence in Biological and Health Security as promising model

On 14th of September 2014, the German-Sudanese Partnership Program for Excellence in Biological and Health Security was launched in an official opening ceremony in Khartoum, Sudan. This new cooperation is an expression of a recently intensified collaboration between the Sudan and Germany.

Joined meetings for technical individuals from both side conducted for 2 days to develop Action plan with time frame and coordination team appointed from both side as well as the area of capacity development designated as follow (Awareness Raising, Biosafety & Biosecurity, Surveillance, Detection and Diagnostics and Networking). The key Partnership Drivers Sudan side: Federal Ministry of Health-(Epidemiology Department- Health Promotion Department) ,National Public Health Laboratory, German Side: Robert Koch Institute (RKI)- GIZ.

Nine B&B ToT workshops out of 9 planned workshops series were conducted, include 32 participants from different institutions & 18 states and acquired knowledge implemented at institutions level in between the workshops.

Three workshops out of three planned workshops were conducted in the area of laboratory networking and agreed network approved from undersecretary council; FMOH. As well as 18 members, Coordination team was a pointed Training course for 3 weeks hold at RKI for 4 Sudanese participants in laboratory diagnosis of highly pathogenic viral infections as well as one hold at NPHL and Central laboratory includes 6 participants. Twelve participants from NPHL and 12 from CL trained on Glove box machine.

KAP study for B&B conducted to identify the gaps in knowledge, attitude and practice, report finalized.

**Out comes:** National Biosafety & Biosecurity Indorsed and the strategic plan nearly to be finalized

Laboratories network established with 18 laboratory members regarding biosafety & biosecurity issues.

Thirty two participants from 8 different institutions and 18 states have been trained as TOT.

The capability of the country in laboratory diagnosis of highly pathogenic viral infections improved Awareness plans and material developed regarding KAP study for B&B conducted to identify the gaps in knowledge, attitude and practice.

In the area of surveillance, data management strengthened at national level as well as surveillance system.

Sudanese Biological Safety Organization created and approved from authorized body in Sudan

The German- Sudanese Partnership program for Excellence in Biological and Health Security not only aim to minimizing biological security risks, such as the outbreaks of highly pathogenic infectious diseases, whole Sudanese health care system will benefit too. The partnership will provide sustainable support to improve the resilience against the natural or intentional outbreaks of dangerous infectious diseases as well as boost life sciences in the Sudan and Germany.

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## Global Health Security Agenda— What Is It, Where Are We And Where Should We Be?

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Introduction - What is it?

Launched in February 2014, GHSA is a global effort to strengthen nations capacity to prevent, detect, and respond to infectious diseases threats using a multilateral and multi-sectorial approach. It provides a platform for countries to share best practices, arguments advocacy for national prioritization of global health security and facilitates compliance of countries to international health security standards. The October 2017 “Kampala Declaration extended GHSA to 2024.

Where Are We?

The new GHSA 2014 comprises of GHSA 2024 Framework, sets new targets, establishes new Tasks Forces and Action Packages Working Groups and while the original 11 Action packages remain priority, focus in 2019 will be through 8 Action Package working groups.

By May 2018, 65 countries of which 20 (31%) are from Africa were members of GHSA. Of these 13 (20%) of which 11(85%) are from Africa had shared their implementation roadmaps with GHSA secretariat. Of the 11 African countries, 10 (91%)

had conducted Joint External Evaluations (JEE), a method adopted by GHSA for assessment of country’s health security core capacities.

Successes have been reported by GHSA countries in Africa including establishment of GHSA Steering Committee (1), National Technical Working Groups and Tasks Forces for AMR, Surveillance, Laboratory (2), development of National Health Security Plans for achieving GHSA and AMR (4), training and human resource capacity building including FELTP programs (5), strengthening One Health Approach (5), establishment of Health Emergency Operating Centers, tabletop and full-scale simulations to test emergency preparedness (1), strengthening biosafety and biosecurity systems (1) and establish inter-country Emergency Operation centers (2)

GHSA has partnered with international organizations to support various aspects of global health security including The Next Generation Global Health Security Network, the PATH Global Health Security Partnership (GHSP) and RTI International.

Where should we be?

GHSA has set a target of more than 100 countries to have completed an evaluation of health security capacity using the JEE platform and have these planning and resource mobilization to address identified gaps.

Challenges and Way Forward

Coordination at country level of the multiple GHSA partners is complex for the Ministry of Health, which can be resolved by use of multi-sectorial Technical Working Groups. Sustainability of high cost for global security which can supported through increased domestic funding and inclusion of global security in the country strategic plans. Monitoring and evaluation is limited with GHSA strongly relying on country self-assessment and reporting. Coordination between human and animal health sectors remains a challenge that can be solved by use of multi-sectorial platforms like Technical Working Groups, task teams and joint planning.



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## Serological Evidence of Chikungunya Virus Among Presumptive Malaria Patients in Brong-Ahafo and Ashanti Regions of Ghana

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**Background:** Malaria and other arboviral infections such as Chikungunya virus (CHIKV) share similar clinical signs and symptoms. These similarities have contributed to the over-diagnosis of malaria and under-recognition of CHIKV in many countries in Africa. This study sought to determine the prevalence of CHIKV infection among presumptively diagnosed malaria patients in the Brong-Ahafo and Ashanti Regions of Ghana. The findings of this study are not only an important step that can guide proper diagnosis and effective treatment of malaria but will also provide a baseline data on the prevalence of CHIKV virus in Ghana.

**Methods:** Venous blood samples were obtained from 400 study participants who have been presumptively diagnosed as having malaria. Samples were tested for the presence of CHIKV specific IgM and IgG antibodies using ELISA and malaria by microscopy respectively.

**Results:** An overall prevalence of CHIKV infection was 16(4.0%). CHIKV specific IgG was 8(2.0%), while that of IgM was 5(1.25%) and IgM/IgG co-infection was 3(0.75%). The study also revealed that CHIKV and laboratory confirmed malaria co-infection was 4(1.0%) while laboratory confirmed malaria infection only was 54(13.5%) and CHIKV infection only was 12(3.0%). The frequent clinical symptoms by CHIKV infected participants was headache and anaemia.

**Conclusion:** Results in the study suggest evidence of CHIKV among presumptively diagnosed malaria patients and this could possibly influence malaria misdiagnosis among patients.

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## Role of Political Commitment in Building National Public Health Institutes

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**Background:** Lessons from Ebola outbreaks have identified the need for strong and coordinated national public health institutes, especially on the African continent. The Nigeria Centre for Disease Control (NCDC) is a young rapidly evolving National Public Health Institute (NPHI), established in the context of limited resources.

Nigeria continues to experience outbreaks of infectious diseases. In the year 2017, the country experienced large outbreaks of Lassa fever, yellow fever, monkeypox, cholera and *Neisseria meningitidis* serogroup C. The value of having a science led national public health institute such as NCDC, has become more obvious.

Building a strong NPHI is especially important in Nigeria with its large population and infectious disease risk profile. The NCDC also serves as the regional hub of the Africa Centers for Disease Control in West Africa.

We describe activities associated with rapid advancement of NCDC, reflecting on the enabling factors.

**Method:** This is a descriptive case report about the developmental evolution of NCDC and the importance of political commitment, leadership, and a legal mandate to its development, over its seven-year history.

We reviewed historical documents including meeting reports, handover notes, scientific publications on Nigeria's Ebola response and previously developed strategy plans of NCDC.

Each document was reviewed by the main author and interviews held with key personnel within and outside NCDC.

**Results:** With the increased political commitment, funding and partnerships, the NCDC now takes the lead in preventing and preparing for public health

emergencies, and in managing the surveillance and reference laboratory architecture for Nigeria.

In its initial four years (2007 – 2011), there was limited growth, accomplishment and institutional support.

In the last three years, NCDC has grown from having less than 100 employees immersed in response activities, to over 200 employees, with increased focus on prevention and preparedness, increased budgetary allocation and partner support. With the increase in human resource capacity, the agency has expanded its functions to include coordinating the surveillance of antimicrobial resistance in Nigeria, risk communications, scientific and operational research and other preventive measures that previously had less attention.

After a protracted process, on the 8th of November 2018, the President of the Federal Republic of Nigeria signed into law the Act establishing NCDC, demonstrating a political commitment to health security. The strong support from an influential Senate committee chairman and Minister of Health ensured the Bill was passed, and the NPHI has become increasingly supported.

More funding has also become available from the World Bank's Regional Disease Surveillance Systems Enhancement project (REDISSE), enabling investments to support key areas.

**Conclusion:** There is a growing paradigm across the African continent and globally, supporting the establishment of NPHIs. It is important to emphasise that in developing a national public health institute, the focus should go beyond technical capability development, to ensuring government integration and strong political commitment.

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## Laboratory Strengthening to Support Biosecurity/Biosafety in Africa

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**Background:** The Mérieux Foundation, an independent family foundation with public interest status, is committed to fighting, in the field, the infectious diseases that affect developing countries by building capacities, particularly in clinical laboratories. The Foundation has projects in over 30 countries, in South America, Africa, the Middle East and Asia. In Africa, the Foundation is particularly active in West Africa (Benin, Burkina Faso, Guinea, Mali, Niger, Senegal, Togo), Tunisia and Madagascar.

**Methods:** The Mérieux Foundation works to increase vulnerable populations' access to diagnostics. To achieve this objective, two main types of laboratories must be reinforced: research and referral laboratories but also clinical biology laboratories. Biosecurity and Biosafety is an essential part of strengthening laboratories and involves developing their infrastructure, equipment and training.

Knowledge-sharing activities, including courses and e-learning, are also a strategic area of focus for the Foundation, and an integral part of its initiatives to strengthen laboratory systems.

**Results:** The Rodolphe Mérieux Laboratories are state-of-the-art laboratories given by the Mérieux Foundation to local public institutions:

In Mali, the Charles Mérieux Center for Infectious Disease received a BSL3 laboratory to enhance tuberculosis research and has developed capacity for the surveillance of emerging pathogens; In Madagascar, the Charles Mérieux Center for Infectious Disease, hosted by the University of Antananarivo of Madagascar, is equipped with BSL2 laboratories with diagnostic capacities in infectious diseases, HIV and leprosy; In Tunisia, the Pasteur Institute will be equipped with a 250 m<sup>2</sup> BSL3 laboratory.

The Foundation is involved in a number of projects seeking to build laboratory networks. Forming such networks strengthen the performance of health systems by enabling expertise to be shared and synergies brought into play. In Africa, the Foundation supports and helped to form two laboratory networks: RESAOLAB, developed with the Ministries of Health of seven West African countries (Benin, Burkina Faso, Guinea, Mali, Niger, Senegal and Togo) and RESAMAD, developed with the Ministry of Health of Madagascar. RESAMAD is helping to strengthen biosecurity by establishing bacteriology testing in its member laboratories. This will make it possible to assess antimicrobial resistance and monitor its evolution over time. Training and e-learning on biosecurity and biomedical waste management also helps to build capacity in this area.

The Mériex Foundation is participating in a project to create a G5 Sahel Biosecurity Network (Burkina Faso, Chad, Mali, Mauritania and Niger) to improve response to biological threats and more efficiently monitor and combat epidemics of highly pathogenic diseases in partnership with the Bundeswehr Institute of Microbiology in Munich and with funding from the GIZ (German Federal Enterprise for International Cooperation). The Foundation has also contributed to the Global Health Security Agenda (GHSA) in particular in Senegal.

**Conclusion:** The Mériex Foundation actively supports the development of biosecurity and biosafety in Africa by working closely with local stakeholders and national authorities, with the aim of making a significant contribution to national preparedness efforts.

