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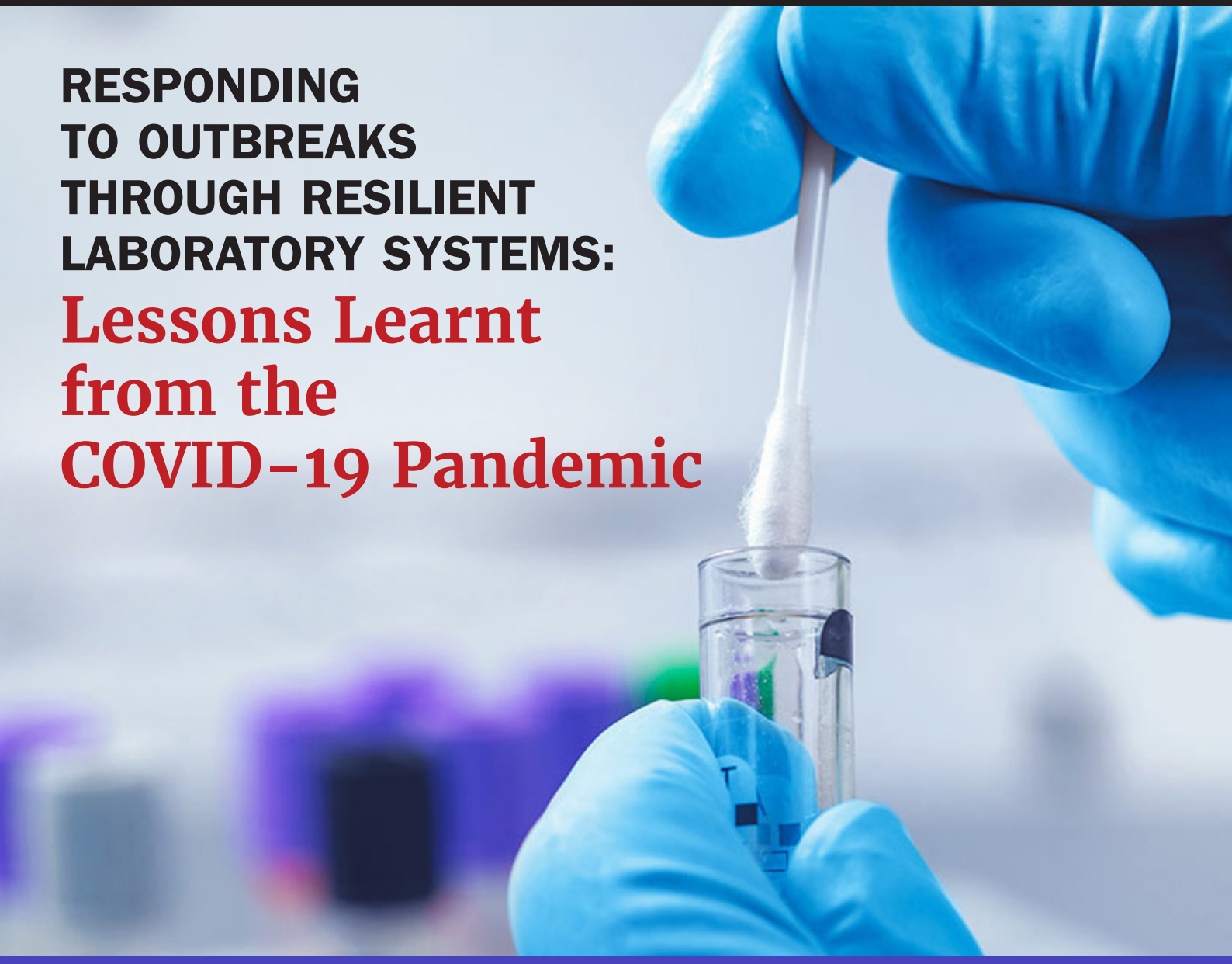
2021



RESPONDING TO OUTBREAKS THROUGH RESILIENT LABORATORY SYSTEMS:

Lessons Learnt from the COVID-19 Pandemic

abstracts

Celebrating Our 10th Anniversary

VIRTUAL: 15-18 NOVEMBER 2021

ORAL SESSIONS at a GLANCE

The Outbreak Effect

ORAL SESSION 2500
Outbreaks, Emerging Pathogens and Disease Burden
Tuesday, 16 November
11:00 – 12:30

CHAIRPERSONS: Nadine Abiola; Marguerite Massinga Loembé

5237272 | Human Papillomavirus Infections and the Impact of Viral Load in Women Attending the Gynecology Clinic at Dr George Mukhari Academic Hospital, South Africa
Varsetile Varster Nkwinika, *Tebogo Lorraine Mashishi, Teboho Amelia Tiiti, Johny Nare Rakgole, Ramokone Lisbeth Lebelo*

5265836 | The Burden of Human Coronavirus Infection in Children Hospitalized with Severe Lower Respiratory Tract Infection in Cape Town, South Africa (2012 – 2013)
Abdulmumuni Samuel Aliyu

5224919 | Bacteria Profile Associated with Bacteriuria in Pregnancy at the Yaounde University Teaching Hospital (CHUY)
Barry Assangwing Nkemontoh, *Moses Njutain Ngemenya*

5266365 | Isolation, Identification and Antimicrobial Resistance Profile of Pathogenic Bacteria Isolated from Clinical Samples in a Rural Remote Community
Paul Olatinwo, *Ifeoluwa Akintayo, Veronica Ogunleye, Anderson Oaikhena, Jolaade Ajiboye, Erkison Odih, Oluwafemi Popoola, Kathryn Holt, Iruka Okeke*

5266726 | Association Significative Entre L'élévation des Taux Antigéniques du Facteur de Von Willebrand et la Mortalité Chez les Patients Atteints de COVID-19
Mohamed El Horri, *Souhil Nour Elain Touati, Imene Harrane, Abdelkrim Chikh Khelifa, Ibrahim Khachaa, Fatima Seghier*

5182313 | Methicillin-Resistant Staphylococcus Aureus in Ibadan, Nigeria: A Community Nasal Colonization Prevalence Study
Ademola Olayinka, *Ibukunoluwa Oginni*

ORAL SESSION 2505
The Role of Laboratories in Outbreak Preparedness and Response
Tuesday, 16 November
11:00 – 12:30

CHAIRPERSONS: Francesco Marinucci; Beatrice van der Puije

5237136 | Cost-Effective Fast Turn-Around Surveillance Method for SARS-CoV-2 Variants of Concern
Eduardo Sanchez, *Nicholas Pinkhover, Kenneth Okello, Kerriann Pontbriand, Liam Garvey, Teddie Proctor, Sara Kendrick, Manoj Gandhi, Jared Auclair*

5237768 | Enhancing Timely Access to Aggregate Laboratory Testing Information in Zambia
Kasimona Sichela, *Reshma Kakkar, Aaron Shibemba, Mutinta Shisholeka, Innocent Chiboma, Phiri Sam, Brian Ntentabunga, Mpande Mwenechanya, Ranjit Warrier*

5226749 | Analysis of Two Approaches for the External Quality Assessment of COVID-19 Testing Laboratories In Burkina Faso
Arnaud Kouraogo, *Patrick Madingar, Charles Sawadogo, Samba Diallo, Blessing Marondera, O. Collins Otieno, Marguerite Loembe Massinga, Pascale Ondea*

5265017 | Establishing a Low-Cost Sub-National Specimen Referral System for Epidemic Response: A Pilot Study
Doofan Abaa, *Augusta Zuokemefa, Anthony Ahumibe, Nwando Mba, Oyebimpe Balogun, Edima Ottoho, Joy Shimang, Kosisochukwu Ejieji, Emmanuel Agogo*

5216791 | Building Laboratory Capacity in PEPFAR-Supported Countries. Will We Be Ready for the Next Pandemic?
Mackenzie Hurlston Cox, Larry Westerman, Heather Alexander, ***Erin Rottinghaus Romano***

5182573 | SARS-CoV-2 Specific Immune Responses in Healthcare Workers With and Without Confirmed Infection at Charlotte Maxeke Johannesburg Academic Hospital (CMJAH), 2020
Nonhlanhla Mbenenge, *Andiswa Simane, Bulelani Manene, Kathleen Subramoney, Ashlyn Davis, Florette Treurnicht*

ORAL SESSION 2510
The Threat of Antimicrobial Resistance
Tuesday, 16 November
11:00 – 12:30

CHAIRPERSONS: Geetanjali Kapoor; Richard Walwema

5237306 | Rectal Carriage of Extended-Spectrum-Beta-Lactamase-Producing Enterobacteriaceae Among Neonates Admitted to a Tertiary Referral Hospital, South-Western Nigeria
Temitope Obadare, *Ebunoluwa Adejuyigbe, Adeyemi Adeyemo, Anthony Onipede*

5237458 | Antimicrobial Susceptibility Patterns of Common Uropathogens During 2018 – 2020 in a Regional Hospital in KwaZulu Natal Province, South Africa
Alicia Naidoo, *Nomonde Mvelase, Khine Han*

5237733 | Detection of Antibiotic Activity in Urine Using A Bioassay in Samples Patients with Suspected Urinary Tract Infections Presenting to Primary Care Clinics
Mutsawashe R Chisenga, *Forget Makoga, Beauty Makamure, Heidi Hopkins, Benjamin Amos, Katharina Kranzer, Ioana Diana Olaru*

5236928 | Class 1 Integron-Integrase Gene(Inti1) Detection in Multi-Drug Resistant Organisms Isolated in Clinical Samples from Niger Delta University, Yenagoa, Bayelsa State
Tolulope Alade

5266255 | Profil de L'antibiorésistances des Germes Responsables D'Infections Urinaires À L'Institut National de Santé Publique de Bamako de 2015 À 2019
Donato Koyalta, *Ibréhima Guindo, Rokia Doumbia, Flabou Bougoudogo*

5239450 | Antibiofilm Formation Activity, Resistant Genes Profiling and Detection of Virulence Factors of Toxigenic Vibrio Cholerae Isolates from Kisumu County, Kenya
Silas Awuor

ORAL SESSION 2515
Policy and Regulation for Resilient Laboratory Systems and Networks
Tuesday, 16 November
11:00 – 12:30