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## The Protective Effect of Isoniazid Prophylaxis on Tuberculosis Incidence Among HIV-Positive Patients Receiving ART in Ethiopian Settings: A Meta-Analysis

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**Background:** Tuberculosis (TB) and HIV make up a deadly synergy of infectious disease, and the combined effect is apparent in resource limited countries like Ethiopia. Previous studies have demonstrated inconsistent results about the protective effect of isoniazid preventive therapy (IPT) on active TB incidence among HIV positive patients receiving ART. Therefore, the aim of this meta-analysis was, first, to determine the protective effect of IPT on active tuberculosis incidence, and second, to assess the pooled incidence of active TB among HIV positive patients taking ART with and without IPT intervention in Ethiopia.

**Methods:** PubMed, Google scholar and Cochran library databases were searched from April 1 to 30, 2018. Two independent authors explored and assessed studies for eligibility, and extracted data based on predefined criteria. Heterogeneity of the included studies was checked by I<sup>2</sup> statistics, whereas publication bias was determined by funnel plot and Egger's regression test. A random effects model was used to estimate risk ratios and the pooled incident TB with the respective 95% confidence intervals using Stata version 11.0 statistical software.

**Results:** Totally, 423 titles were retrieved and 7 studies met the inclusion criteria. Accordingly, IPT has been reduced the risk of TB incidence by 73%, risk ratio (RR) 0.27 (95% CI; 0.16–0.43%), compared to no IPT group. Moreover, IPT treatment for 12 months has reduced incident TB by 91% (RR: 0.09, 95% CI: 0.04 to 0.21), whereas 6 months IPT intervention has averted TB incidence by 63% (RR: 0.37, 95% CI: 0.26 to 0.52). The overall pooled incidence of active TB among HIV infected patients receiving ART with and without IPT was

3.79% (95% CI; 2.03%–5.55%) and 16.32% (95% CI; 11.57%–21.06%) respectively.

**Conclusion:** IPT has reduced the risk of incident TB among HIV positive patients receiving ART in Ethiopian settings. Moreover, the duration of IPT intervention has effect on its protective role. Thus, scaling up the isoniazid preventive therapy program and its strict compliance is necessary to avert HIV fueled tuberculosis in Ethiopia.

Study protocol registration: CRD42018090804.

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## Fatal Rift Valley Fever Outbreak Caused by Exposures to Meat from Sick and Dead Livestocks: Uganda, July 2018

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**Background:** Rift Valley Fever (RVF) is a viral hemorrhagic fever that can be fatal to humans and livestock. During June–October 2018, an upsurge of RVF cases occurred in western and central Uganda. We investigated to identify the scope of the outbreak and exposure factors, and recommend evidence-based control measures.

**Methods:** We defined a probable case as acute onset of unexplained fever with thrombocytopenia or leukopenia, plus  $\geq 1$  of: unexplained bleeding, blurred vision, jaundice, or unexplained death during June–October 2018 in a resident of eight affected districts. A confirmed case was a probable case with a positive serum test for RVF by RT-PCR. We reviewed medical records and searched communities for cases. In a case-control study, we compared exposures of cases and age-, sex-, and neighbourhood-matched controls. We also reviewed livestock surveillance data for RVF-specific IgM antibodies.

**Results:** We identified 19 cases (17 confirmed, 2 probable); 13 (68%) died. The attack rate (AR) was 19 times as high in males (8.7/1,000,000) as in females (0.46/1,000,000). Stratified epidemic

curves indicated multiple point-source outbreaks following dissecting/butchering livestock that had been sick or died of unknown causes (“sick/dead livestock” hereafter). Of the 18 case-patients included in the case-control study and 90 controls, 10 case-patients (56%) and seven controls (7.8%) had a history of butchering/dissecting/carrying sick/dead livestock (ORMH=23, 95%CI=4.6-109). Exposure to raw meat from healthy livestock was not significantly associated with RVF (ORMH=3.3, 95%CI=0.36-31). Of 100 livestock serum samples, 72 (72%) were IgM-positive for RVF.

**Conclusions:** This outbreak was caused by exposure to raw meat from sick/dead livestock. RVF infection in area livestock appeared to be widespread. We recommend banning the processing of meat from sick/dead livestock. RVF surveillance data between human and livestock health sectors should be shared to facilitate early warning and detection for RVF.

Key words: Rift Valley Fever; Outbreak; One Health; Global Health Security; Uganda.

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## Comparison of Singleplex Versus Multiplex Real-Time PCR Assays for the Simultaneous Detection of Chikungunya, Dengue and Zika Virus RNA

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**Background:** Diagnostic laboratories tend to increase the diagnostic capacity but also like to reduce costs, and here the multiplex real-time PCR strategy (amplification of multiple targets in a single reaction) is believed to be a good approach. On the other hand, singleplex PCR, the amplification of a single target plus an internal control, usually leads to a higher sensitivity, one of the main goals in molecular diagnostics to avoid erroneous results. Since false-negative test results can have serious implications, a comparison of 2 commercial multiplex real-time PCR assays (applied biosystems

/ ThermoFisher, and Fast Track Diagnostics) and 3 single plex real-time PCR assays (Altona Diagnostics) will be compared for single and also for simultaneous detection of Chikungunya virus, Dengue virus and Zika virus RNA.

**Materials & Methods:** WHO International Standard RNA for Zika Virus was resolved as described in the user instructions. The RNA was extracted by QIAamp Viral RNA Kit (Qiagen, Germany) and the extracted RNA diluted in half log steps from 10E4 IU/μl to 0 IU/μl. Dengue Virus (type 1) and Chikungunya Virus (both ZeptoMetrix, US) in culture fluid were used for the set-up of the same dilution serial as described before.

The singleplex and multiplex real-time PCR assays were tested in triplicates for all dilution steps on an ABI7500 (Applied Biosystems, US).

Afterwards, the dilution serials were mixed to simulate co-infections in the following way:

(1) All three pathogen dilutions were mixed in parallel (e.g.: ZIKV 10E4 IU/μl + CHIKV 10E4 IU/μl + DENV 10E4 IU/μl, etc.)

(2) Parallel mix of ZIKV and CHIKV dilutions (e.g.: ZIKV 10E4 IU/μl + CHIKV 10E4 IU/μl, etc.), same for ZIKV and DENV dilutions (3) and DENV and CHIKV dilutions (4).

(5) ZIKV and CHIKV dilutions were mixed counter-directional (e.g.: ZIKV 10E4 IU/μl + CHIKV 0 IU/μl; ZIKV 3,16E4 IU/μl + 3,16E0 IU/ml, etc.), same for ZIKV and DENV dilutions (6) and DENV and CHIKV dilutions (7).

All 7 dilution set-ups were tested with the real-time PCR assays and results were compared.

**Results:** All real-time PCR assays performed well and results are generally comparable. The time needed from sample to result was comparable for both, multiplex and singleplex assays, since the singleplex assays share the same PCR temperature profile which allows the customer to combine all three assays in one PCR run.

In all 3 single pathogen dilution serials (ZIKV, CHIKV and DENV) the results of all assays (multiplex and singleplex) were very good and, based on the limited data, sensitivities comparable. The differences in sensitivities become more obvious in the simulated co-infections (mixed dilution serials). In mixed infections the singleplex real-time PCRs gave generally better results than the multiplex assays.

**Conclusions:** Sensitivity is an important factor in diagnostics and even though multiplex real-time PCR is an interesting approach, singleplex PCR is still the better option avoiding false-negative results.

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## Implementation of One Health Approach in Sudan: A Review of 20 Years of Experience

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**Background:** The One Health concept is a worldwide strategy for expanding interdisciplinary collaborations and communications in all aspects of health care for humans, animals and the environment. One health focuses on improving health and well-being through the prevention of risks and the mitigation of effects of crises (e.g. emerging diseases) that originate at the interface between humans, animals and their various environments.

The one health approach plays a significant role in the prevention and control of zoonoses. 75% of new emerging human infectious diseases are defined as zoonotic.

Sudan has a large population of livestock which considered as an important source of national income. Zoonoses are of great public health concern in Sudan due to the high cross-border movement of people, livestock and wildlife and other drivers of disease emergence and spread. In addition to internal conflict, Sudan geopolitically location within unstable region which often trigger mass mobility of people and animals. The movement of animals is difficult to be controlled. In rural and nomadic communities people live in close contact with their animals and this increase their susceptibility to zoonotic infections.

The overall objective of this review is to determine the status of the one health approach and its applications to zoonoses.

The specific objectives are to clarify One health practice in Sudan, to display the major zoonotic diseases and to highlight best practice, challenges and possible solutions.

**Material and Method:** A cross-sectional study using documentation approach was carried out to analyze one health applications to zoonoses in Sudan in resources from 1997 to 2018, representing a 21-years review. The documentation review included resources found on the records of Ministry of Health, besides internet search. All the results were then categorized by their year of implementation, the activity types, percentage of

implementation, and geographic distribution. SWOT analysis was conducted to analyze the collected data.

**Results:** All related documents were reviewed for the defined period of time to scan , Disease Surveillance, Early Preparedness, Response and Coordination. zoonotic diseases of greatest public health concern within Sudan, are RVF, CCHF, Ebola, Avian influenza, Brucellosis, Rabies, Anthrax, Bovine TB, Plague and Leishmaniasis. The activities counted were :monthly and annual reports shared between the partners , zoonotic diseases profile, investigation forms and case definition of Zoonotic Diseases, Memorandums of understanding, one health high technical committee, joint outbreak investigation, joint awareness activities and training workshops and state zoonotic focal persons.

**Conclusion:** There is a big need to sustain and strengthen coordination through regular joint meetings and operationalization of the memorandums of understanding for enhancing integrated perspective within human, animal and environment sectors, beside the need of developing further efforts towards engagement with the global community serving as the unit of a one health approach. Implementation of One Health platform among relevant sectors will be the stone corner to the early detection and response to both emerging and neglected zoonotic diseases to avoid its effects in humans, global health security and economies.

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## Reference Intervals of Routine Clinical Chemistry Parameters Among Apparently Healthy Young Adults in Amhara National Regional State, Ethiopia

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**Background:** Clinical laboratory reference intervals (RIs) are essential for clinical diagnosis, treatment

and therapeutic monitoring. Locally established RIs are required to correctly interpret clinical laboratory results. In Ethiopia, clinical laboratory test results are interpreted based on RIs derived from a western population. Therefore, the aim of this study was to establish reference intervals for routine clinical chemistry parameters among apparently healthy young adults in Amhara National Regional State, Ethiopia.

**Methods:** A multicenter cross-sectional study was conducted among blood donors in Amhara National Regional State, Ethiopia from March 2016 to May 2017. A total of 1,175 apparently healthy study participants were included in the study from four blood banks in the region. All clinical chemistry parameters were analyzed using Mindray BS-200E full automated clinical chemistry analyzer. The 95% RIs were estimated using reference limits at 2.5th percentile for the lower reference limit and 97.5th percentile for the upper reference limit. Kolmogorov–Sminorv and Wilcoxon rank-sum tests were used to check data distribution normality and whether partitions were needed between variables, respectively.

**Results:** RIs established include: ALT 5.13-42.88 U/L for males and 4.3-37 U/L for females; AST 12.13-46.88 for males and 10-43.8 U/L for females; ALP 77.2-475.8 U/L for males and 89-381 U/L for females; amylase 29-309.8 U/L for males and 29-287.9 U/L for females; GGT 7-69.8 U/L for males and 6-39.1 U/L for females; total bilirubin 0.11-1.18 mg/dl for males and 0.08-0.91 mg/dl for females; creatinine 0.48-1.13 mg/dl for males and 0.47-1.09 mg/dl for females; total cholesterol 78.13-211.75 mg/dl for males and 83.6-202.7 mg/dl for females; total protein 5.7-9.7 g/dl for males and 5.6-9.47 for females; triglycerides 36-221.9 mg/dl for males and 35.3-201.5 mg/dl for females; urea 12-43 mg/dl for males and 10-38.7 mg/dl for females; and uric acid 2.7-6.9 mg/dl for males and 2.1-5.9 mg/dl for females.

**Conclusions:** This study has established RIs for routine clinical chemistry parameters. These RIs are important as they support the interpretation of clinical laboratory results for medical decision making and other health-related activities.

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## Rapid Detection of Drug-Resistant *M. tuberculosis* from Presumptive Drug-Resistant Tuberculosis Patients in Ethiopia

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**Background:** Resistance to rifampicin has mainly been associated with mutations in the *rpoB* gene. Accurate and rapid detection of drug-resistant strains of TB is critical for early initiation of treatment and for limiting the transmission of drug-resistant TB. Xpert<sup>®</sup> MTB/RIF (Cepheid, Sunnyvale, CA, USA) is real-time PCR technology that uses molecular beacons to detect rifampicin resistance in the *rpoB* gene. In this study we investigated the accuracy of Xpert MTB/RIF for detection of rifampicin (RIF) resistance and whether the detection of RIF-resistance predicts the presence of multidrug resistant (MDR) TB in Southwest Ethiopia.

**Methods:** Cross-sectional study was carried out at Jimma University-Mycobacteriology Research Center, Jimma, Southwest Ethiopia. A total of 67 smear-and/or- culture positive pulmonary TB patients with increased suspicion of drug resistance were included in this study. Genotype MTBDRplus line probe assay (LPA) and Xpert MTB/RIF tests were done directly on smear-positive sputum specimens and on the cultured isolates for smear-negative specimens. We used the routine drug susceptibility test (LPA) as the reference standard for confirmation of rifampicin (RIF) and isoniazid (INH) resistance.

**Results:** Using line probe assay, 32.8% (22/67) of the patients were rifampicin resistant, 35.8% (24/67) were isoniazid-resistant and 31.3% (21/67) were multidrug-resistant TB (MDR-TB) (resistant to both rifampicin and isoniazid). The most common mutation in RIF resistance was at -MUT Ser531Leu (82.4%). More than 85% of INH resistant have mutation at codon 315 of *katG*. 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) were 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 resistant 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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## Association of Human Leukocyte Antigen-C Class Allele Sharing and Heterosexual HIV-1 Transmission Amongst Serodiscordant Couples in Nigeria

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**Background:** Certain biological and behavioural risk factors have previously been documented to increase the chances of heterosexual HIV-1 transmissions among serodiscordant couples. These included increased HIV -1 RNA (>1500 copies/ml), Sexually Transmitted Infections, oral/anal sex, increased number of sexual partners, age and sex. Few studies have also reported the association between HLA-B allele and increased risk of HIV-1 transmission in serodiscordant couples. However, information on shared HLA-C alleles by serodiscordant couples is scarce and virtually non-existent in Nigeria. Therefore, this study aimed to determine the association between sharing of HLA-

C, at allele and group level at HLA-C Loci with increased risk of HIV-1 transmission amongst serodiscordant couples in Nigeria.

**Methods:** A total 224 serodiscordant couples who signed informed consent document were enrolled into this programme. Extracted genomic DNA was used for HLA class 1 genotyping using allele-specific primers for PCR. Sequencing was done by Sanger method, using Biosystems™ 3130xl Genetic Analyzer. HLA-C Typing, was done using Codon Express 201010. Data entry and statistical analysis was done with SPSS and Kaplan–Meier analysis.

**Results:** Their age ranged from  $\geq 21$ - < 50years. Within HIV-1 status at HLA-C allele level: Couples who do not share HLA-C haplotypes was 57.5% and couples that shared HLA-C allele at allele level were 42.5%.  $P=0.013$ . Risk estimate at 91% CI: 1.033 at lower limit and 3.299 at upper limit. Again, within HIV-1 status at HLA-C allele group level: Couples who do not share HLA-C was 68.8% while couples sharing HLA-C at group level were 31.2%.  $P=0.001$ . Risk estimate at 91% CI: lower limit: .302 and upper limit.646.

**Conclusions:** After adjustment for other biological and behavioural risk factors associated with heterosexual transmission of HIV-1 in this group, sharing HLA-C allele at group level and at allele level by couples was independently associated with increased risk of HIV-1 transmission amongst serodiscordant couples in Nigeria.

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## Serological Prevalence of Hemorrhagic Fever Viruses in Equatorial Africa

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**Background:** The 2014 - 2016 outbreak of Ebola virus disease (EVD) in West Africa has changed our understanding of viral hemorrhagic fevers. What was previously thought to be a sporadic, localized disease is now perceived as a more widespread threat to public health in heavily populated regions. The re-emerging epidemic illustrated the need for epidemiological investigations of the serological prevalence and geographic range of hemorrhagic fever viruses (HFV) as well as the development of novel serological assays for their detection and surveillance. A total of 2,430 serum samples were tested for antibodies specific for Ebolavirus (EBOV), Marburgvirus (MBGV) or Lassa virus (LASV) proteins to determine the overall seroprevalence for these viruses in the respective populations. Serological assays for the detection of antibodies against EBOV glycoprotein (GP), matrix protein (VP40) and nucleoprotein (NP) as well as MBGV and LASV glycoproteins included novel micro-neutralization and luciferase immunoprecipitation system (LIPS) assays.

**Methods:** A serological survey of 2,430 serum samples from different sources was conducted to determine the prevalence of hemorrhagic fever viruses, including Ebola, Marburg and Lassa viruses, in Equatorial Africa. Serum samples were screened for neutralizing antibodies in a pseudotype micro-neutralization assay and for Ebolavirus by a newly developed luciferase immunoprecipitation system (LIPS) assay. Specimen seroreactive for Filoviruses were confirmed by enzyme-linked immunosorbent assay (ELISA).

**Results:** Our results suggest a serological prevalence between 2 and 3.5 % for Ebolavirus and less than 1 % for Marburgvirus in the Republic of the Congo and the Democratic Republic of the Congo (DRC), which both have reported Ebolavirus outbreaks in the past. Surprisingly, a seroprevalence for Marburgvirus of > 6 % was found in Cameroon and Ghana, suggesting the circulation of Filoviruses or related viruses outside of known endemic areas that remain undetected by current surveillance efforts. Overall, the detection of VP40-specific antibodies resulted in higher rates of positive samples than the neutralization assay in all examined sample sets. Antibody-positive samples for Ebolavirus were not detected in the 1997 HIV surveillance samples from Ghana (n=48) by any of the assays while the VP40-LIPS assay resulted in 1/160 reactive case (0.94%) in Uganda and 4/96 (4.17%) in Cameroon. In this study we found approximately 2% EBOV prevalence rates for both the Republic of Congo and a blood donor cohort in Kinshasa, DRC, respectively. These results



agree with a recent serological survey in 2011 of blood donors in the Republic of Congo that reported a 2.5% EBOV prevalence. In our study of 160 serum samples collected in 1999, Owando returned the highest prevalence of the three different locations surveyed in the Republic of Congo. However, at 3.13% this prevalence rate could have been missed using the smaller sample size.

**Conclusion:** In summary, by using a multi-serological-assay approach with stringent assay cut-offs normalized by background assay reactivity in the general local population, our data suggest that EBOV exposure outside of recognized outbreaks is likely a rare event. Nevertheless, serological evidence of past EBOV exposure was detected throughout different regions of Central Africa.

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## Bacterial Etiology of Fever in Children in Gabon

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**Background:** Fever is one of the main reasons of pediatric consultation in sub-Saharan Africa. Malaria is the most frequently suspected cause, posing a major problem, the misguided prescription of antimalarial drugs to febrile children, including those with negative diagnostic tests to malaria. The decrease in the prevalence of malaria in the early 21st century has shown the involvement of common and emerging bacteria in fever in Africa. Unfortunately, in a sporadic context existence of the main viral causes such as Chikungunya and Dengue, studies are lacking in Gabon leading underestimation of fever causes and seriously compromise the febrile children care.

**Objective:** This study aimed to evaluate the presence of emerging, common bacteria as well as plasmodial and filarial parasites in febrile gabonese children younger from 0 to 16 years old.

**Method:** From 2012 to 2016, 1,363 DNA extracts from blood samples of 1,203 febrile children and 160 afebrile children were analyzed using molecular tools (PCR coupled to sequencing).

**Results:** Overall, *Rickettsia felis* was the most common bacterium detected in 54 cases including 50 (4.4%) febrile children, followed by *Staphylococcus aureus* in 29 cases including 26 (2.2%) febrile children, *Streptococcus pneumoniae* in 12 (1%) febrile children, *Salmonella* spp. in 11 (1%) febrile children, *Borrelia* spp. in 2 afebrile patients, *Tropheryma whipplei* in 1 febrile child and *Streptococcus pyogenes* in 1 febrile child. The *Plasmodium* and *Mansonella perstans* DNAs were detected in several cases, mainly in 912 and 61 febrile children, respectively. Other filarial parasites, such as *Loa loa* and a potential new species provisionally called *Mansonella* sp "DEUX" were detected, in 7 and 12 febrile children, respectively.

**Conclusion:** This work demonstrated that bacteremia, including those related to fastidious bacteria such as *R. felis*, previously unknown, are common during fever in children in Gabon. Their co-circulation with plasmodial and filarial parasites underlines the importance to improve the management of fever in Gabon by, systematically, screened bacteria in both positive and negative malaria cases.

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## How to Make Diagnostics for (Re-)Emerging Viruses Available in the Affected Regions?

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**Background:** The recent outbreaks of Ebola (2013-2018) and Zika (2015-2016) caused a huge health threat in the affected regions where diagnostic tools are largely lacking and exemplify how challenging an emergency response can be. These outbreaks have sparked global epidemic preparedness and prompted industry to develop diagnostics tests besides new vaccines and

medicines. The ultimate impact of all these efforts depend on whether these tests will continue to be available for future outbreaks.

**Materials & Methods:** We have been involved in the development of two diagnostics tests: one for Ebola (Cnops et al., 2016 J Infect Dis.), and a second multiplex test for the combined detection of multiple arthropod-borne viruses and co-circulating pathogens (e.g. Plasmodium). Together with a company that already had a suitable PCR platform available, our approach was to develop a field-adapted, sample-in result-out test targeting multiple pathogens that cause clinically indistinguishable acute febrile illness.

**Results:** The Ebola test, which received FDA EUA in May, 2016, is nowadays not readily available as it takes more than 3 months to be produced upon request. Likewise, 10 out of the 14 Ebola virus diagnostic tests that were listed by FDA and WHO for use in emergency situations, are currently not commercially available as we observed in a recently performed query on the availability of these tests. Preliminary results of the multiplex test demonstrated its successful evaluation in a reference center at the Institute of Tropical Medicine Antwerp (Belgium) and in a field setting by Institut Pasteur Dakar (Senegal) (Cnops et al., ICREID 2017, abstract 30). The development of this multiplex test however is now halted at this stage of a prototype test.

**Conclusions:** Our observations demonstrate that there is need for re-thinking a suitable (business) model for the development of diagnostics for emerging infectious diseases. We call for a global alliance on diagnostics that defines the current and future diagnostic needs, that aligns R&D efforts through strategic partnerships, that fosters access to clinical specimens for performance evaluation and, finally, that enables access to the diagnostics in the affected countries.

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## One Health: Integrated Surveillance Systems for West Nile Virus in Tunisia, 2017-2018

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**Background:** The surveillance and control of WNV is complex and requires the establishment of a surveillance system integrating both human surveillance, animal surveillance (avian and equine), entomological and environmental. The occurrence of WNV outbreaks in Tunisia led to the necessity for creation and implementation of integrated surveillance systems for the timely and accurate forecast of imminent epidemics, but also for the planning of control.