CHAIRPERSONS: Karidia Diallo; Tjeerd Datema

5236634 | Mise En Oeuvre D'un Programme National D'Evaluation Externe de la Qualité Au Togo De 2016 À 2019: Leçons Apprises Et Pistes D'amélioration en Biochimie et Diagnostic du Paludisme
Kafui Codjo Kouassi, *Améyo M. Dorkenoo, Komi Gbada, Yaovi-Gameli Afanyibo, Minogblon Têko, Adjane Koura*

5226104 | Equipment Management in Veterinary Laboratories: Implications for Pandemic and Epizootic Disease Preparedness and Learning Lessons from Past Disease Events
Jennifer Lasley, *Emmanuel Appiah, Kazunobu Kojima, Stuart Blacksell*

5250738 | Country Adherence to WHO 2019 Recommendations on HIV Testing Strategies: A Policy Review Across the WHO African Region
Emmanuel Fajardo, *Céline Lastrucci, Nayé Bah, Casimir Manzengo Mingiedi, Ndoungou Salla Ba, Fausta Shakiwa Mosha, Magdalena Barr-Dichiara, Muhammad Shahid Jamil, Anita Sands, Cheryl Johnson*

5281982 | Development of the Regional Biosafety and Biosecurity Legal Framework for the African Union Member States
Noumedem Kenfack Jaurès Arnaud, ***Talkmore Maruta***

5266578 | Assessment of Viral Load Suppression Rates Among Paediatric Patients Living with HIV in Western Nigeria
Saheed Usman

5237301 | Strengthening Laboratory Capacity for Detection and Surveillance of Antimicrobial Resistance: Bungoma County Referral Hospital in Kenya
Joshua Odero, *Josiah Njeru, Sheilla Chebore, Joan Wasike, David Wanikina, Susan Githii, Evelyn Wesangula, David Mungai, Anicet Dahourou, David Mutonga*

Laboratory Response and Lessons Learnt

ORAL SESSION 3500 — **Wednessday, 17 November**
Strengthening Laboratory Systems and Networks for Routine and Emergency — **11:00 – 12:30**

CHAIRPERSONS: Nadine Abiola; Shirley Lecher

5237182 | **Operational Feasibility of Screening Blood Samples with a CD4 Count of 100-200 Cells/µl for Cryptococcal Antigen in an Established Reflex Programme in South Africa**
Lindi Coetzee, *Greg Green, Miriam Mwamba, Naseem Cassim, Nelesh Govender, Deborah Glencross*

5236684 | **Improving Antimicrobial Resistance Surveillance Through Linking Laboratory Information Management Software with Hospital Information Systems in Vietnam**
Huong Lien Pham, *To Nhu Nguyen, Si Tuan Ngo, Duc Kien Pham, Ngan Giang Vo, Tuan Truong Nguyen, Le Van Ngoc Truong*

5236801 | **Diagnosis of Tuberculosis Infection to Species Level Amongst Multidrug Resistant Tuberculosis Patients for Better Patient Management and Improved Treatment Outcome**
Cornelius Gweba, *Chinonso Mfoneddie, Divine Onwubuariri, Chijioke Anya, Anuli Emeka-Amadi, Precious Uzor, Chike Ezeanya, Meshak Panwal, Mosunmola Iwakun, Abdullahi Abubakar*

5261476 | **The Use of InTray COLOREX Screen and ESBL for Bacterial Identification and ESBL-Detection from Blood and Urine Cultures in Harare, Zimbabwe**
Mutsawashe R Chisenga, *Forget Makoga, Gwendoline Chimhini, Beauty Makamure, Heidi Hopkins, Katharina Kranzer, Ioana Diana Olaru*

5250745 | **Increased Viral Load Testing Capacity with Installation of Solar Power Systems in Zambia**
Lugard Sichalwe, Clement Phiri, Aaron Lunda Shibemba, ***Christine Mfula****, Delhan Hamomba Milimo, Valery Kadima, Mary Chileshe-Lombe, Sarah Snyder, Noah Hull, George Mwakanandi*

5239225 | **Étude de la Cinétique des Anticorps Anti-RBD Et Anti-N Du SARS-COV2 Dans un Échantillon de la Population Tunisienne**
Mariem Gdoura, *Habib Halouani, Donia Sahli, Meriem Ben Hmida, Imen Abouda, Wafa Chamsa, Henda Triki*

ORAL SESSION 3510 — **Wednessday, 17 November**
Workforce Development and the Laboratory Profession — **11:00 – 12:30**

CHAIRPERSONS: Nicolas Steenkeste; Suzanne Kiwanuka

5237326 | **Implementation of the ASLM SARS-COV-2 Antigen RDT Training Package: Field Experiences from South Africa**
Lynsey Stewart-Isherwood, *Abel Makuraj, Anura David, Francinah Nonyane, Shazia Basseer, Sandra Maphumulo, Mashate Silver, Violet Gabashane, Pedro Da Silva, Wendy Stevens*

5237490 | **Impact of the National Health Laboratory Service Extension for Community Healthcare Outcomes Programme on Teaching and Training of South African Laboratorians and Healthcare Workers During the COVID-19 Pandemic**
Leyya Essop, *Babatyi Malope-Kgokong, Adeboye Adelekan, Karidia Diallo*

5330258 | **Situational Analysis of the Response to HIV Viral Load Results Requiring Attention in PEPFAR/CDC Supported Primary Healthcare Facilities in South Africa**
Leigh Berrie, *Paulah Wheeler, Ntombifikile Mtshali, Njeri Kamere, Joslyn Walker, Tinyiko Khosa, Sandile Prusente, Karidia Diallo*

5265935 | **Use of Precise Duty Rosters to Reduce Staff Work-Over Load: A Quality Improvement Intervention**
Charles Olanya, *Ben Okello, Mathew Komakech, Norbert Adrawa, Emma Welikhe*

5227945 | **Converting a Highly Interactive Laboratory Accreditation Curriculum to On-line Learning in Resource-Limited Settings: A Study of Effectiveness, Feasibility, and Costs for Multi-Country Implementation**
Katy Yao, *Elde Mil Paladar, Beatrice Van Der Puije, Janet Scholtz, Davis Ashaba, Kennedy John Matovu, Monte D. Martin, Luciana Kohatsu*

5260785 | **Antimicrobial Resistance Surveillance Curriculum Development: A Kenyan Experience**
Sheilla Chebore, *Joshua Odero, David Mungai, Josiah Njeru, David Mutonga, Anicet Dahourou, Susan Githii, Emmanuel Tanui, Eveyline Wesangula, Jedidah Kahura*

ORAL SESSION 3520 — **Wednessday, 17 November**
Science and Technology to Support Cost-Effective and Integrated Laboratory Networks — **11:00 – 12:30**

CHAIRPERSONS: Paolo Maggiore; Anafi Mataka

5237287 | **Independent Evaluation of the WHO Prequalified M-PIMA HIV-1/2 Viral Load Assay**
Demetrius Mathis, *Katrina Sleeman, Guoqing Zhang, Stephen Jadczak, Heather Alexander, Clement Zeh*

5237665 | **Variable Performance of Chromogenic Agars When Screening for Multi-Drug Resistant Organism (MDRO) Colonization in the Antibiotic Resistance in Hospitals and Communities (ARCH) Study in Kenya**
Susan Bollinger, *Robert Mugoh, Sylvia Omulo, Linus Ndegwa, Beatrice Oduor, Charchil Ayodo, Moureen Jepleting, Douglas Call, Ulzii Luvsansharav, Rachel Smith*

5216247 | **ELABS: Innovative Digital Tool for Strengthening the Clinic-laboratory Interface: Results From a Scaled-Up Programme in South Africa**
Portia Sejake, *Lynsey Stewart-Isherwood, Kumbirai Chigudu, Veronica Mkuyamba, Fadzai Marange, Lesley Scott, Leigh Berrie, Karidia Diallo, Wendy Stevens*

5205993 | **Evaluation of the Abbott Alinity M HIV-1 Assay for Viral Load Testing Using Plasma and Dried Blood Spots**
Lisa Guerrero, *Shon Nguyen, Katrina Sleeman, Guoqing Zhang, Heather Alexander, Clement Zeh*

5211793 | **Evaluation of the HIV-1 Viral Load Assay on the Cobas® 4800 Platform for Early Infant Diagnosis**
Katrina Sleeman, *Demetrius Mathis, Guoqing Zhang, Heather Alexander, Clement Zeh*

5266597 | **Introduction of a Viral Load Data Management System in Ghana**
Kwame Asante, *Shannon Emery, Reshma Kakkar, Phillip Boakey, Francis Frimpong, Lucy Maryogo-Robinson*

ORAL SESSION 3530 — **Wednessday, 17 November**
Pathogen Genomics to Control Diseases — **11:00 – 12:30**

CHAIRPERSONS: Sikhulile Moyo; Gerald Mboowa

5237542 | **Human Coronavirus Circulation Prior to Sars-Cov-2 Epidemic in Zambia: 2019-2020**
Miniva Mwanza, *Paul Simusika, Edward Chentulo, Agness Mushabati, Simon Kawesha, Aaron Shibemba, Jonas Hines, Sam Yingst, Mwaka Monze*

5263904 | **Sars-Cov-2 Lineages Among Clinical and Community Surveillance Samples Submitted to an Academic Virology Laboratory, Gauteng, South Africa, March 2020-February 2021**
Kathleen Subramoney

5240427 | **Molecular Characterization of Plasmids Encoding CTX-M Extended Spectrum β-lactamases Among Escherichia Coli Clinical Isolates in Ethiopia**
Abebe Aseffa Negeri

5266354 | **First Laboratory Confirmation and Sequencing of Zaire Ebolavirus in Uganda After Introduction of Cases from the 10th Ebola Outbreak in the Democratic Republic of the Congo, June 2019**
Luke Nyakarahuka, *Sophia Mulei, Jackson Kyondo, Alex Tumusiime, Baluku Jimmy, Stephen Balinandi, Julius Lutwama*

5266700 | **Strategie de Surveillance Génomique du SARS-CoV-2 au Gabon**
Samira Zoa Assoumou, *Armel Mintsa, Benedicte Ndeboko, Ludovic Mewono, Rodrigue Bikangui, Marien Juliet Verald Magossou, Georgelin Nguema Ondo, Joel Fleury Djoba Siawaya, Jean Bruno Lekana-Ndouki, Ayola Akim Adegnika*

5239530 | **Carbapenemase-Producing Enterobacteriaceae in Malawi: Genomic Composition and Features of Plasmids Encoding Carbapenemases**
Geoffrey Kumwenda, *Yo Sugawala, Watipaso Kasambala, Yukihiro Akeda, Kazunori Tomono, Shigeyuki Hamada*

Ownership, Partnership and Innovation

ORAL SESSION 4500 — **Thursday, 18 November**
Research for Better Laboratory Systems and Networks — **11:00 – 12:30**

CHAIRPERSONS: Linda Oskam; Collins Odhiambo

5228417 | **Field Evaluation of the Asanté HIV-1 Recency Assay for HIV Diagnosis and Recent Classification Using Samples from the Nigeria HIV/AIDS Indicator and Impact Survey**
Ernest Yufenyuy, *Mervi Detorio, Jeni Vuong, Amy Zheng, Olumide Okunoye, Mcpaul Okoye, Bharat Parekh*

5228079 | **Dried Tube Specimens for Quality Assurance in the Implementation of Rapid Tests for Recent HIV-1 Infection**
Keisha Jackson, *Mervi Detorio, Jeni Vuong, Latasha Williams, Bharat Parekh, Ernest Yufenyuy*

5265071 | **Approaches for Improving the Turnaround Time for Viral Load Testing Services in the Eastern Province of Zambia**
Lugard Sichalwe, *Gideon Zulu, George Mwakanandi, Wessy Miyanda, Martin Mwanza, Cletus Kabwe, Charles Shumba, Goodsons Mukosa Mpumba, Clement Phiri, Ranjit Warrier*

5225238 | **LabBook 3.0, an Opensource LIS Developed to Facilitate Data Exportation to DHIS2 and WHONET**
Anja Mampianina Ramilson, Mafoudji Kande, Oumar Kanté, Alexandre Charles, Philippe Meurier, Philippe Brun, Aicha Marceline Sarr, Laurent Raskine, François-Xavier Babin, ***Nicolas Steenkeste***

5266585 | **Peut-On Utiliser L'Antithrombine À la Place du Facteur v dans L'évaluation de L'insuffisance Hépatocellulaire Chez les Patients Cirrhotiques ?**
Mohamed El Horri, *Abdelkrim Chikh Khelifa, Ibrahim Khachaa, Malika Baghdadi, Fatima Seghier*

5239491 | **Performance Evaluation of the Panbio ™ Covid-19 Antigen Rapid Test Device Compared to a PCR-Based Point of Care Test**
Bonolo Mashishi, *Bhaveshan Reddy, Nonhlanhla Mbenenge, Kathleen Subramoney, Florette Treurnicht*

ORAL SESSION 4550 — **Thursday, 18 November**
Partnership, Policy and Regulation to Improve Access and Equity of Diagnostic Tools — **11:00 – 12:30**

CHAIRPERSONS: Francesco Marinucci; Anafi Mataka

5237213 | **Assessing the Costs of Extending Cryptococcal Antigen (CrAg) Reflex Testing in South Africa up to a CD4 Count of 200cells/µl**
Lindi Coetzee, ***Naseem Cassim***, *Deborah Glencross*

5237045 | **Cartographie des Laboratoires au Mali**
Ousmane Traoré, *Adama Sangaré, Souleymane Ongoiba, Sekou Traoré, Boubacar Doumbia, Samba Diallo, Ashenafi Aytenew, Seydou Fomba, Sere Keita, Yaya Coulibaly*

5265966 | **Impact of COVID-19 Pandemic Mitigation Strategies on Viral Load Coverage, Viral Suppression and Continuity of Treatment in PEPFAR Supported Facilities in the Hhohho and Shiselweni Region at Eswatini**
Tandzile Zikalala, *Sindisiwe Dlamini, Kikanda Kindandi, Lydia Mpango, Fannie Khumalo, Christopher Makwindi, Philisiwe Khumalo*

5265948 | **Public-Private Collaborative Approach to Strengthening Clinical Laboratory Capacity in Routine and Emergency Diagnostics Services: Lessons from Nigeria**
Farouk Umaru, ***Adebola Adekoya***, *Dolapo Oyedipe, Florence Ajimobi, Emily Kaine*

5264009 | **Development of An All-In-One Transportable Clinical Bacteriology Laboratory: Feedback from Testing the Mini-Lab Prototype in Haiti**
Jean-Baptiste Ronat, *Alessandra Natale, Céline Langendorf, Bernard Baillet, Céline Franquesa, Thomas Kesteman, Jan Jacobs, Olivier Vandenberg, Thierry Naas, Jacques Boncy*

5223605 | **An Effective Implementation of Antigen Rapid Diagnostic Test (Ag – RDT) for COVID-19: A Program to Increase Testing Capacity in the African Region**
Aytenew Eshete, *Yenew Kebede, Pascale Ondoa, Abebaw Kebede, Halifa Said*

ORAL SESSION 4575 — **Thursday, 18 November**
Harnessing the Power of Community — **11:00 – 12:30**

CHAIRPERSONS: Helen Etyaale; Suzanne Kiwanuka

5236713 | Reaching the Unreached for HIV Viral Load Testing During the COVID-19 Pandemic: A Community-Led Camp Approach in Northeastern India
Nangjong Tangha, Naresh Goel, Bhawna Rao, Vijay Yeldandi, Anita Singh, Anwar Parvez, Melissa Nyendak, Ramesh Reddy Allam, Sanjeev Verma, ***Sunita Upadhyaya***

5262192 | Routine Viral Load Testing: Community-Led Campaigns to Increase Demand for the Test that Counts
Bactrin Killingo, Helen Etya'ale, ***Pontsho Pilane****, Susan Perez, Wame Jallow*

5262097 | Description of Women Attending First Antenatal Care Visits at Saboti Sub County Hospital from March to December 2020
Isaac Njihia

5266674 | Maximizing the Benefits of Laboratory Tests During COVID-19 Pandemic by Systematically Engaging Community Networks and Leadership Structures in COVID-19 Suspect Identification (Alerts Approach)
Monkoe Leqheka

5266149 | Assessing the Feasibility of Use of a Digital Health Solution to Support Antigen RDT (AgRDT) Screening (Professional Collection and Testing) at Taxi Ranks in Johannesburg, South Africa
Mohammed Majam*, Vanessa Msolomba, Rigveda Kadam, Olukunle Akinwusi, Paula Akugizibwe*

5266087 | Evidence of Reduced Academic Performance Among School Children with Helminthic Infection in Spite of Nutritional Status
Emmanuel Timmy Donkoh*, Samuel Asamoah, Abdul Sakibu Raji, John Ekow Otoo, Dorice Akosua Berkoh, Kenneth Bentum Otabil, Michael Tawiah Yeboah, Simon Kofi Adams, Benedicta Atulbire Aganiba, Samuel Fosu Gyasi*

ORAL SESSION 4580 — **Thursday, 18 November**
The One Health Approach to Shape New Laboratory Systems — **11:00 – 12:30**

CHAIRPERSONS: Renuka Gadde; Beatrice van der Puije

5237350 | A Holistic Health System Strengthening Approach in Building AMR Diagnostics Networks: Lessons from Kenya
Josiah Njeru*, Joshua Odero, Sheila Chebore, David Mungai, Anicet Dahourou, Emmanuel Tanui, Evelyn Wesangula, Susan Githii, David Mutonga*

5266359 | Antimicrobial Resistance Genes of Escherichia Coli Isolated from Household Water in Municipal Ibadan, Oyo State Nigeria
Ifeoluwa Akintayo*, Jesutofunmi Odeyemi, Olumuyiwa Alabi, Jeremiah Oloche, Chukwuemeka Nwimo, Oluwafemi Popoola, Iruka Okeke*

5266041 | Identification of Aedes Vectors in Arbovial Diseases Transmission Areas in Darfur, Western Sudan
Muzamil Mahdi Abdel Hamid*, Abubaker Salih, Arwa Elaagip, Musab Albsheer*

5182344 | Occurrence of Multidrug Resistant Escherichia Coli in Contaminated Wells in Ile-Ife, South West, Nigeria: A Public Health Concern
Babatunde Odetoyin*, Mercy Fagbewesa*

5264212 | A Multisectoral Collaboration to Develop Laboratory Leaders and Support a One Health Approach to Laboratory System Building
Jocelyn Isadore*, Virginie Dolmazon, Paula Gomez, Aftab Jasir, Varsha Kumar, Jennifer Lasley, Samantha Musumeci, Lidewij Wiersma, Burton Wilcke, Shannon Emery*

POSTERS at a GLANCE

The Outbreak Effect

Outbreaks, Emerging Pathogens and Disease Burden

5225280 | Impact of the Covid-19 Pandemic on Severe Childhood Malaria at the University Hospital of Brazzaville
Armel Landry Batchi-Bouyou

5225310 | High SARS-CoV-2 IgG/IGM Seroprevalence in Asymptomatic Congolese in Brazzaville, the Republic of Congo
Armel Landry Batchi-Bouyou, *Francine Ntoumi*

5226455 | Studies on Microbial Contamination of Cut and Exposed Onions
Agi Vivian

5237063 | Dengue Serotypes 2 and 4 Detected in Suspected Malaria Patients Attending Some Selected Health Centers in Jos, Nigeria
Nantip Miri*, John Mawak, Nyam Chuwang, Shedrach Acheng*

5237580 | Environmental Surveillance of Crimean-Congo Hemorrhagic Fever Virus in Ixodid Ticks Infesting Livestock in Uganda: Findings from a Prospective Nationally Representative Survey
Jackson Kyondo*, Stephen Balinandi, Luke Nyakarahuka, Alex Tumusiime, Sophia Mulei, Jimmy Baluku, Julius Lutwama, Teddy Kayiki Muwawu, Trevor Shoemaker, John Klena*

5237707 | Urinary Schistosomiasis Among Children Under Ten Years in Tudun Wada Area of Kaduna South Local Government, Kaduna State, Nigeria
Jonathan Onyekachi Peter*, Hadiza Ahmad, Olufunke Deborah Abolarin*

5237849 | Reported Reactions Post Covid-19 Vaccination
Adaora Onwuka

5262081 | Impact of COVID-19 on HIV Viral Load for PEPFAR Countries
Shirley Lecher*, George Alemnji, Heather Alexander*