**Aim:** The general objective of this device is to detect early viral circulation, to take appropriate information, prevention and control measures and to propose a model for predicting VWN in Tunisia. To strengthening collaboration between the various sectors involved in surveillance, the Ministry of Agriculture.

**Methods:** Since October 2016, we formed a multisectoral committee to draft an integrated surveillance system protocol, Ministry of Health, Observatory of New and Emerging diseases, primary care direction, hygiene direction, Institute of Pasteur of Tunisia. Ministry of Agriculture National Institute of Meteorology and NGO. Findings: Three sites have been identified for the implementation of the integrated system, governorates of Gabes, Monastir and Bizerte. This program will start in May 2018.

**Human surveillance:** a network of 5 laboratories was established in order to enhance the surveillance efforts. In case of a positive result, an epidemiological investigation of the case is initiated by the regional team. Bird active surveillance: early detection of West Nile virus circulation via sentinel domestic birds, serological monitoring, repeat samples twice a month, will begin in June and will

end in November (6 months). The early detection of the circulation of the virus in the mosquito.

**Discussion and Conclusion:** This project will test the system in 3 pilot sites and then generalize it to the whole country. The most important is the collaboration between ministry of health and agriculture and to establish a regular communication and exchange of information between the different sectors.

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## Comprehensive Integrated Training for Filovirus Research Capacity Building in a Rural Hospital: The JMEDICC Approach and Experience

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The Joint Mobile Emerging Disease Intervention Clinical Capability (JMEDICC) is a collaboration between United States and Ugandan research entities aiming to deploy experimental therapeutics for future filovirus outbreaks in Uganda along with high dependence clinical care. Data from the WHO interim reports showed that healthcare workers were 28-36 times more likely to contract Ebola in the 2014-16 West Africa outbreak. Recently in DRC, by August 21st 2018, 13 of the 96 cases in the North Kivu Ebola outbreak were healthcare workers. Therefore there is a need to equip the current generation of medical workers with skills to deliver quality care to filovirus disease patients while maintaining the highest standards of safety through Infection Prevention and Control (IPC) practices.

From April 2017, an in-country team of 26 full-time staff was hired and stationed at Fort Portal regional referral hospital (FPRRH) where they are working

alongside Uganda Ministry of Health at FPRRH staff on a sepsis Observational research protocol to appreciate the best practices of sepsis management. They all received standard Ministry of Health (MoH) Approved training in IPC, Viral Hemorrhagic Fever (VHF) case management and cadre-specific training in Integrated Management of Adolescent and Adult Illnesses (IMAI).

A review of the current National Guidelines for Ebola Marburg outbreak Management was done at the start of the program to appreciate the scope of skills required, and gaps in implementation in our local setting. This informed the development of a JMEDICC a training plan with assessment tools to monitor continuous improvement.

The team, under the supervision of senior IPC Trainers, proposed solutions tailored to the local context, which were then deployed in weekly training drills, reviewed, and further assessment of gaps done to fine tune the processes. The multiple tasks that the team trained on were further integrated into clinical scenarios with mock patients under investigation for VHF. This process underwent a quality check by external experts who trained with the team until consensus on best practice was reached. This translated into standard operating procedures and guidelines for which every member of the team was tested for competency where applicable or used in a joint exercise with the local and national stakeholders and assessed for feasibility. The team had an excellent opportunity of managing a confirmed case of Congo Crimean Hemorrhagic fever for 3 weeks, which provided an extra layer of individual and process assessment to better prepare the team for management of more virulent VHF such as Ebola and Marburg virus diseases.

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## Trend in Age-Sex Distribution of HIV Infection in Ogun State, Nigeria (2012-2015): Implications for Control Programmes

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**Background:** Ogun State has the second highest HIV prevalence in South-West Nigeria. Specific HIV information for local action is lacking. There is a need to have a clear picture of the age and sex distribution of HIV infection in Ogun State to help guide targeted control programmes.

**Purpose:** To describe the trend in age and sex distribution of HIV infection in Ogun State, Nigeria.

**Methods:** We reviewed records of HIV counselling and testing between 2012 and 2015 from Ogun State AIDS and Sexually Transmitted Infection Control Programme. Proportions were used to describe the age and sex distribution of HIV in the state while chi-square test for trend was used to determine the trend of HIV across age-group over the study period at p-value < 0.05.

**Findings:** A total of the 417,535 clients were tested for HIV from 2012-2015, out of which 260,959 (62.5%) were females. The age-group 25-49 years constituted the highest proportion of those tested (57.0%) and had the highest prevalence of HIV (5.8%) while the age-group 15-19 years accounted for the lowest proportion of those tested (8.5%) as well as the lowest prevalence of HIV (1.3%). There was no statistically significant change in the overall trend of HIV prevalence between 2012-2015. When disaggregated by age-group, only the age-group 15-19 years (p= 0.003) and 20-24 years (p= 0.04) showed a statistically significant downward trend in the prevalence of HIV.

**Conclusion:** HIV prevalence decreased significantly among the age-groups 15-19 and 20-24 years. However, the burden of HIV was highest among those aged 25-49 years. Therefore, we recommended that control measures should be targeted at those aged 25-49 years.

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## Molecular Epidemiology of Rotaviruses in Northwest Ethiopia After National Vaccine Introduction

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**Background:** Rotaviruses mortality among infants and young children is high in Sub-Saharan Africa. Recently, Ethiopia introduced the monovalent rotavirus vaccine in its national immunization program to decrease the burden of rotavirus disease and mortality. Rotavirus surveillance in Ethiopia is based largely on data provided by sentinel hospitals in its capital Addis Ababa.

**Objective:** To assess rotavirus abundance and diversity in outpatient infants and children outside of Addis Ababa in the early post-introduction period.

**Method:** Fecal samples were obtained from children aged less than five years presenting with diarrhea at outpatient health institutions in two cities in Northwest Ethiopia, Gondar and Bahir Dar, from November 2015 to April 2016. Basic demographic data were assessed. Real-time RT-PCR was used to detect rotavirus A RNA. Based on sequences of VP4 and VP7 gene segments phylogenetic analysis was performed.

**Results:** Rotavirus wildtype positivity was 25% (113/450) and higher in Gondar (34%) than in Bahir Dar (18%). Rotavirus infection was less common in infants below 6 months than in children of all other age-groups. Rotavirus genotype distributions were distinct between Bahir Dar and Gondar. In total, wildtype G3P[8], G2P[4], G9P[8], G12P[8], and G3P[6] rotaviruses were detected in 68 (60.2%), 21 (18.6%), 13 (11.5%), 9 (8.0%), and 2 (1.8%) of the positive samples, respectively. Wildtype G1P[8] strains were absent. The phylogenetic analysis revealed close relatedness of the current rotavirus strains with Ethiopian strains of the pre-introduction period.

**Conclusion:** In the early period after the introduction of vaccination, rotaviruses were frequent and were diverse in Northwestern Ethiopia. High phylogenetic relatedness with strains of the pre-vaccine era, indicate absence of early vaccine-induced strain replacement. Future surveillance studies should be carried out throughout the country to gain comprehensive data on rotavirus strain diversity and to monitor the effect of the ongoing vaccine program on the disease burden and eventual rotavirus strain replacement.

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## Mapping African Mobile Health Readiness

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**Background:** With more than 11% of the sub-Saharan African population accessing health services via their mobile phones in 2017, mobile phone penetration in the region expected to grow to 52% by 2025, and outbreak response teams increasingly relying on mobile devices for rapid case reporting; mobile health and epidemiology platforms offer a novel way to provide health advice, report symptoms remotely in the absence of other health infrastructure, and form an early warning system for infectious disease outbreaks. We have mapped the potential use and coverage of these mobile interventions across sub-Saharan Africa to determine the connectivity needs of African health systems, enable geographically tailored and targeted interventions at the village level, and provide a platform for integration with current mobile surveillance infrastructure to inform epidemiological efforts.

**Materials & Methods:** Geographic information systems were used to collate open-source datasets of cellular network coverage, health facility location and type, population density, road infrastructure, and demographic and health indicators such as pregnancies and vaccine coverage.

**Results:** A web-based interactive map was produced visualising mobile health readiness across

sub-Saharan Africa. Additionally, the percentages of health facilities and populations in range of cellular networks were identified for each country. Areas of potential outbreak risk with poor connectivity were identified as cold spots, and areas with poor access to other health infrastructure but with cellular network coverage were identified as opportunity areas.

**Conclusions:** This platform has the potential to inform regional health policy and investment in cellular network infrastructure, improve access to care and advice through targeted mobile health interventions, and inform emergency preparedness and response plans.

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## High Level of Human Astroviruses Circulation in Wastewater of Dakar, Senegal

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**Background:** Acute gastroenteritis (AGE) is a major public health problem, causing a significant mortality especially in developing countries where children under the age of 5 years are frequently affected by precarious hygiene conditions. Among the responsible pathogens agents of AGE, viruses are the predominant etiology. Human Astroviruses (HAsTV), which are positive RNA viruses, represent the third viral etiology for AGE after Rotavirus and Noroviruses. Their role in the epidemiology of AGE in Senegal is poorly known.

**Objective:** The purpose of this study was to retrospectively evaluate the prevalence and genotypes of human Astrovirus (HAsTV) circulating in the environment from wastewater collected in urban Dakar.

**Methods:** We collected by grab method 67 wastewater at Camberene's sewage treatment plant in Dakar region (in 2016 and 2017). After concentration by a biphasic method using polyethylene-glycol (PEG) and Dextran, those samples were stored at -80 °C in the laboratory. After extraction of viral RNA, we conducted

molecular characterizations by an (hemi) nested PCR and partial Sanger sequencing of the viral genome for positive specimens.

**Results:** The prevalence of Astroviruses in effluents was 21% (n=14/ 67). Phylogenetic analysis of the sequences revealed the presence of genotypes HAstV-1(21.43 %), HAstV-2 (7.14%) and HAstV-5 (71.43%). All strains found belong to genogroup I and formed a single cluster.

**Conclusion:** The high detection rate of HAstV in this study indicates that these viruses circulate at a relatively high frequency in the local population. Our data demonstrate that environmental monitoring might be an effective method to identify HAstV strains in circulation with the aim to develop specific prevention strategies.

Key words: Human Astrovirus – Acute gastroenteritis – Wastewater – Dakar.

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## Temporal Trend of Measles Cases and Potential Impact of Vaccine on Outcomes in Jigawa State, Nigeria, 2013-2017

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**Introduction:** Measles is a vaccine-preventable viral disease that is highly infectious and mostly affects children less than five years old. In Nigeria, the burden is highest in the North. We reviewed Jigawa State measles surveillance data over a five-year period to identify its trend, determine the magnitude, vaccination status and disease outcomes.

**Materials & Methods:** We conducted a secondary data analysis of measles specific Integrated Disease Surveillance and Response (IDSR) records for Jigawa State covering a period between January 2013 and December 2017. We sorted, extracted and cleaned relevant variables from the IDSR line list; these

included number of cases and deaths, date of onset, vaccine doses and laboratory results. We calculated frequencies and proportions and obtained odds ratios (OR) with 95% confidence interval (CI) using Microsoft Excel 2016 and Epi Info 7.

**Results:** A total of 6,214 cases were recorded with 955 (15.4%) confirmed by laboratory investigation. The highest number of cases – 2,434 (39.2%) was in 2013 while the least – 838 (13.5%) was in 2017. Overall case fatality rate was 1.71%. The attack rate was 110/100,000. Age specific attack rate was highest among those less than five years (503/100,000). Only 1,185 (19.7%) had at least one dose of measles vaccine. Compared to those who had never received the measles vaccine, those who received at least one dose were less likely to have died (OR= 0.43, 95% CI: 0.22-0.82). The trend of measles followed the same pattern throughout the years with cases peaking in March, then gradually decline through the year.