5265424 | Prevalence of Hepatitis B, Its Associated Factors and The Level of Knowledge in the Buea Regional Hospital
Elisabeth Zeuko'o Menkem*, Claudia Nzechieu Noumbissie*

5265514 | Sero-Epidemiology of HIV-1 Among the People Living in Rural Communities of Federal Capital Territory Abuja, Nigeria; An Outreach Experience
Mohammed Shehu Busu*, Yakubu Ya'aba, Moses Njoku, Salihu Izebe Kasim, Aisha Abubakar, Mary Usoroh, Emmanuel Asawa, Shamsiya Shehu, Peters Oladosu, Peter. Adigwe Obi*

5265981 | Systematic Testing with COVID-19 Antigen Rapid Diagnostic Tests on Inpatient Admission Increases COVID-19 Case Detection in Homa Bay (Kenya)
Msfocp Labo*, Norah Odidi, Newton Ambaisi, Sonia Guiramand, Marie-Josee Uwimbabazi, Clair Mills*

5266112 | Characterization of Shiga Toxin-producing Escherichia Coli in Raw Beef from Informal and Commercial Abattoirs
Lamech Mwapagha*, Kaarina Nehoya, Ndinomholo Hamatui, Renatus Shilangale, Harris Onywera, Jeya Kennedy*

5266566 | Prevalence of Anaemia in Children Attending Yusuf Dantsoho Memorial Hospital, Tudun Wada, Kaduna South Local Government Area of Kaduna State, Nigeria
Jonathan Onyekachi Peter*, Gabriel Patrick, Amina Muazu, Olufunke Deborah Abolarin*

5266589 | COVID-19 Case Management and Co-Morbid Illness; Outcome in a Low Resource Setting in Western Nigeria
Saheed Usman

The Role of Laboratories in Outbreak Preparedness and Response

5228188 | Analysis of Laboratory Turnaround Time of the Positive Covid-19 Cases in Zambia-2020 to 2021
Thelma Shinjeka, *Situmbeko Mwangala, Kunda Musonda, Mwaka Monze, Otridah Kapona, Nyambe Sinyange*

5228408 | Panbio Rapid Antigen Test Not Useful in Hospitalised Paediatric Patients
Mathilda Claassen, *Marieke Van Der Zalm, Gert Van Zyl, Wolfgang Preiser, Helena Rabie*

5266052 | Performance Evaluation of SARS-CoV-2 Antibody Test (Lateral Flow Method) at Bacteriology and Virology Laboratory, Aristide le Dantec Hospital, Dakar
Awa Ba, *Aissatou Ahmet Niang, Gora Lo, Assane Dieng, Khardiata Gueye Ndiaye, Abou Koundio, Ibrahima Faye, Halimatou Diop-Ndiaye, Makhtar Camara*

5266197 | Detection of SARS-CoV-2 Infection by RT-PCR In North-Central Nigeria
Christopher Chime, *Monday Tola, Abubakar Abdullahi, Manji Obed, Sam Peters, Charles Mensah, Patrick Dakum, Alash'le G Abimiku*

5266385 | Process of Laboratory Setup and Quality Indicator Monitoring for SARS-CoV-2 Molecular Testing in Response to an Outbreak in a Resource-limited Setting in Kenya
Jully Okonji, *Edwin Ochieng, Noah Hull, Rufus Nyaga, Reshma Kakkar, Samantha Musumeci, Maria Landron*

The Threat of Antimicrobial Resistance

5199901 | Evaluating Fluoroquinolone Resistant and Susceptibility Pattern in Seven States at Seven Tertiary Health Facilities in North Western Nigeria
Adeola Adeleye, Auwalu. H Arzai, ***Feyisayo Jegede***, *Feyisayo Jegede*

5237179 | Blood Culture Testing Outcomes Among Non-Malarial Febrile Children at Antimicrobial Resistance Surveillance Sites in Uganda, 2017-2018
Rogers Kisame

5237189 | Point Prevalence Survey of Antimicrobial Use at Three Rural District Hospitals in Rwanda
Sandra Urusaro, Mariella Munyuzangabo, Carol M. Mugabo, Jean De Dieu Gatete, Emmanuel Kayitare, Jean Claude Munyemana, Esperance Uwayitu, Marthe Yankurije, Alphonse Nshimiryo, ***Fredrick Kateera***

5237435 | Phenotypic Profile and Antibiogram of Biofilm-Producing Bacteria Isolates from Diabetic Foot Ulcers in Zaria, Nigeria
Yahaya Usman, *Adamu Girei Bakari, Idris Nasir Abdullahi, Abdurrahman Elfulaty Ahmad, Fatima Bello, Solomon Atiene Sagay, Adebola T. T. Olayinka*

5265102 | Bacteremia Isolates Before and During the COVID-19 Pandemic in Ibadan, South West Nigeria
Ifiok Udofia, *Ibadan Setaplus Nigeria Investigators*

5266202 | Molecular Studies of Primary Drug-Resistance in Mycobacterium Tuberculosis Among Presumptive Tuberculosis Patients in North West, Nigeria
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ORAL SESSIONS

Tuesday, 16 November | 11:00 – 12:30
THE OUTBREAK EFFECT

ORAL SESSION 2500
OUTBREAKS, EMERGING PATHOGENS AND DISEASE BURDEN

CHAIRPERSONS:
Nadine Abiola; Marguerite Massinga Loembé

5237272 | Human Papillomavirus Infections and the Impact of Viral Load in Women Attending the Gynecology Clinic at Dr George Mukhari Academic Hospital, South Africa

Varsetile Varster Nkwinika[1], Tebogo Lorraine Mashishi[2], Teboho Amelia Tiiti[3], Johny Nare Rakgole[2], Ramokone Lisbeth Lebelo[2]
[1]South African Vaccination and Immunisation Centre (SAVIC), Sefako Makgatho Health Sciences University, South Africa;
[2]National Health Laboratory Service (NHLS), Department of Virological Pathology, Sefako Makgatho Health Sciences University, South Africa;
[3]Department of Virological Pathology, Sefako Makgatho Health Sciences University, South Africa

BACKGROUND: There is an unacceptably high incidence rate of cervical cancer in South Africa. High viral load levels of High-risk human papillomavirus (HR-HPV) is associated with persistent infection and development of CIN 2 or worse (CIN 2+). Data on the relationship between viral load and the degree of cervical lesion is controversial. This study reports on the prevalence of HR HPV infections and the impact of viral load at different stages of cervical lesions.

METHODS: Analytical study design was used. Ethical clearance was received from the Sefako Makgatho Health Sciences University Research Ethics Committee (SMUREC) with reference number SMUREC/M/44/2018: PG. A total of 306 endo-cervical samples were collected from women aged 18 years and older, and preserved in ThinPrep PreservCyt® Solution (Hologic Inc.). HR HPV DNA was extracted using Abbott mSample Prep System DNA. The HPV genotyping and viral load quantification were performed using Anyplex™ II HPV28 Detection assay (Seegene HPV assay). Liquid-based cytology slides were prepared using ThinPrep T5000™ system and stained manually using Pap stains. Inferential data analysis and logistic regression analysis was performed using IBM SPSS v23 software.

RESULTS: There was high HPV DNA prevalence (69.0%) and the most prevalent HR HPV types were HPV 16 [67/306 (21.9%)]; HPV 66 [57/306 (18.6%)] and HPV 58 types [54/306 (17.6%)]. HPV DNA prevalence increased from 12.3% in women with normal cytology to 14.1% in women with HSIL. High viral load levels were more suitable for predicting the progression of (4.7%) HSIL cases, with OR of 3.306, (95% CI = 1.539–7.101, P=0.003).

CONCLUSION: The risk of CIN significantly increases with high viral load. Thus, viral load may be used as a surrogate indicator for persistence and predict risk of cervical lesions. Our findings suggest that patients with high viral loads are at risk for disease progression and should be managed carefully.

5265836 | The Burden of Human Coronavirus Infection in Children Hospitalized with Severe Lower Respiratory Tract Infection in Cape Town, South Africa (2012 – 2013)

Abdulmumuni Samuel Aliyu
University of Cape Town, South Africa, Nigeria

BACKGROUND: In order to better understand the epidemiology and burden of human coronaviruses (HCoV) - NL63, HKU1, OC43, and 229E in South Africa, their role in the etiology of childhood pneumonia needs to be described.

METHODS: We used data collected between September 2012 – September 2013 from children aged <13 years with lower respiratory illness at Red Cross War Memorial Children's Hospital. Respiratory samples including a nasopharyngeal swab (NP) and induced sputum (IS) were taken and tested for the four strains of coronaviruses using FTD33 multiplex real-time PCR.

RESULTS: A total of 460 respiratory samples were analyzed. of these, 258 (56.0%) were male and 19 (4.1%) HIV infected. The median age of the children was 8 (IQR 4-18) months. Nasopharyngeal (NP) samples were obtained from 460 children while induced sputum (IS) was not available for six children due to sample loss prior to analysis, leaving 454 available for analysis. A total of 42 (9.1%, 95% CI 6.7- 12.1%) participants tested positive for HCoV in at least one of the two specimens. PCR was able to detect a total of 35 (7.7%) cases from the 454 tested IS specimens compared to 23 (5.0%) detected out of 460 NP samples. The commonest detected HCoVs was OC43 with 20 (4.3%) detected from either NP/IS specimen. Infants aged 6 – 18 months had a higher positivity for HCoV compared to other age groups.

CONCLUSION: Human coronaviruses are common in young infants with lower respiratory illness. Optimal management outcomes of patients will depend upon robust epidemiological data and information.

5224919 | Bacteria Profile Associated with Bacteriuria in Pregnancy at the Yaounde University Teaching Hospital (CHUY)

Barry Assangwing Nkemontoh[1], Moses Njutain Ngemenya[2]
[1]District Hospital Limbe, Cameroon; [2]University of Buea, Cameroon

BACKGROUND: The increased risk of bacteriuria in pregnancy poses threats to mother and fetus. Diagnosis of bacteriuria in most local settings is via urinalysis and urine microscopy causing empiric treatment based on limited available data on uropathogens and their antibiotic resistance pattern (ARP). With rising resistance rates and significant geographical variation of uropathogens to antibiotics, studies to increase knowledge on spectrum of bacteria associated with bacteriuria in pregnancy (BiP) and their ARP at local and national levels are important in setting up an evidence based empiric treatment for BiP.

METHODS: All pregnant women with at least 48 hours of no antibiotic therapy were conveniently and consecutively selected for this cross-sectional descriptive study following their consent. Aseptic collection of urine specimen preceeded macroscopic and biochemical analysis, inoculation onto CLED and MacConkey media, then microscopic and cytologic analysis. Antibiogram was based on the disk diffusion principle. Testing for Asymptomatic bacteriuria (ASB) was based on guidelines outlined by the Infectious Diseases Society of America. API 20E was implemented in identifying isolates. Logistic regression and chi-square test were performed using EPI info version 7.2 statistical software.

RESULTS: Significant bacteriuria was seen in 26.2% and ASB in 9.5% of the 84 study participants. Pyuria (OR=6.7, 95% CI=1.4-30.8, P=0.01) was the strongest predictor of bacteriuria. Escherichia coli and Coagulase negative staphylococci were the most common uropathogens. Less than 20% of isolates were resistant to nitrofurantoin and gentamicin.

CONCLUSION: Bacteriuria occurs in 1 of every 4 pregnant women and ASB in 1 of every 10 pregnant women. Uropathogens prevalent in bacteriuria were equally prevalent ASB. Nitrofurantoin and gentamicin can empirically treat BiP. Isolates that were resistant to atleast one antiobiotic (86.7%) were the most frequent cause of BiP.

5266365 | Isolation, Identification and Antimicrobial Resistance Profile of Pathogenic Bacteria Isolated from Clinical Samples in a Rural Remote Community

Paul Olatinwo[1], Ifeoluwa Akintayo[1], Veronica Ogunleye[2], Anderson Oaikhena[1], Jolaade Ajiboye[1], Erkison Odih[3], Oluwafemi Popoola[2], Kathryn Holt[4], Iruka Okeke[1]
[1]Department of Pharmaceutical Microbiology, Faculty of Pharmacy, University of Ibadan, Nigeria., Nigeria; [2]College of Medicine, University of Ibadan, Nigeria., Nigeria; [3]University of Copenhagen, Copenhagen, Denmark., Nigeria; [4]Department of Infectious Diseases, Central Clinical School, Monash University, Australia, Australia

BACKGROUND: Effective surveillance for antimicrobial resistance is necessary to quantify the problem and measure the impact of interventions. In Nigeria, as in most of Africa, surveillance sentinels are tertiary care centres, which largely manage referral cases. We hypothesized that these sentinels yield surveillance data that is less representative of other settings. We equipped a remote rural laboratory to offer basic clinical bacteriology services and compared the spectrum of isolates, and their resistance profiles to tertiary care-derived data.

METHODS: A remote laboratory at rural Ibarapa, Oyo State, Nigeria was equipped and staffed to offer bacteriological services. Blood and other clinical specimens received from Ibarapa Central Local Government Area and environs were processed using standard microbiological procedures. Isolates were identified biochemically and disc-diffusion antimicrobial susceptibility testing was conducted according to Clinical Laboratory Standard Institute protocols. Statistical comparisons were done using the Fischer's exact test.

RESULTS: The Ibarapa laboratory processed 184 clinical specimens between March 2020 and July 2021 with a median time for return of clinical bacteriology results of 3 days. Seventy-six isolates from over 12 genera were obtained with recovery rates of 8 (10.5%), 10 (13.2%), 58 (76.3%) from blood, urine and swab cultures, respectively. Organism isolation profiles were compared with data from a proximal sentinel site and *Klebsiella* and *Staphylococcus aureus* isolates were highly prevalent at both. Resistance profiles were markedly different for many agents with amikacin and beta-lactam resistance unseen and significantly lower ($p<0.05$) in *Klebsiella* from Ibarapa, compared to the tertiary sentinel. We also recorded markedly higher gentamicin and cefoxitin resistance among Ibarapa *S. aureus* isolates ($p<0.02$)

CONCLUSION: This study found significantly different resistance profiles from those of a nearby tertiary hospital surveillance site in addition to diverse pathogens at the rural laboratory. National surveillance systems should include sentinels below the tertiary care level.

5266726 | Association Significative Entre L'élévation des Taux Antigéniques du Facteur de Von Willebrand et la Mortalité Chez les Patients Atteints de COVID-19

Mohamed El Horri[1], Souhil Nour Elain Touati[1], Imene Harrane[1], Abdelkrim Chikh Khelifa[1], Ibrahim Khachaa[1], Fatima Seghier[2]
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INTRODUCTION: La coagulopathie associée à la covid-19 a un impact pronostic important et est corrélée à l'issue défavorable des patients. Les taux élevés d'antigène du facteur de Von Willebrand, plaident en faveur d'une inflammation endothéliale importante et constituent le reflet fidèle de cette coagulopathie. L'objectif de notre étude était d'étudier la valeur pronostique de ce marqueur dans la COVID-19.

MATÉRIEL ET MÉTHODES: Une cohorte pronostique a été réalisée, portant sur des patients admis pour prise en charge d'une infection respiratoire par le SARS-Cov-2. Toutes les données cliniques et paracliniques ont été enregistrées à l'admission, ainsi que le dosage antigénique du Facteur de Von Willebrand par méthodes immuno-turbidimétrique. Les patients ont été suivis pendant la durée de l'hospitalisation. Le critère de jugement était la survenue du décès.

RÉSULTATS: 55 patients atteints de COVID-19 ont été inclus dans cette étude. 70.9% des cas étaient des hommes, avec une moyenne d'âge de 64 ans [IC : 59 – 68]. 74.5% des formes étaient modérées, 14.5% sévères et 11% critiques. Au cours de cette cohorte, 29.1% des patients sont décédés.

L'élévation du VWF-Ag au-delà de 487.2%, prédisait la mortalité avec une sensibilité 56.25% de et une spécificité de 84.62%. Cette valeur seuil était significativement associée au décès chez les patients atteints de COVID-19, avec un H.R = 5.88 [IC : 1.63 – 21.19]. Les patients qui avaient des taux supérieurs à cette valeur seuil avaient une probabilité de survie de 37.1% à 13 jours d'hospitalisation contre 90.9% chez ceux qui avaient des taux inférieurs à cette valeur seuil (p = 0.032 ; Khi-deux = 4.596).

CONCLUSION: Considérée comme témoin d'une stimulation massive des cellules endothéliales, l'élévation des taux antigéniques du facteur de Von Willebrand constitue de fait, un marqueur de mauvais pronostic chez les patients atteints par la covid-19.

5182313 | Methicillin-Resistant Staphylococcus Aureus in Ibadan, Nigeria: A Community Nasal Colonization Prevalence Study

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BACKGROUND: Nasal carriage of Community-Acquired Methicillin-resistance Staphylococcus aureus (CA-MRSA) is recognized for its rapid community spread and tendency to cause various infections especially in communities with a large population where personal hygiene is poor. We sought to investigate the prevalence and evaluated the possible risk factors of CA-MRSA among healthy population.

METHODS: Nasal swabs from healthy volunteers using the multi-stage sampling technique were cultured for Staphylococcus aureus. Isolates were identified by conventional biochemical tests, Microbact™12S identification kit and 16SrRNA. Antibiotic susceptibility testing was performed using the Kirby-Bauer disc diffusion technique. Isolates were further investigated for methicillin-resistance by using the cefoxitin disk diffusion test. MecA and Nuc genes of the isolates were amplified via polymerase chain reaction.

RESULTS: The results showed 9.4% prevalence of MRSA nasal carriage. The residents of Ibadan North local government area (Fisher's Exact = 1.8962, P = .028) and Egbeda local government area (Fisher's Exact = 2.7222, P = .006) are likely to carry MRSA than any other local government area in Ibadan, Nigeria. The antimicrobial resistance patterns of the isolates revealed high resistance to Oxacillin (96.9%). PCR analysis showed that mecA gene was present in all 66 (100%) MRSA isolates. Male-gender ($\chi 2 = 8.849$, P = .003), Adults; 40-50 years old ($\chi 2 = 9.842$, P = .002), low educational background ($\chi 2 = 36.817$, P < .001), recent hospital visitation ($\chi 2 = 8.693$, P = .003) are some of the factors that are observed in this study to be associated with MRSA infection

CONCLUSION: The study established a high prevalence and resistance burden of CA-MRSA in the population. This poses a serious public health concern in the region and necessitates the demands for continuous surveillance on the colonization state of CA-MRSA.

ORAL SESSION 2505
THE ROLE OF LABORATORIES IN OUTBREAK PREPAREDNESS AND RESPONSE

CHAIRPERSONS:
Francesco Marinucci; Beatrice van der Puije

5237136 | Cost-Effective Fast Turn-Around Surveillance Method for SARS-CoV-2 Variants of Concern

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BACKGROUND: SARS-CoV-2 Variants of Concern (VOC) like the highly transmissible delta (B.1.617.2) variant pose a serious threat to global public health. It is critical to conduct surveillance testing as the pandemic moves into an endemic phase. While whole genome sequencing (WGS) is conventionally used for surveillance testing; it is costly, resource intensive and turn-around time is not quick enough if any public health counter measures were to be implemented. In this study, we describe an alternative, low-cost quick PCR-based method for the detection and discrimination of 4 currently designated VOCs; *alpha* (B.1.1.7), beta (B.1.351), *gamma* (P.1), and delta (B.1.617).

METHODS: 46 SARS-CoV-2 positive samples were evaluated using an 8 Mutation of Concern (MOC) panel (N439K, K417T, D215G, Del.H69/V70, E484K, P681R, L452R, Q27STOP) at the Life Science Testing Center at Northeastern University. RNA was extracted using the MagMax™ Viral/Pathogen II Nucleic Acid Isolation Kits in conjunction with Agilent Bravo™ Liquid Handlers followed by PCR on the Applied Biosystems™ QuantStudio™ 6 instrument. Results of the MOC panel were verified against WGS using the Ion Torrent GeneStudio-S5 System. In addition, strain identification was assessed against self-reported vaccinated status.

RESULTS: The 8-MOC panel was able to reliably identify the 46 SARS-CoV-2 VOC samples; *alpha* (n=21), *beta* (n=2), *gamma* (n=5) and delta (n=18). The PCR-based genotyping results were in complete agreement with WGS results. Majority of the positives (41/46) were identified in unvaccinated cases and breakthrough infections were identified in 5 cases (1 *beta*, 1 *gamma*, 3 *delta*). All breakthrough infections were associated with mild symptoms.