**Conclusion:** Measles remains a public health concern in Jigawa State, though declining over the years. There was low vaccination coverage among cases. Receiving at least one dose of the vaccine reduces fatality among the cases. We sensitized communities on the importance of routine immunization (RI) and recommended to the state and federal ministries of health to strengthen RI and implement other control strategies e.g. two-dose measles vaccination schedule for successful eradication of measles.

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## Assessment of Knowledge Gap and High Risk Practices in Lassa Fever Endemic Communities of Esan West Local Government Area, Nigeria

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**Background:** Esan West Local government area in Nigeria has remain endemic for Lassa fever since

advent of the disease in 1969. Over the years, efforts at halting community transmission of the virus with successive yearly outbreak of the disease has not yielded a corresponding reduction in incidence. This study therefore sought to assess the knowledge gap and high risk practices in these communities with a view to proffering enduring solution to the seasonal outbreak of Lassa fever in the area.

**Materials and Method:** By means of a cluster random sampling technique, the knowledge and high risk practices of 280 permanent residents of 3 Lassa fever endemic communities in Esan West LGA was assessed using an interviewer administered structured questionnaire. The data was analysed using SPSS version 20 and statistical significance using chi-squared test was done at 0.05 significance level. The findings in 2018 were compared with a similar study in same locations with same study instruments ten years previously (2008).

**Results:** The knowledge of the respondents on Lassa fever has risen from 35.2 % in 2008 to 86.5 % in 2018, while the safe practices increased marginally from 36.3 % to 41.3 % ( $P < 0.05$ ). Only 31.4% of the subjects live in rat proof houses as at 2018 compared to 27.4% in 2008. The major sources of information on Lassa fever for the two sets of respondents was essentially from communal gatherings which happened mainly during the seasonal outbreaks. The traditional practice of drying food items on unprotected ground surfaces including poor refuse disposal methods have remain largely unchanged. Farming and local trading remain the dominant occupation in the two groups (45.6% and 51.2%). There was no statistical significant difference in the knowledge levels and safe practices between the two groups with respect to sex, occupation and marital status ( $P > 0.05$ )

**Conclusion:** There has been an appreciable increase in the level of knowledge of Lassa fever in the study area without a corresponding reduction in high risk practices and behaviour. An assessment of current community education methods and engagement strategies is imperative, while maintaining efforts at reducing the contribution of socio-economic and environmental factors such as poor housing conditions and poor environmental sanitation. Collaboration with local government authorities by Non-governmental Organizations is advocated to achieve a sustainable control program for Lassa fever in endemic communities.

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## Cholera: Outbreak in Algeria

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**Background:** Cholera is an epidemic diarrheal disease, strictly human, of bacterial origin with *Vibrio cholerae*, transmitted by the digestive tract; it is a disease of the faecal peril. It is highly contagious, particularly in areas affected by natural disasters, armed conflict and in countries where wastewater is not adequately treated. In Algeria cholera has recently reappeared in 6 wilayas after the last isolated cases reported in 1996; the last epidemic dates back to 1986.

The objective of our study is to describe the cholera epidemic that has recently affected the region and its management within our department.

**Material and Method:** We carried out a study concerning 215 cases of patients hospitalized at the department of infectious diseases in Boufarik hospital, Blida from August 12 to September 29, 2018.

**Results:** 215 patients in care, average age 38.5 years; 155 adults and 60 children (of which 6 infants), sex ratio 0.76.84 cases, including 64 from 14 families, were confirmed with *Vibrio cholerae* O1 serotype Ogawa by stool culture and / or rapid diagnostic test (Crystal VC). A water source was found in Oued Béni Azza (river) located in Blida. The cholera syndrome was characterized by the occurrence of acute watery diarrhea, rice water with vomiting observed in 61% of cases, diarrhea in 32% of cases and 7% were healthy carriers.

3.3% of the patients consulted in a phase of collapse with impregnable blood pressure, hypokalemia was founded in 21% of cases, 14% had functional renal insufficiency, 6 of which required hemodialysis and 2 had been intubated. Our patients received rehydration combined with cyclin antibiotic therapy for adults and Erythromycin for children. The antibiogram performed on the first strains revealed resistance to aminopenicillins and cotrimoxazole.

The evolution was favourable for the majority of our patients with only 3 deaths.

**Conclusion:** Cholera remains a threat to public health worldwide, an indicator of the lack of social equity and the lack of social development. Improving water supply, sanitation and raising the level of hygiene remain the best ways to fight the disease.

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## Genetic Diversity of Mycobacterium bovis and Its Zoonotic Potential in Ethiopia: A Systematic Review

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**Background:** Understanding the types of Mycobacterium bovis (M. bovis) strains circulating in a country and exploring its zoonotic potential has a significant contribution in the effort to design control strategies. The main aim of this study was to review and compile the results of studies conducted on M. bovis genotyping and its zoonotic potential of M. bovis in Ethiopia.

**Methods:** A systematic search and review of articles published on M. bovis strains in Ethiopia were made. PubMed and Google Scholar databases were considered for the search while the keywords used were "Mycobacteria," "Mycobacterium bovis," "Bovine Tuberculosis" and "Ethiopia."

**Result:** Fourteen studies were considered in this review and a total of 31 distinct strains of M. bovis (N=211) were obtained; the most dominant strains were SB0133 (N=62, 29.4%), SB1176 (N=61, 28.9%), and followed by SB0134 and SB1476 each (N=18, 8.5%). The clustering rate of M. bovis strains was found to be 42.0%. On the other hand, 6 strains of M. bovis were reported from human namely; SB0665 (N=4), SB0303 (N=2), SB0982 (N=2), SB0133 (N=1), SB1176 (N=1), and 1 new strain. Similarly, a total of 8 strains (N=13) of M. tuberculosis bacteria were also identified from animal subjects; namely SIT149 (N=3), SIT1 (N=2), SIT1688 (n=2), SIT262

(N=2), SIT53 (N=1), SIT59 (N=1), and one new-Ethiopian strain.

**Conclusion:** The result showed that the genetic diversity of M. bovis strains reported from Ethiopia are less diversified. The result also underlines that there is an ongoing active transmission of M. bovis and M. tuberculosis between human and animals in Ethiopia because a significant number of both M. tuberculosis and M. bovis strains were reported from both human and animals.

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## Hepatitis C Virus Testing and Treatment Among Persons Receiving Buprenorphine in an Office-Based Program for Opioid Use Disorder in Nigeria

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**AIMS:** IN NIGERIA, HEPATITIS C VIRUS (HCV) INFECTION IS PRIMARILY SPREAD THROUGH INJECTION DRUG USE. THERE IS AN URGENT NEED TO IMPROVE ACCESS TO CARE FOR HCV AMONG PERSONS WITH OPIOID USE DISORDERS WHO INJECT DRUGS. THE PURPOSE OF OUR STUDY WAS TO DETERMINE THE PREVALENCE OF HCV, PATIENT CHARACTERISTICS, AND RECEIPT OF APPROPRIATE CARE IN A SAMPLE OF PATIENTS TREATED WITH BUPRENORPHINE FOR THEIR OPIOID USE DISORDERS IN A PRIMARY CARE SETTING.

**METHODS:** THIS STUDY USED RETROSPECTIVE CLINICAL DATA FROM THE ELECTRONIC MEDICAL RECORD. THE STUDY POPULATION INCLUDED PATIENTS RECEIVING BUPRENORPHINE IN THE OFFICE BASED OPIOID TREATMENT (OBOT) CLINIC WITHIN THE ADULT PRIMARY MEDICINE CLINIC AT LAGOS MEDICAL CENTER BETWEEN OCTOBER 2008 AND AUGUST 2015 WHO RECEIVED A CONCLUSIVE HCV ANTIBODY AB TEST WITHIN A YEAR OF CLINIC ENTRY. WE COMPARED CHARACTERISTICS BY HCV SEROSTATUS USING PEARSON'S CHI-SQUARE AND PROVIDED NUMBERS/PERCENTAGES RECEIVING APPROPRIATE CARE.



**RESULTS:** THE SAMPLE COMPRISED 300 PATIENTS. SLIGHTLY LESS THAN HALF OF ALL PATIENTS (N = 134, 27.7%) WERE HCV AB POSITIVE, AND WERE SIGNIFICANTLY MORE LIKELY TO BE OLDER HAUSAS AND YORUBA'S, HAVE DIAGNOSES OF POST-TRAUMATIC STRESS DISORDER (PTSD) AND BIPOLAR DISORDER, HAVE PRIOR HEROIN OR COCAINE USE, AND BE HIV- INFECTED. AMONG THE 134HCVAB POSITIVE PATIENTS, 126 (67.7%) HAD DETECTABLE HCV RIBONUCLEIC ACID (RNA) INDICATING CHRONIC HCV INFECTION; ONLY 8 PATIENTS (2.21%) WITH CHRONIC HCV INFECTION EVER INITIATED TREATMENT.

**CONCLUSIONS:** NEARLY HALF OF PATIENTS (47.7%) RECEIVING OFFICE-BASED TREATMENT WITH BUPRENORPHINE FOR THEIR OPIOID USE DISORDER HAD A POSITIVE HEPATITIS C VIRUS ANTIBODY SCREENING TEST, ALTHOUGH INITIATION OF HCV TREATMENT WAS NEARLY NON- EXISTENT (2.21%).

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## Prevalence of Intestinal Coccidian Parasite and Associated Risk Factors Among HIV-Infected Individuals in Asella and Adama Teaching Hospitals

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**Background:** Intestinal coccidian parasitic infections are the major causes of diarrheal disease in low-income countries; mainly in HIV infected patients. The prevalence of intestinal coccidian parasites is underestimated as the routinely practiced stool wet mount is not able to detect those parasites.

**Objectives:** The objective of this study was to determine the prevalence of intestinal coccidian parasites and associated risk factors among HIV infected patients in Asella and Adama Teaching Hospitals, Ethiopia.

**Methodology:** An institutional based cross sectional study was conducted among HIV patients with diarrhea who attended the ART clinic of Asella and Adama Teaching Hospitals from March 30, 2018 to August 15, 2018. A total of 222 participants were included in the study. Stool samples were collected and examined at Hirsch Institute of Tropical Medicine for parasites using direct smear, modified Ziehl-Neelsen (ZN) and Auramine O staining techniques. Collected Data was entered and analyzed using SPSS version 21. Kappa test was used to assess agreement between test methods and P values < 0.05 was taken as statistically significant value.

**Results:** The overall prevalence of intestinal parasitic infection among HIV infected individuals on ART was 18.92 % (42/222).The prevalence of intestinal coccidian parasites were 22/222 (9.9%) in HIV infected patients on ART. Intestinal coccidian parasitic infection was associated with CD4+ T-cell count <200 cells/μl [AOR, 95% CI: 10.4 (38.88, 2.8), P<0.05]. The most prevalent parasite was *E.histolytica* 15/222 (6.75%), followed by *Cryptosporidium* species 11/222 (4.95) and *Isospora belli* 11/222 (4.95%), *G.lambliia* 5/222 (2.25%) and *Taenia* species 1/222 (0.45%). Having Auramine O staining as a reference, the sensitivity and specificity of modified ZN were 50% and 100% respectively.

**Conclusions:** Intestinal coccidian parasitic infections were detected in 9.9 percent of HIV infected patients. Low CD4 count was significantly associated with opportunistic intestinal parasitic infection. Having a latrine facility or contact with pet animals were not significantly associated with parasitic infections. Auramine O staining was more sensitive compared to Modified ZN in diagnosis of intestinal coccidian parasite in our setup.