DISCUSSION: PCR-based genotyping using a MOC panel is an accurate method for identification of known SARS-CoV-2 variants. It offers a high throughput, economical and quick solution for SARS-CoV-2 surveillance, especially in areas where sequencing capacity is limited and allows to preserve precious WGS resources for identification of new variants.

5237768 | Enhancing Timely Access to Aggregate Laboratory Testing Information in Zambia

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BACKGROUND: Zambia has over 389 hospitals and health centers providing laboratory services across the country with varied levels of available and standardized electronic information management systems, leading to limitations in required aggregation of national laboratory diagnostic data. Timely access to aggregate test information remains key to epidemiological surveillance, planning and policy guidance. The Ministry of Health (MoH), working closely with the Association of Public Health Laboratories and other collaborating partners, instituted a process to ensure data accuracy and appropriate access to these laboratory data.

METHODS: A single unlimited countrywide license was negotiated with a commercial Laboratory Information Management System (LIMS) provider and adopted for use in public health laboratories across the country. The Open Laboratory Data Repository (OpenLDR), an open source, laboratory data warehouse, was deployed at MoH to aggregate information from laboratories using LIMS. A LIMS dashboard with key performance indicators (KPI) was developed with input from stakeholders in the National Laboratory Technical Working Group (TWG).

RESULTS: The LIMS was deployed in thirty-five laboratories in the ten provinces against a target of 60 by September 2021 under this unlimited license. Data from laboratories was routinely aggregated to the OpenLDR in near-real-time via internet, making on-demand information access a reality. The HIV program KPIs were completed on the dashboard providing aggregate HIV viral load and early infant diagnosis test information to guide laboratory diagnostic network optimization and programme planning. Rights to the LIMS dashboard were disseminated to both MoH and organizational partners to enhance data use and decision making.

CONCLUSION: Standardization and integration of electronic health systems remains fundamental to the efficiency and improvement of health care services. The unlimited country LIS license in Zambia enables more laboratories to improve their data management and allows for managed access, timely data acquisition and use of laboratory data by all stakeholders.

5226749 | Analysis of Two Approaches for the External Quality Assessment of COVID-19 Testing Laboratories In Burkina Faso

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BACKGROUND: External Quality Assessment (EQA) in COVID-19 diagnostic laboratories is imperative to ensure quality laboratory services. In 2020, with the closure of borders, samples for external quality control (EQC) were unlikely to be available in local commerce. This is how ASLM, in collaboration with the Department of Medical Biology Laboratories (MoH) of Burkina Faso, organized two different EQA approaches in COVID-19 testing laboratories.

METHODS: Faced with the difficulty of accessing QC in local commerce, the first approach was to retest samples taken from 10 laboratories using rRT-PCR platforms by the Flu National Reference Laboratory (F-NRL). Then, during the second approach, 15 laboratories were enrolled in an EQA PT program with the Canadian supplier Oneworld Accuracy (1WA) for two rounds.

RESULTS: The retesting carried out by F-NRL focused on 150 samples (10 negative samples and 05 positive samples per laboratory) collected in 10 COVID-19 molecular diagnostic laboratories, which made it possible to observe 05 discordant laboratories. Subsequently, these laboratories benefited from formative supervision focused on corrective actions.
For 1WA EQA PT program, 15 sample panels were sent to 15 laboratories. After submitting their test results to the OASYS online platform in the first round, only one lab was non-compliant. Immediate formative supervision was organized in this laboratory. During the second round of EQA organized by the same supplier, all 15 registered laboratories were compliant.

CONCLUSIONS: These two EQA sessions assessed competence, laboratory performance, reliability of analytical methods and accuracy of reporting, as well as monitoring of unacceptable EQA results. Indeed, these two evaluation procedures revealed non-conformities in the laboratories which made it possible to establish corrective actions for formative supervision.

5265017 | Establishing a Low-Cost Sub-National Specimen Referral System for Epidemic Response: A Pilot Study

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BACKGROUND: The absence of standardized referral systems in Nigeria has resulted in underutilization of in-country PCR testing capacity, long laboratory testing turn-around time (TAT), high cost of specimen shipment, low accessibility to laboratory testing and immense biosafety and biosecurity concerns. Specimen referral systems (SRSs) are required to increase access to testing and reduce testing turnaroundtime.

METHODS: Using the hubs and spokes distribution model, we mapped COVID-19 sample collection centers (CCCs) to testing laboratories in two states and contracted a third-party logistics company to transport samples using bikers. We developed a Specimen Referral Management System (SRMS) to monitor the referral pathway and provided hands-on training to health workers on utilization of this system. After successful establishment of the SRS and field deployment of data tools, we used data generated to conduct analysis on referral cost and SRMS utilization. 135 health workers were trained in SRMS, biosafety, and biosecurity in both states. We also conducted informant interviews with bikers to identify challenges with sample pick and delivery.

RESULTS: 30 CCCs were mapped to four laboratories in Edo and 15 CCCs were mapped to two laboratories in Nasarawa state. 2165 samples were shipped at USD 1030.5 over a two-month period, making the average cost of shipping a sample USD 0.47. Only 3% of samples shipped were logged in SRMS. The key factor contributing to low utilization of the SRMS was low ownership of smartphones among riders.

CONCLUSION: A major factor determining the usefulness of establishing intra-state SRSs in the volume of samples available for transport. Specimen referral during pandemics can be cost effective if bikers are used to transport samples over relatively long referral routes (9.8-120km). Arrangement of SRSs in simple algorithms with stakeholder's roles clearly delineated increases overall efficiency of the system and minimizes the occurrence of missed sample pick-ups.

5216791 | Building Laboratory Capacity in PEPFAR-Supported Countries. Will We Be Ready for the Next Pandemic?

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BACKGROUND: The COVID-19 pandemic has relied on existing laboratory networks and continues to test existing laboratory capacity and quality globally. This abstract illustrates how U.S. President's Emergency Plan for AIDS Relief (PEPFAR) programs have scaled up quality laboratory testing from 2018 to 2020.

METHODS: Data were cleaned and analyzed using PEPFAR's Monitoring, Evaluation, and Reporting standardized datasets at the global (all PEPFAR countries) level, by testing site, test type, and year (2018-2020). A site (laboratory or point-of-care (POC)) is defined as a point within a facility that performs any of the following tests: HIV serology, Early Infant Diagnosis of HIV (EID), HIV viral load, TB diagnostics: GeneXpert, AFB, or culture, or CD4. A single laboratory will likely have multiple sites. Laboratory quality was assessed by enrollment in continuous quality improvement (CQI) programs, accreditation/met qualifications for certification at labs/POC sites, and enrollment in proficiency testing (PT).

RESULTS: Across PEPFAR in 2018, 2019, and 2020 65% (n=34,030), 67% (n=36,883), and 73% (n=37,657) of all testing sites (laboratory and POC) were enrolled in CQI respectively. The number of sites certified/accredited increased each year from 2018-2020 (n=2,279, 2,792, 3,791). Three of the seven test types reported their greatest number of sites certified/accredited in 2020 from 2018-2020: serology (1,750, 2,299, 3,176), EID (37, 49, 76) and TB GeneXpert (127, 121, 167). PT enrollment was reported for 65% (38,194), 75% (42,972), and 68% (38,660) of sites across the three fiscal years.

CONCLUSIONS: Despite the challenges of 2020, the PEPFAR program globally continued to report an increase in the percent of sites enrolled in CQI and the number of sites accredited/certified. PT enrollment decreased in 2020 at the global level. Quality laboratory testing is the backbone of health systems; continuous efforts to strengthen laboratory quality are needed to fight current pandemics and prepare for future outbreaks.

5182573 | SARS-CoV-2 Specific Immune Responses in Healthcare Workers With and Without Confirmed Infection at Charlotte Maxeke Johannesburg Academic Hospital (CMJAH), 2020

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BACKGROUND: Healthcare workers (HCWs) are a high-risk group for the severe acute respiratory syndrome-coronavirus-2 (SARS-CoV-2) infection, the aetiological agent of coronavirus disease of 2019 (COVID-19). There is limited knowledge of viral dynamics and immune response kinetics following SARS-CoV-2 infection that disadvantages the use of antibody tests in diagnostic laboratories. In this study, our overall aim was to determine the seroprevalence and characterize the SARS-CoV-2 specific immune responses in HCW with and without confirmed SARS-CoV-2 infection, Gauteng, South Africa, 2020.

METHODS: A descriptive analysis of serum samples collected from volunteers Charlotte Maxeke Johannesburg Academic Hospital (CMJAH) HCWs beginning of the 2nd-wave (November 2020). Samples were tested for SARS-CoV-2 IgG antibodies using the Abbott Diagnostics SARS-CoV-2 IgG enzyme-linked immunosorbent-assay on Architect i1000sr immunoassay-analyzer (Abbott Laboratories, USA). Participants were requested to complete a questionnaire indicating their demographic data and details about exposure to SARS-CoV-2 infection.

RESULTS: Seventy-six of 79 (96.2%) HCWs were included for data analysis, comprising laboratory workers (LW) (77.6%, 59/76), National Health Laboratory Service (NHLS) phlebotomy staff (7.9%, 6/76), hospital HCWs (5.3%, 4/76) and other health staff (OHS) (9.2%, 7/76). Most of the participants were middle age (mean = 42.5; SD = 14.5). Fourteen of 76 (18.4%) reported having a co-morbid disease. The prevalence of SARS-CoV-2 IgG positivity was 34.2% (26/76); of these, 9.0% reported no symptoms and 25.2% had symptomatic illness. None of the seropositive HCWs reported COVID-19 related hospitalization. Fifty participants (65.8%) tested negative for SARS-CoV-2 IgG (LW 51.4%, NHLS phlebotomy-staff 1.3%, CMJAH HCW 5.3% and OHS 7.9%).

CONCLUSION: The seroprevalence was high amongst HCWs following the 1st-wave; however, the susceptible pool size was also of concern. Thus, SARS-CoV-2 IgG plays a significant role in determining the immunity gap for persons with an increased risk of infection and COVID-19 and will contribute to surveillance estimates of the burden disease.