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## Hemorrhagic Fevers Co-Infection in Darfur Region, Sudan

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**Background:** Hemorrhagic fevers are a main health threat in Sudan. Basically, viral hemorrhagic fevers such as dengue, Yellow fever represent a main health problem for health care providers. The aim of this study is to assess the hemorrhagic fever circulation in the Darfur region in 2014.

**Materials & Methods:** A total number of 86 who admitted with hemorrhagic fever symptoms was included in this study. The blood sample was collected from each patient. An investigation was done for a panel of hemorrhagic fever agents, including dengue, yellow fever, Chikungunya, and Crimean Congo Hemorrhagic fever. Enzyme linked Immunoassay (ELISA) IgM was done for all these pathogens. Data was analyzed by STATA-13 and descriptive and analytical statistics was created. Fisher's exact test was used to build an association between dependent and independent variables.

**Results:** A total number of 86 participants were included in the study with a mean age  $25.5 \pm 13.2$ . The number of females was 15 (17.4%) and number of males was 71 (82.6%). 32 patients were reported in South Darfur, 20 (23.2%) in West Darfur, 16 (18.65) in North Darfur, 15 (17.4%) in Central Darfur, and 3 (3.5%) in East Darfur. 38 (43.7%) samples were positive for yellow fever and were reported from all five states. A total numbers of 23 samples were positive for dengue virus, 5 samples positive for Chikungunya. 15 samples were yellow fever and dengue co-infected. Two samples were yellow fever and Chikungunya co-infection. Three samples were positive for both dengue virus and Chikungunya. There was a statistical significant association between gender and dengue infection (0.006). There was no association between gender and other viruses.

**Conclusion:** This study concluded that the viral hemorrhagic fevers are prevailing in Darfur States. Vector control activities should be considered in order to cut the transmission circle of these viruses. Encourage community member to improve their environmental hygiene and raise awareness toward mosquito control measures.

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## Success of Epidemiological Response to Lassa Fever Outbreak in Ondo State, Southwest Region, Nigeria, September to November 2018

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**Background:** Lassa Fever, a zoonotic acute viral hemorrhagic illness caused by Lassa virus of the family Arenaviridae, was suspected in the death of a student in Ondo State on the 20th October, 2018. The Nigeria Centre for Disease Control (NCDC) had reported 254 cases with 137 deaths nationwide as at 14 March, 2016 (Case Fatality Rate (CFR) of 53.9%). The NCDC received the notification on the same day and constituted a rapid response team. We investigated to confirm the outbreak, identify possible source and institute mitigating measures to stop the outbreak.

**Methods:** State Lassa Fever Emergency Operation Center was activated. Pillar groups for coordination, case management, surveillance, risk communication, Infection Prevention and Control and environmental management were identified and constituted. We defined suspected case as "Any person managed as a patient; or working or living within Ondo State presenting with fever  $\geq 38.0^{\circ}\text{C}$ , and at least one of the following signs: generalized body weakness, sore throat, abdominal pains, bloody diarrhoea, bleeding from gums, bleeding into skin (purpura), bleeding into eyes and urine, history of travelling and has received standard treatment for fever without response or has had contact with a known case between 30th September and 4th November 24, 2018". A confirmed case as "any suspected case that tested positive on Lassa virus RT-PCR laboratory investigation". We actively searched for cases through laboratory and hospital registers from October to November, 2018 and environmental assessment for rat infestations in the affected communities. Blood samples were collected from

suspected cases for serological test at reference laboratory in Irrua for confirmation. Contact tracing was done and identified contacts were monitored for 21 days counting from last contact date with a confirmed case for sign of fever ( $\geq 38.0^\circ\text{C}$ ) and/or any other suspect-related signs. We generated univariate analyses of the variables using 2016 Microsoft Excel and Epi Info 7.

**Results:** The index case was a 12-year-old male who presented with fever, general body weakness and rectal incontinence and died a few hours later. Sixty cases were listed: 17 confirmed and 43 suspected cases with 4 deaths (CFR: 23.5%). Among confirmed cases, age-group 30-49 years were mostly affected (53%). The median age was 35 years (range: 6 months to 75 years) and 9 (53%) were females. Four of 18 Local Government Areas (LGA) of the state recorded at least a case. Akure North LGA recorded 1 (6%), Akure South LGA 2 (12%), Ose LGA 3 (18%), Owo LGA 10 (59%) while one of the cases was from Edo State. A total of 562 contacts were listed and monitored, three (0.5%) developed fever during monitoring and one (1) tested positive. There were evidences of rat infestations in the affected communities.

**Conclusions:** Lassa fever outbreak was confirmed in the state. Activation of emergency operation center in response to the outbreak assisted in identifying cases, limiting spread and reducing mortality. We conducted sensitization of health workers and community members, coordinated environmental sanitation and derating of affected households.

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## Evaluation of Meningitis Surveillance System in Kebbi State, Nigeria, 2014-2016

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**Background:** Cerebrospinal meningitis (CSM) is an epidemic-prone vaccine-preventable disease. It is associated with high fatality when untreated and high frequency of severe sequelae. A robust surveillance system is a key to meningitis control.

We assessed the attributes of Meningitis Surveillance System in Kebbi State.

**Materials & Methods:** We used CDC updated guidelines for evaluating public health surveillance system. We reviewed the surveillance record from January 2014 to December 2016. We interviewed key informants and administered a semi-structured questionnaire to 21 Disease Surveillance and Notification Officers (DSNOs) from the all the Local Government Areas in the state.

**Results:** There were 2,628 suspected cases of CSM reported during the period under review. Among them, only 216 (8.2%) had samples taken with 117 confirmed positive for *Neisseria meningitidis*. All the respondents found the system to be complex as specialized training is required for sample collection. Ninety-six percent (96%) reported that the case definition was broad. All the respondents were willing to continue to participate in the CSM surveillance, while 86% of the respondents were willing to handle the addition of an extra information or indicators to the system. Lack of means of transportation and the need for training on lumbar puncture were their main challenges.

**Conclusion:** CSM surveillance system in Kebbi State is sensitive, acceptable, flexible but complex. We recommended training of clinicians and DSNOs on lumbar puncture to improve sample collection.

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## Evaluation of Acute Flaccid Paralysis Surveillance in Gombe State, Nigeria, April 2018: A Peer Review Approach

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**Background:** Polio eradication remains a key goal of the Global Polio Eradication Initiative. Nigeria is the only polio-endemic country in Africa. As the country moves closer to the polio eradication goal, there is a constant need to maintain a high quality acute

flaccid paralysis (AFP) surveillance system that will promptly detect any polio virus occurring in the country. Although the AFP surveillance system is highly sensitive, apparently perfect surveillance core indicators across some states are issues of concern. We evaluated the reported high non-polio AFP and stool adequacy rates in Gombe State to determine the concordance for both indicators as well as the specificity of the system.

**Materials & Methods:** We obtained AFP line list from the state and reviewed AFP cases verified as true and adequate. We defined a true AFP case as any case of sudden flaccid weakness of one or more limbs in a child less than fifteen years old or in whom a clinician suspects poliomyelitis and stool adequacy as two stool specimens in an AFP case collected within 24-48 hours apart and  $\leq 14$  days from onset of paralysis. We used the World Health Organization (WHO) standard checklist and Open Data Kit (ODK) to verify key information from parents and/or care givers which include age of the child, history of onset of sudden flaccid weakness of limb, date of onset of paralysis and stool specimen collection methods. We determined the concordance for non-polio AFP and stool adequacy rates. We identified reasons for discordance and updated the state AFP surveillance data base.

**Results:** A total of 121 AFP cases were reviewed. The state reported a non-polio AFP and stool adequacy rates of 26.1/100,000 and 98% respectively. However, the non-polio AFP rate was found to be 19.1/100,000 (72.7% (88/121) were true AFP cases) and the stool adequacy rate was 83.5% (101/121). The main reason for classifying cases as not true AFP was non-flaccid paralysis in 31 (94%) of 33 cases while stool specimens not collected within 24-48 hours apart was the main reason for classifying cases as inadequate in 16 (80%) of 20 cases.

**Conclusion:** Although the AFP surveillance system in Gombe State is sensitive, the specificity is suboptimal. There was discordance in the reported non-polio AFP and stool adequacy rates because of case misclassification and inappropriate stool specimen collection methods. This may result to missed cases of true AFP. We shared our findings with the State Ministry of Health and developed an improvement plan for the state. We sensitized the disease surveillance and notification officers (DSNOs) on case detection and investigation. We recommended regular training and re-training of the DSNOs on adherence to AFP case definition and proper stool specimen collection for successful eradication of polio.

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## Investigation of an Unusual Surge in Malaria Cases at Gidan Dugus, Dutse Local Government Area (LGA), Jigawa State, November 2017

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**Background:** Malaria is a potentially life-threatening disease especially in the tropics caused by Plasmodium specie. Plasmodium falciparum infection carries a poor prognosis when poorly managed. Though Nigeria is endemic, it has recorded outbreaks of severe malaria, especially among children aged 6 months to 3 years. In November 2017, we investigated a report of unusual surge in malaria cases in Dutse, Jigawa State. We investigated the outbreak to confirm, characterize and institute control measures.

**Method:** A descriptive study was conducted. A case was defined as any child less than 15 years of age residing within 5km of Gidan dugus in Dutse LGA with fever of less than two(2)weeks with or without abdominal discomfort, altered stool pattern, cough, jaundice, purulent eye discharge, bleeding and body swelling. We conducted active case searches in community and health facilities, key informant interviews, obtained blood samples, Questionnaires on risk assessment and vaccination coverage were administered. We obtained verbal autopsy and supported management of comorbidities.

**Results:** One hundred and sixty (160) cases were identified. The median age group was 1-5years, 89 (55.6%) were males. The most affected age group was 1-5years (77.5%). The commonest presentations were fever 132 (82.5%), diarrhea 109 (68%) and cough/catarrh in 105 (66%). Fourty of the suspected cases had their blood samples collected, 30 (75%) were confirmed to have malaria using thick film microscopy, with 28 (93.3%) showing Plasmodium falciparum on thin film, 2 (6.7%) had mixed infection with Plasmodium vivax. Other

baseline investigations like full blood count and differentials showed severe anaemia(60%) and leukocytosis, liver function tests and urinalysis were carried out. Twenty-seven (90%) revealed very high alkaline phosphatase. Samples tested negative for viral haemorrhagic fevers.

**Conclusion:** The outbreak was confirmed severe malaria that was poorly managed and complicated with severe anemia at Gidan Dugus, Dutse LGA Jigawa State. We recommended early detection, prompt diagnosis and effective treatment of non-severe and severe malaria, provide and sustain essential medicines and other required supplies for case management and sensitization with training of health workers on Infection Prevention and Control (IPC) standards, surveillance and proper documentation.

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## Community Engagement Strategies in Lassa Fever Control: Lessons from the PHC Approach in Nigerian Endemic Communities

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**Introduction:** Lassa fever, a viral hemorrhagic illness found in parts of West Africa has transited from its typical occurrence in epidemic proportion to an all year round phenomenon particularly in high endemic communities of Edo state, Nigeria. One of the suggested ways to reduce the incidence of Lassa fever is to directly engage the communities in formulating and implementing control strategies.

**Methodology:** From records available at the Institute of Lassa fever Research and Control (ILFRC) in Irrua Specialist Teaching Hospital (ISTH), Edo State, Nigeria, Communities with sustained transmission as evidenced by cases admitted at the isolation ward were identified and 3 communities with the highest records of cases were selected. Two of the three communities were in rural areas

and the remaining one was located in urban area. Advocacy visits to the Primary Health Care Coordinator and his team which included the Disease Surveillance and Notification Officer and the Health Education Officer were made. Visits were made to the Community heads in the company of the PHC team, who introduced the study team to the Community head and details including the purpose of the intended study. The community head then convened a meeting of the elder's council who heads various quarters or subdivisions. A convenient date for both parties was fixed to discuss modalities of engagement in a formal community entry ceremony. The ceremony attended by 12 members of the research team and members of the elders' council was mainly interactive sessions during which the study details were explained including potential benefits. Fears, anxieties, misconceptions were handled during the Q&A sessions. The forum appointed representatives or liaison from each of the quarters who was to act as tour guide to conduct the field teams during the preliminary data gathering. The ceremony ended with a light refreshment.

**Results:** Community entry ceremony in the 3 communities had all members of the elders council in attendance as follows: Ihunmudumun 56 (94%), Egoro-egware 37 (96%), Ebudin 90 (98%). The experience in all the 3 communities was similar in terms of attitude and practice, fears and misconceptions on Lassa fever. Awareness of the dangers of Lassa fever and preventive measures was however highest at Ebudin (72%), followed by Ihunmudumun (62%) and Egoro-egware (51%). 100% of the elders in each community gave their consent to participate the entire data gathering exercise and to cooperate with the research team. Lack of feedback from researchers on research projects was seen as a major obstacle to their continued participation or reception to other researchers and community based projects. They all expressed the need for a feedback

**Conclusion:** Using the Primary health care approach as a community entry point is a strategy that can be employed for Community based control programs of highly infectious diseases in West Africa.

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## Sero-Prevalence of Hepatitis B Virus Infection and Associated Risk Factors Among Medical Waste Handlers in Kenyatta National Hospital, Nairobi, Kenya

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**Background:** Infectious and hazardous wastes generated in healthcare facilities, if not properly disposed, pose enormous risk to patients, staff, waste handlers, and the community. Medical waste contains a wide range of potentially harmful microorganisms among which Hepatitis B virus are the most significant pathogens. In developing countries, management of medical wastes has not received sufficient attention and the priority it deserves due to limited resources. Hazardous and non-hazardous wastes are non-segregated thus creating a great health risk to medical waste handlers. This study is aimed to determine the sero prevalence of Hepatitis B Virus infection and risk profile among medical waste handlers in Kenyatta National Hospital.

**Material and Methods:** A cross sectional study was conducted among medical waste handlers at the Kenyatta National Hospital. A structured predesigned and tested questionnaire was used to capture socio demographic data and factors associated with Hepatitis B Virus infection. Serum samples were obtained from each participant and analyzed for Hepatitis B surface Antigen using the enzyme linked immune absorbent assay. Data analysis was done using SPSS version 22.0. Prevalence was calculated as a proportion of participants who were sero reactive to Hepatitis B Surface Antigen. Risk profile was compared between the infected and the non-infected group using Fishers exact test and significance interpreted at 5%.

**Results:** A total of 185 medical waste handlers were recruited. The mean age was 41.5 years (SD 10.3

years) and 53% were females. About a third (31.9%) had college level of education, 83.8% were aware of HBV, 3.8% had ever taken HBV test and only 27% had been vaccinated. The median duration of exposure to medical waste was 15 years (IQR 7.5-20 years). Prevalence of HBV infection was 2.7% (5 medical waste handlers). There was no significant difference between the infected and uninfected participants in relation to risk profile ( $p > 0.05$ ). However, it was noted that all the infected participants had never received a training on medical waste handling and infection control, none had been vaccinated, had reported needle pricks and medical waste splashes on to their mucous membranes. PEP accessibility was at 8.1% and 28.1% incidences were reported in the occurrence register.

**Conclusion:** The prevalence in medical waste handlers indicated intermediate endemicity population. Efforts to eliminate HBV in this population need to focus on increasing awareness, screening, offering universal vaccination and ensure all handlers are trained on infection control.

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## Suspect Cases' Experience and Community Trust in Ebola Care Services During the 2013-2016 West Africa Epidemic

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**Background:** When an epidemic has been declared, fear in communities (at national level and in neighbour at-risk countries) and precautions among health workers encourage the identification of alert cases, who may show signs leading them to be categorized as suspect cases. For many of them, Ebola laboratory test result is negative and they are later considered non-cases. Their experience during the diagnosis process shapes their perception of health services' answer for Ebola patients. It

influences their willingness to further seek care for themselves or for their families. How do the suspect cases (that are not subsequently confirmed) report their experience of the diagnosis and care process? What are the medical or social consequences of being categorized a suspect case? Does it lead them to encourage care-seeking in health facilities in case of Ebola suspicion?

**Materials & Methods:** A qualitative study was conducted in Senegal and Cote d'Ivoire, two countries with high risk epidemic situation for Ebola in 2015-2016, in urban and rural sites. Semi-structured interviews were held with 7 people who had been considered suspect cases and with caregivers for 5 more suspect cases (or groups of cases who received care together) that could not be interviewed. Interviews with cases were held either a few hours or days after their release from the isolation ward. When the person could not be traced, caregivers were interviewed a few weeks later. Data were recorded or noted, translated and coded for thematic analysis.

**Results:** Cases' reports are dominated by their difficulties in experiencing the diagnosis and isolation process, who led most of them to quit the isolation ward rapidly when they got their negative lab test result. They report failures in health services at several levels: insufficient means and preparation; lack of care for their vital needs and lack of treatment for their on-going ailments; lack of listening, explanation and consideration for their families. They also complain about suffering from being isolated and lacking material help such as electricity provision for their mobile phones to be able to communicate. Some of them report violent reactions by health agents due to fear and insufficient communication about biosecurity precautions. Some responders experienced unexpected secondary social effects such as stigma in their communities for being considered an Ebola case. Several factors may explain these **Findings:** the lack of preparedness in health services confronted to their first Ebola epidemic; caregivers' focus on Ebola diagnosis more than patients; fear of contagion on both parts.

**Conclusion:** Non-confirmed suspect cases mostly complained about their treatment in health services. Their perception may be explained by several factors related to the lack of experience and preparedness in health services, that might not occur again after mobilization and training. However, these results also bring key considerations for increasing the acceptability of suspect cases diagnosis and care, that may be

useful to define operational procedures and trainings for health professionals. Improving suspect cases' experience will help building trust in the community about care for Ebola.

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## Adaptation of Local Rabies Virus Isolates to High Growth Titer and Pathogenicity Study to Develop Vaccinal Strain in Ethiopia

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**Background:** Rabies is a zoonotic viral disease which causes acute encephalitis in humans and animals. The case is most severe in developing countries where cell culture derived anti-rabies vaccines are un-affordable or the available nervous tissue-derived vaccines are of questionable immunogenicity and may cause neurological complications. The aim of this study was to adapt local rabies virus isolates on cell lines and mice brain, and to study pathogenicity to intramuscular route of inoculation to develop vaccine strain locally.

**Materials and Methods:** The viruses were isolated from rabid dogs' brain and human saliva and adapted to Swiss albino mice brain and cell lines (BHK-21 and Vero) by several blind passages (35 times) to increase viral titer. The viral titer were controlled by titration at each blind passage both in vivo and in vitro. For Pathogenicity study, mice were inoculated intramuscularly with 250MICLD50/0.1 ml of each adapted virus isolates and observed for 45 days.

**Results:** By titration, a minimum of 1.5 million virus TCID50/ml (in vitro) and 750 thousand viruses MICLD50/0.03 ml (in vivo) virus titer were obtained. According to Pathogenicity study, only two virus isolates, human origin sululta (HOS) and dog origin (DO) caused 12.5% death, which shows incomplete attenuation.

**Conclusion:** Increase in viral titer was significant and it was observed for high viral titer by in vitro virus propagation. Death due to intramuscular inoculation can indicate the phylogroup origin of the viruses showing decline in virulence due to several blind passages. Adaptation of the viruses to mice brain and cell lines to increase virus infectivity titer significantly affects viral virulence to intramuscular inoculation. Further, genetic relationship with fixed rabies virus strain need to be studied by molecular techniques and vaccinal strain should be used from locally isolated viruses.

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## Molecular Epidemiology of Human Papillomaviruses from Cervical Samples in Ethiopia: A Systematic Review

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**Background:** Over 99% of cervical cancer cases are associated with infections of Human papillomaviruses (HPVs). In order to draw up optimal vaccination strategies and HPV based cervical cancer screening, collected data on the genotype distribution of HPVs is crucial that is otherwise missed in Ethiopia. Therefore, the aim of this study was to review and compile the results of studies conducted on HPV genotyping in Ethiopia.

**Methods:** Published articles were systematically searched starting from conception to 27 July 2018 using comprehensive search strings from PubMed/Medline and SCOPUS. Besides, other databases like Google Scholar and the Google databases were also searched manually for grey literatures. Two of the authors of this review independently appraised the studies for scientific quality and extracted the data using the Joanna Briggs Institute (JBI) tools. The pooled HPV

genotype distribution was presented with descriptive statistics and summary measures.

**Results:** The included studies were undertaken in three different areas of the country (Central, Southwest and South) between 2010 and 2014. Some 859 women (age range 15-85 years) with different kinds of cervical abnormalities were included, from whom a total of 534 HPV sequences were reported. Of the reported genotypes, the proportion of HR-HPVs was at 80.4 to 100%. The top five genotypes were HPV 16 (45.3%; 95%CI: 41.1-49.6%), HPV 52 (9.4%; 95%CI: 7.2-12.1%), HPV 18 (8.2%; 95%CI: 6.2-10.9%), HPV 58 (6.9%; 95%CI: 5.1-9.4%) and HPV 45 (5.2%; 95%CI: 3.7-7.5%). The combined prevalence of HPV 16/18 was at 53.6% (95%CI: 49.3-57.8%). Some other reported high risk HPV groups were HPV 31 (3.9%), HPV 33 (2.8%), HPV 39 (2.4%), HPV 51 (1.1%), HPV 56 (3.7%) and HPV 68 (2.4%). HPV 6 at 2.8% (95%CI: 1.7-4.9%) was the predominant low risk type.

**Conclusions:** In this review, HPV 16 in particular, but also HPV 52 and 18, warrant exceptional consideration in vaccination and HPV based cervical screening programs in Ethiopia. To the best of our knowledge, this review represents the first of its kind to establish the genotype distribution of HPV from different kinds of cervical lesions in Ethiopia although it is synthesized out of very few studies. Hence, additional nationwide data are needed to strengthen our finding.

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## Cold Chain Management for Vaccines in Remote Fishing Communities Around Lake Victoria, Uganda in Preparation for HIV Vaccine Efficacy Trials

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**Introduction:** Vaccines are easily adversely affected by extreme temperatures. In many parts of low income countries, the supply of electricity or liquid petroleum gas to power a cold chain is erratic.



Therefore, alternative means have to be relied upon to ensure vaccine potency.

**Methods:** During a simulated vaccine efficacy trial in fishing communities, we shipped and stored Engerix® B and TYPHIM Vi® vaccines in a 2-8°C temperature environment facilitated by reusable Credo Cubes™. The cubes were prepared by disassembling and keeping the plates in a 2-8°C refrigerator for at least overnight before use. When they were to be used, these plates were reassembled and left to stand until the internal temperature in the cubes came to within 2-8°C. The payload was then packed with temperature data loggers and sent to the fishing communities; Nsazi island 2 hours away and Kigungu mainland site 30 minutes away from the main hub.

**Results:** Between January and July 2017, we made 77 shipments; 14 to Nsazi and 44 to Kigungu. The total hours of use were 2797 hours (33.8% to the island and 66.2% to the mainland). On 91% of the shipments the required temperatures were achieved within 20 minutes of setting up the Credo Cubes™ and 99% within the first hour. The longest storage was 103 hours 46 minutes. The mean kinetic temperatures were maintained between 2-8°C with the highest being 7.3°C and lowest 3.0°C.