ORAL SESSION 2510
THE THREAT OF ANTIMICROBIAL RESISTANCE

CHAIRPERSONS:
Geetanjali Kapoor; Richard Walwema

5237306 | Rectal Carriage of Extended-Spectrum-Beta-Lactamase-Producing Enterobacteriaceae Among Neonates Admitted to a Tertiary Referral Hospital, South-Western Nigeria

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BACKGROUND: Rectal carriage of Extended-spectrum β-lactamase-producing Enterobacteriaceae (ESBL-PE) by neonates increases the chances of neonatal infections by these drug-resistant organisms. This study investigated the epidemiology and resistant determinants of ESBL-PE colonising rectums of neonates admitted to a tertiary hospital in South-west Nigeria.

METHODS: A cross-sectional study conducted from September - November 2019. Involved sampling of neonatal stool within the first 24 hours of admission and then weekly until discharged or deceased. Stool isolates were identified by standard biochemical methods, and antibiotic susceptibility testing was by modified Kirby-Bauer method. Phenotypic testing for ESBL production was by standard protocol. Polymerase-chain-reaction protocols were used to determine ESBL- genes. Chi Square was used to determine association and logistic regression for independent risk factors.

RESULTS: Stool samples from 127 neonates yielded 182 non-duplicate Enterobacteriaceae from 59 neonates; 105 (57.7%) were phenotypically confirmed ESBL-PE. The ESBL coloniser prevalence was 46.5% (59/127). At the point of admission, 23 neonates were colonised with ESBL-PE and 36 neonates over the course of the study. ESBL-PE acquisition rate was 34.6% (36/104). Common ESBL-PE isolated were *Klebsiella Pneumoniae* 16.2% (17/105), *Enterobacter cloacae* 16.2% (17/105), *Klebsiella oxytoca* 13.3 % (14/105), *Enterobacter agglomerans* complex 13.3 % (14/105), *Escherichia coli* 9.5% (10/105), *Citrobacter freundii* 6.7% (7/105) and *Cirtobacter sedlakii* 4.8% (5/105), *Klebsiella ornithinolytica* 4.8% (5/105). Sixty-four isolates haboured 122 ESBL-determining genes including blaCTX (47/122), blaTEM (47/122) and *bla*SHV (28/122) with multiple genes detected in majority (43, 67.2%) of isolates. Prolong rupture of membrane (AOR=0.297; p <0.004), number of neonates in the same admission cubicle (AOR=0.053; p < 0.001) and presence of a known ESBL-PE coloniser in the admission cubicle (AOR=2.272; p < 0.004) were the independent risk factors for ESBL-PE rectal colonisation.

CONCLUSIONS: Rectal colonisation by ESBL-PE is high and this underscores the need for review of the neonatal admission protocols and care in our hospitals.

5237458 | Antimicrobial Susceptibility Patterns of Common Uropathogens During 2018 – 2020 in a Regional Hospital in KwaZulu Natal Province, South Africa

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BACKGROUND: Urinary tract infections (UTIs) are a common bacterial infection, affecting millions worldwide and amounting to billions in health care cost. Globally, treatment options for UTIs have been well established, with ciprofloxacin being considered the drug of choice when treating uncomplicated UTIs. However, the rampant misuse of antibiotics has led to an overwhelming increase in antimicrobial resistance. Although this is seen in multiple studies around the world, there is a dearth of information on antimicrobial resistance rates from the developing world, specifically South Africa. The objective of this study was to describe the antimicrobial susceptibility patterns of common uropathogens isolated from urine specimens collected from a regional hospital located in KwaZulu-Natal, South Africa.

METHOD: A retrospective analysis of antimicrobial susceptibility data of positive urine specimens from RK Khan Hospital, a regional hospital in KwaZulu-Natal, South Africa during 2018 – 2020 was carried out. The VITEK® 2 – (Biomerieux) automatic system was used to perform identification and sensitivity, and results were interpreted using Clinical and Laboratory Standards Institute breakpoints. The data was collected from the laboratory information system.

RESULTS: Between 2018 and 2020, 4272 urinary organisms were isolated,among these 3044 uropathens met the criteria. of which, *Escherichia coli* was the most frequent cause of UTI (1603; 53%), followed, at a distant second, by *Klebsiella* spp (437;14%). Both *E. coli* and *Klebsiella* spp showed high rates of resistance to AMC (29.8% and 42.3%) and ciprofloxacin (37.7% and 30.4%). Nitrofurantoin resistance was low for *E. coli* at 6.2% but high for *Klebsiella* spp at 61.3%.

CONCLUSION: *E.coli* remains the most commonly isolated uropathogen. Resistant rates for frequently prescribed oral treatment options namely AMC and ciprofloxacin are alarmingly high for both *E. coli* and *Klebsiella* spp. This highlights the importance of regular local antimicrobial surveillance so as to inform appropriate empiric therapy.

5237733 | Detection of Antibiotic Activity in Urine Using A Bioassay in Samples Patients with Suspected Urinary Tract Infections Presenting to Primary Care Clinics

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BACKGROUND: Antibiotics prior to sample collection can affect the yield of cultures leading to diagnostic uncertainties and incorrect prescriptions. Because of socioeconomic constraints, patients may access antibiotics in the informal sector or through private pharmacies to avoid clinic visits. This study aimed to evaluate a simple urine bioassay to investigate prior antibiotic exposure among patients presenting to primary care with suspected urinary tract infections (UTIs) in Harare, Zimbabwe.

METHODS: Participants with UTI symptoms were prospectively enrolled in ten primary healthcare clinics and urine samples were collected. For the bioassay, stored urine aliquots were tested. A uniform lawn of the indicator organism *Escherichia coli* ATCC25922 was inoculated on Muller Hinton agar. Blank filter paper discs were dispensed on the inoculated plate and 20µL sample were added followed by incubation at 37C for 24 hours before reading. Any inhibition of growth was considered positive for the presence of antibiotic traces.

RESULTS: The study enrolled 1164 patients and 1129 (97.0%) had urine samples stored and were analysed. Median age was 35.9 years, 724 (64.1%) were female and 380 (36.8%) were HIV-positive. The antibiotic assay was positive in 264 (23.4%) patients. Urine culture yield was lower in patients with a positive bioassay than in those with a negative result, 25.0% vs. 32.8%, p=0.02. of the 264 patients with a positive bioassay, 116 (43.9%) patients reported either having taken antibiotics prior to clinic presentation or being on co-trimoxazole prophylaxis while 148 (56.1%) did not report any prior exposure.

CONCLUSION: The results of this study highlight the high prevalence of antibiotic use occurring in the community prior to accessing healthcare with most use not being reported by patients. The disc-diffusion based antibiotic bioassay is a simple and inexpensive way of determining prior antibiotic exposure. The method may be considered to evaluate community antibiotic use.

5236928 | Class 1 Integron-Integrase Gene(Inti1) Detection in Multi-Drug Resistant Organisms Isolated in Clinical Samples from Niger Delta University, Yenagoa, Bayelsa State

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BACKGROUND: Integrons are common features of bacterial genomes that allow efficient capture and expression of new genes which are embedded in gene cassettes. Class 1 integron are mostly identified among clinical Gram negative bacteria as the major factor responsible for drug resistance. This study was aimed at detecting the presence of the integron-integrase 1 gene (inti1) in Gram negative bacteria.

METHODS: A total of 121 clinical samples were collected, of which 99(81.8%) were urine samples, 5(4.13%) were Endocervical swabs, 4(3.31%) were sputum samples, 4(3.31%) were High vaginal swabs, 6(4.95%) were wound samples and 3(2.48%) were ear swabs, 45(37.2%) samples were collected from males and 76(62.8%) were collected from females. The samples were analysed and the isolates were determined using Standard Bacteriological methods. Antibiotic susceptibility testing was carried out using Modified Kirby Bauer disc-diffusion method and the genomic DNA was extracted by boiling method. The presence of Inti1 gene was determined using Polymerase Chain Reaction. The findings showed that out of 121 samples analysed, a total of 95 isolates were obtained from the samples with *E.coli* having a high prevalence of 32(33.7%), followed by *Klebsiella oxytoca* 30(31.6%), *Klebsiella pneumonia* 21(22.1%), *Pseudomonas aeruginosa* 6(6.31%), *Enterobacter aerogenes* 3(3.2%) and *Citrobacter freundii* 3(3.2%). Antibiotics susceptibility pattern showed the resistance percentage of each of the antibiotics used; Gentamicin (50.5%) Pefloxacine (68.4), Narivid (67.4%), Streptomycin (81.1%), Septrin (66.3%) Chloramphenicol (70.5%), Spectinomycin (53.7%), Ciprofloxacin (56.8%), Amoxacillin (53.7%) and Augmentin (88.4%). Out of the 30 isolates selected for molecular analysis, the Inti 1 gene was detected in 26 isolates.

CONCLUSION: This study showed that there is high prevalence of class 1 integron in multi-drug resistant Gram negative bacteria. To prevent the development of multi-drug resistance bacteria, the judicious use of antibiotics should be avoided.

5266255 | Profil de L'antibiorésistances des Germes Responsables D'Infections Urinaires à L'Institut National de Santé Publique de Bamako de 2015 À 2019

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CONTEXTE : L'infection du tractus urinaire est l'une des pathologies les plus fréquemment rencontrées. Il s'agit d'évaluer le profil de l'antibio-résistance des germes responsables d'infections urinaires isolés de janvier 2015 à juillet 2019 à l'Institut National de Santé Publique (INSP) de Bamako, au Mali.

MATÉRIELS ET MÉTHODES : Il s'agit d'une étude, transversale, descriptive à collecte rétro-prospective, portant sur 1098 cultures positives des Examens Cytobactériologiques des Urines réalisés à L'INSP de Bamako. Les échantillons sont ensemencés dans des milieux de culture différents. L'incubation se fait à 37°C pendant 18 à 24 heures. L'identification et l'antibiogramme des bactéries ont été faite à l'aide de la galerie API 20 E de Biomérieux® et de l'Automate VITEK 2 Compact.

L'analyse des données a été effectuée sur le logiciel IBM SPSS (Statistical Package for the Social Sciences version 13.0) puis traité sur Excel 2016.