**Conclusion:** It is feasible to transport and store vaccines in remote fishing communities for more than 100 hours with little reliance on electricity. Further experimentation is needed to study vaccines that require frozen storage temperatures.

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## Vaccine Development and Participation in Sub-Saharan Africa: How Willing Are Young People in Western Nigeria?

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**Background:** An estimated 36.7 million people live with HIV/AIDS in 2015, with more than 3 million people living with the virus in Nigeria, ranking the country among the top three most affected.

Because adults are mostly affected by this epidemic, their inclusion in HIV vaccine trials is of utmost importance in obtaining an effective and acceptable vaccine. This study is thus aimed at evaluating the factors determining adults (young persons) willingness-to-participate (WTP) as well as their entire knowledge and perception about HIV vaccine trials.

**Methods:** Data was obtained from 3500 young persons (18-49 years) recruited by a multi-stage sample technique. The cross-sectional study was carried out using a face-to-face interview. An informed consent was obtained through a pre-tested structured questionnaire, with questions addressing socio-demographics, HIV vaccine studies knowledge and perception, sexual behaviour and possible stigma from HIV vaccine trial participation. Data was analysed using SPSS software, with significance fixed at P<0.05.

**Results:** The mean age ± SD was 27.53 ± 3.46 years. 1094 (31.3%) expressed their willingness to definitely participate in the vaccine studies while 999 (28.5%) reported that they may participate especially if a very tangible incentive will be given. Unwillingness to participate was associated with safety concerns (12.0), side effects (5.0%), fear of HIV infection from vaccine (4.1%), time required for study (1.9%) and partner's sexual intercourse refusal (1.2%). 983 (28.3%) reported people in good health, HIV negative individuals and at low risk of HIV infection, are eligible for HIV vaccine trial. There was a significant association between willingness to participate in HIV vaccine trials and age as well as gender.

**Conclusion:** Participation in an HIV vaccine trial in a Nigerian context is likely to be influenced by comprehensive education about the vaccine trial concept, addressing issues relating to concerns and possible risks pertaining to participation as well as incentives, as the WTP in the vaccine trial is quite low probably due to the participants' perception and inadequate knowledge as evidenced in this research.

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## Phased Information Sharing Before Screening: A Strategy for Recruitment of Participants in an Expedited Phase 1 Ebola Vaccine Trial in Uganda

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**Introduction:** The 2013-2016 Ebola epidemic in West Africa was a public health crisis that necessitated rapid development of novel interventions including vaccines. Ebola vaccine clinical trial sites had to develop recruitment strategies to enable them enrol participants in shorter time spans than usual. While most other trials use a single protocol specific study information sharing session, we explored a phased study information sharing approach as a strategy for rapid recruitment at MRC/UVRI & LSHTM Uganda Research Unit site in Masaka.

**Methods:** The MRC/UVRI & LSHTM Uganda Research Unit site was one of the sites in Africa participating in the Crucell Holland B.V sponsored phase 1 vaccine trial to evaluate the safety, tolerability and immunogenicity of heterologous prime-boost regimens using Ad26.ZEBOV and MVA-BN-Filo, in healthy adults (EBOVAC1). The site used a phased information sharing approach to groups of potential participants before screening between April and August 2015 in 3 sessions. The first session focused on Ebola virus disease while the second was about vaccines, their development, and a brief summary of the trial. During the third session, each volunteer went through the Informed consent (IC) process individually with a study staff prior to signing the IC form. During each session, participants attending were recorded on study attendance logs. We summarised the outcome of these sessions using frequencies and percentages.

**Results:** The first session involved 270 (65.6% male) volunteers. Of these, 233 (63.9% male) progressed to the second session, while 180 (63% male) progressed from the second to the third session. At third session, 98% (176/180) of volunteers passed a test of understanding questionnaire and proceeded to sign the IC form. Of the 176 volunteers, 47 (27%)

met enrolment eligibility criteria (screening to enrolment ratio of 4:1). The recruitment to the study took only 5 months.

**Conclusion:** Using a phased study information sharing approach before screening enabled rapid enrolment of participants in this expedited research project, and is recommended in other similar projects.

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## HIV Vaccine Most Wanted in Sub-Saharan Africa—Yet to Come

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The South African AIDS Vaccine Initiative (SAAVI) was established in 1999 as an initiative of South African Government and is a lead program of South African Medical Research Council (MRC). SAAVI coordinates and support the development of testing of HIV Vaccines in South Africa with the aim to find an affordable, effective and locally relevant HIV vaccine. SAAVI works with local and international partners to achieve the common aim of finding successful HIV vaccine.

Sub-Saharan Africa is home to two-thirds of all people living with HIV/AIDS and main driver is unprotected heterosexual sex, according to joint United Nations program on HIV/AIDS or UNAIDS. South Africa has the unfortunate distinction of claiming the world's highest HIV/AIDS burden, with an estimated 6.3 million people living with HIV/AIDS. Seroconversions are increasing at about 370,000 per year in sub-Saharan Africa that is about 1000 new infection every day. About 20% of South African adults—that's one in five people are living with the virus, reports UNAIDS. Young women are twice as likely to be infected as young man.

Scientists have attempted to develop a vaccine for HIV for more than three decades claimed an estimated 35 million of lives; a preventable has recommended elaisive. The genetic diversity of the virus and its unique ability to replicate unrelentingly despite everything the immune system can throw

at it- are among the reasons this is proven to be extraordinary challenges to produce a Vaccine.

The only HIV-vaccine clinical trial that has shown potential so per is the United States and Thai Military vaccine, RV144 demonstrated a modest 31% efficacy at the end of the three year study.

The first in a series of trials designed to build on the success of RV 144 has now passed a key test in South Africa. A safely trail using the vaccine regimen from RV144-but with an added booster shot 12 months afterwards-has shown to be safe for South Africans and demonstrated "robust immune response. A successful safety trail was necessary to move forward with extensive clinical research .The research was first presented in late October in 2014 by a South African scientist in Cape Town.

The Clinical trials of modified vaccine tailored in South Africa is ongoing process from early January 2015.Only difference in this vaccine is that it have added protein that will target the HIV strain prevalent in South Africa.

Sub-Saharan Africa badly needs HIV- Vaccine to reduce the morbidity and mortality of AIDS victims, - As these parts of the hemisphere prevails the highest incidence of HIV/AIDS in the world.

We are working on it. Let's wait for the right time.

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## **Tackling the HIV/AIDS Pandemic in Africa: The Need to Explore and Develop Traditional Medicine (Herbal Medicine) Approach**

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Plants, herbs and ethnobotanicals have been used since the early days of humans. They have contributed significantly to global health. Medicinal plants form the basis of today's modern medicine and contribute largely to commercial drug preparations. About 25% of drugs prescribed worldwide are derived from plants. Traditional

herbal medicine has become a subject of global health discuss; and have contributed greatly to combating infectious disease outbreaks and epidemics.

In China, traditional Chinese medicine was very strategic during the outbreak of severe acute respiratory syndrome (SARS). In Nigeria, Medicinal and aromatic plants have demonstrated its contribution to the treatment of diseases such as HIV /AIDS, malaria and many others.

HIV/AIDS is still a major threat to public health especially in developing countries; thereby placing a huge economic burden on third world economies. Despite huge investments targeted towards achieving global cure, the disease is still a major threat. In order to achieve the United Nations 'getting to Zero' target for HIV/AIDS prevention, there is need to explore multiple treatment approaches targeted towards achieving the desired goal. Developing treatment to diseases challenging Africans could require exploring treatment approaches using resources indigenous to the people. The Alma Ata declaration of 1978 made recommendations for effective health care which should be available and accessible by all. It also made recommendations for the use of methods which are practical, scientifically sound, socially acceptable and made available at a cost which the community could afford.

This presentation shall critically examine the possibility of exploring traditional medicine approach for the treatment of HIV/AIDS; and the need to scientifically develop promising molecules which have been identified to be effective for the treatment of HIV/AIDS.

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## The Emerging Infection Task Force of the European Society for Clinical Microbiology and Infectious Diseases

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Emerging infections are caused by new microorganisms (SARS, MERS, Nipah Virus etc.) new susceptibility patterns to antibiotics, microorganisms emerging in new geographical areas, changing pathogenicity, infecting new groups of people for instance new age groups or emerging in immune-compromised hosts.

Diagnosis of infections is sometimes difficult. Between 38% and 76% of pneumonia cases never obtain an etiological diagnosis no matter whether we use culture or molecular methods (1). In a recent review of infections in the central nervous system (2), 58% (1504/2583) of CNS infections in one study failed to find an etiology. It is in these groups of patients with at present illness without a microbial explanation, that we have to look for new or emerging pathogens.

The key to obtain this objective is a closer collaboration between clinical doctors and the laboratory. Indeed not all laboratories are equipped to investigate for merging or new pathogens and for pathogens from other parts of the world, should the patient has a travel history.

We argue that the logistics of bringing samples from the clinical front line to the investigative laboratory is the prime problem in surveillance and diagnosis of new pathogens and emerging, known pathogens.

1. Hammitt LL et al. Addressing the Analytic Challenges of Cross-Sectional Pediatric Pneumonia Etiology Data. *Clin Infect Dis.* 2017;64(suppl.3):S197-S204.

2. Erdem H et al. The burden and epidemiology of community-acquired central nervous system infections: a multinational study. *Eur J Clin Microbiol Infect Dis.* 2017;36:1595-1611.

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## Molecular and Serological tools for detection and characterization of MERS-coronavirus infections

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**Background:** Middle East respiratory syndrome coronavirus (MERS-CoV) is an emerging zoonotic disease that is endemic in dromedary camels in the Middle East and Africa. In humans, it causes an infection ranging from asymptomatic or mild respiratory symptoms to severe acute respiratory disease, accounting for 35% fatality among diagnosed cases. Despite the high prevalence of MERS-CoV in African dromedaries, no human cases have been reported from this region so far. Active and fully validated molecular and serological surveillance tools need to be available in MERS-CoV endemic and resource-limited settings like Africa to monitor for possible future outbreaks.

**Materials & Methods:** We validated two different S1 ELISA platforms, a commercial and our in-house ELISA, compared to a plaque reduction neutralization test (PRNT) as a gold standard using a well-defined cohort. We used MinION molecular technology for complete genome characterization of MERS-CoV.

**Results:** We set up and validated an in-house S1 ELISA which is able to specifically detect MERS-CoV positive sera from mildly-infected patients and camel contacts- having low antibody titers - with no false positives or negatives in the tested cohorts. This S1 ELISA showed high sensitivity and specificity for MERS-CoV sera which correlated well with the PRNT results. On the contrary, the commercial S1 ELISA, used for seroepidemiological studies, showed false positive results due to cross-reactivity with some HCoV-OC43 positive sera. Additionally, the sensitivity of this platform was lower compared to our in-house test, as it was able to detect only 20% of the camel contact positive sera and mildly infected patients. This indicates that we might be underestimating the true prevalence of MERS-CoV when not using a specific and sensitive assay. In

addition to serological assays, we also successfully sequenced the complete genome of MERS-CoV strains from samples of the Middle East and Africa using a portable molecular device, MinION.

**Conclusions:** For the prevention of emerging infections, active surveillance and proper diagnostic

tools are essential particularly in highly endemic regions. Our in-house serological ELISA and the portable MinION molecular tools can be applicable in the surveillance and characterization of MERS-CoV infection in regions like Africa.



# **2<sup>nd</sup> International Conference on (Re-)Emerging Infections Diseases**

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