RÉSULTATS : 22 germes différents ont été isolés dont 3 étaient majeurs, à savoir Escherichia coli, Klebsiella pneumoniae, Staphylococcus aureus qui représentaient 86,4% du total des isolats. L'amoxicilline, l'Amoxicilline/Acide clavulanique et la Cefalotine ont été les antibiotiques les moins efficaces sur les espèces d'Entérobactéries avec des résistances respectives de 99,5%, 73,9% et 82,2%.

La résistance des Bactéries Non Fermentaires (BNF) la plus élevée était à la piperacilline/tazobactam (66,7%) et la plus faible était avec Ticarcilline/acide clavulanique avec (0%).Les Cocci à Gram positifs ont une résistance de 64,2% à la nitrofurantoine, et la plus faible avec la Vancomycine (6,0%).

Les Entérobactéries ont exprimé le phénotype PHN (pénicillinase de Haut Niveau) à hauteur de 26,1% , le phénotype BLSE (Bêtalactamase à Spectre Elargi) à hauteur de 36,5%.

CONCLUSION : La connaissance des bactéries responsables constitue un outil précieux pour le choix de l'antibiothérapie de première intention qui nécessite d'être adaptée au site de l'infection et au terrain sous-jacent.

5239450 | Antibiofilm Formation Activity, Resistant Genes Profiling and Detection of Virulence Factors of Toxigenic Vibrio Cholerae Isolates from Kisumu County, Kenya

Silas Awuor
Masogo Sub County Hospital, Kisii University, Kenya

INTRODUCTION: *Vibrio cholerae* can switch between motile and biofilm lifestyles with some of its strains forming biofilms in addition to production of various virulence traits and possessing antimicrobial resistance traits.

METHODOLOGY: A total of 119 *Vibrio cholerae* 01, biotype El Tor isolates collected during 2017 cholera outbreak in Kisumu County were used for this study. Biofilm assay, resistant genes profiling and detection of virulence factors were also done by use of standard procedures.

RESULTS: of the 101 confirmed *Vibrio cholerae* isolates, 80.2% isolates possessed the cholera toxin gene (*ctxA*), 98.0% harbored the *toxR* gene, 80.2% harbored the *inDS* gene, and 93.1% possess the SXT integrating conjugative element. Out of those 7 isolates which were resistance to most drugs four isolates strains and P. aeruginosa ATCC 10145 as a positive control formed biofilms while 71.42% of the isolates produced protease, 85.71% produced phospholipases, 71.42% of isolates has the ability to produce lipase and 100% were able to produce the haemolysin.

CONCLUSION: An understanding of this intricate signalling pathway is essential for the development of methods to treat and prevent the devastating condition caused by *V. cholerae*.

ORAL SESSION 2515
POLICY AND REGULATION FOR RESILIENT LABORATORY SYSTEMS AND NETWORKS

CHAIRPERSONS:
Karidia Diallo; Tjeerd Datema

5236634 | Mise En Oeuvre D'un Programme National D'Evaluation Externe de la Qualité Au Togo De 2016 À 2019: Leçons Apprises Et Pistes D'amélioration en Biochimie et Diagnostic du Paludisme

Kafui Codjo Kouassi[1], Améyo M. Dorkenoo[2], Komi Gbada[3], Yaovi-Gameli Afanyibo[4], Minogblon Têko[5], Adjane Koura[6]
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INTRODUCTION : L'évaluation externe de la qualité (EEQ), une des exigences de l'ISO 15189, aide à garantir l'exactitude des résultats en biologie clinique. L'objectif de cette étude était de mettre en exergue les pistes d'amélioration de la qualité des examens.

MATÉRIEL ET MÉTHODES : Il s'est agi d'une étude transversale, conduite dans 42 laboratoires médicaux. Des échantillons-tests fournis par le prestataire « One World Accuracy » du Canada, pour 49 examens de biochimie et des lames de goutte épaisse-frottis sanguin (GE/FS) ont été distribués une fois par semestre à tous les laboratoires participants (LP). Un groupe WhatsApp des responsables qualité de ces laboratoires a été créé pour le suivi des soumissions des résultats sur une plateforme dédiée et la gestion des résultats non-conformes. Les critères utilisés pour déterminer le taux de conformité étaient : i) les limites acceptables du Clinical Laboratory Improvement Amendements des Etats-Unis et ii) ceux de l'OMS pour le diagnostic du paludisme et l'identification de l'espèce. A été considéré comme satisfaisant, un niveau de performance d'au moins 80% de résultats conformes sur 2 campagnes successives selon l'OMS-AFRO.

RÉSULTATS : De 2016 à 2019, le nombre des LP est passé de 11 à 42. Transaminases, Gamma-Gglutamyl-Transférase, Phosphatase alcaline, Triglycérides ont été les examens ayant maintenu un taux de conformité ≥ 80% et ce à tous les trois niveaux de la pyramide sanitaire. Quant à la GE/FS, un niveau de performance acceptable a été obtenu en 2017, par 42% des LP pour la positivité du test et l'identification correcte de l'espèce plasmodiale.

CONCLUSION : l'expérience du programme d'EEQ au Togo a montré l'importance de cet outil pour l'amélioration de la fiabilité des résultats. Bien que la majorité des examens évalués ait atteint un niveau de performance acceptable, certains, surtout ceux de réalisation fréquente dont la glycémie, la créatininémie, la calcémie, la magnésémie, l›hémoglobinémie et la GE méritent qu'une attention particulière leur soit accordée.

5226104 | Equipment Management in Veterinary Laboratories: Implications for Pandemic and Epizootic Disease Preparedness and Learning Lessons from Past Disease Events

Jennifer Lasley[1], Emmanuel Appiah[2], Kazunobu Kojima[3], Stuart Blacksell[4]
[1]Preparedness & Resilience Department, International Standards & Science Directorate, World Organisation For Animal Health, Oie, France; [2]Digital Transformation & Information Systems Department, General Directorate, World Organisation For Animal Health, Oie, Ghana; [3]Global Infectious Hazards Preparedness Department, World Health Organization, Who, Switzerland; [4]Mahidol-Oxford Tropical Research Medicine Unit, Faculty of Tropical Medicine, Mahidol University, Thailand

BACKGROUND: Since the emergence of pandemic avian influenza, significant investments have been made into diagnostic and research laboratories in low-resource settings to detect emerging diseases as early and as close to their source as possible. often new, sophisticated equipment, such as real-time PCR and biosafety cabinets (BSC), are provided alongside consumables, reagents, and relevant training to achieve this goal. These investments have expanded diagnostic technical capacity in many countries, but challenges have emerged regarding sustainability to ensure laboratory equipment is safe and in good working order.

METHODS: We sought to quantify the amount of laboratory equipment in public veterinary laboratories and the situation regarding maintenance and calibration. Survey responses were received in mid-2019 describing approximately 40 items of common laboratory equipment.

RESULTS: This study recorded 68,445 pieces of equipment from 223 veterinary laboratories in 136 countries. 22% of equipment was not properly maintained, 46% was not properly calibrated, and 11% was out of service. There were notable differences in equipment maintenance and service capacity between income levels and geographical regions that raise concerns regarding the sustainability of donated equipment. Competencies to maintain and calibrate equipment existed in-house for 18% of equipment, and within one's country for 74% of equipment. In-house and local capacity for equipment maintenance and calibration also demonstrated notable differences by region and income.

CONCLUSIONS: The results presented here provide an opportunity to reflect and act on how to best support laboratories during and after the global response to the COVID-19 pandemic. The findings will inform stakeholders to better understand the challenges faced related to equipment management, to better plan to sustain investments made by partners, to design innovative and contribute towards more effective investments, as well as encourage manufacturers in their efforts to design fit-for-purpose equipment for low-resource settings.

5250738 | Country Adherence to WHO 2019 Recommendations on HIV Testing Strategies: A Policy Review Across the WHO African Region

Emmanuel Fajardo[1], Céline Lastrucci[1], Nayé Bah[2], Casimir Manzengo Mingiedi[3], Ndoungou Salla Ba[4], Fausta Shakiwa Mosha[5], Magdalena Barr-Dichiara[1], Muhammad Shahid Jamil[1], Anita Sands[6], Cheryl Johnson[1]
[1]Global HIV, Hepatitis And Sti Programmes, Who, Switzerland; [2]Regional office For Africa, Inter-Country Support Team For Western Africa, Who, Mali; [3]Regional office For Africa, Inter-Country Support Team For Central Africa, Who, Gabon; [4]Regional office For Africa, Inter-Country Support Team For Western And Central Africa, Who, Burkina Faso; [5]Regional office For Africa, Inter-Country Support Team For Southern Africa, Who, Zimbabwe; [6]Incidents And Substandard/Falsified Medical Products Team, Regulation And Prequalification Department, Who, Switzerland

BACKGROUND: In 2019, the World Health Organization (WHO) released updated guidelines on HIV testing services (HTS) recommending: a standard "three-assay" testing strategy requiring three consecutive reactive test results to make an HIV-positive diagnosis; dual HIV/syphilis rapid diagnostic tests (RDTs) as the first test in antenatal care (ANC); and discontinuation of the use of western blotting (WB) for HIV diagnosis. Here we update a 2018 policy review and assess country adoption of these new guidelines in the WHO African region.

METHODS: Between May and July 2021, we undertook a comprehensive desk review of national HTS policies. Adherence to WHO recommendations was categorized as fully adherent, mostly adherent, somewhat adherent and not adherent based on the number of compliant and noncompliant testing strategy characteristics identified compared to the WHO's 2019 HTS guidelines.

RESULTS: National policies were reviewed for 87% (n=41/47) of countries in the WHO African region, 41% (n=17) were published before 2019, and 49% (n=20) adhered to WHO guidance. Between 2018 and 2021, adherence to WHO recommendations in the region increased from 28% (n=9/32) to 49% (n=20/41). Using a two-assay testing strategy was the most common reason for non-adherence: 29% (n=12) and 24% (n=10) in low (<5%) and high (>5%) prevalence countries. Five countries still recommended the use of WB in their HIV testing algorithm, and only 53% (n=21) recommended HIV retesting before ART initiation. Use of dual HIV/syphilis RDTs in ANC was recommended in 43% (n=17) of policies.

CONCLUSIONS: Adherence to WHO-recommended testing strategies has increased in the African region. While WB was only used in a few countries, concerted efforts are needed to discontinue this technology in favour of RDTs. Countries should plan to accelerate their transition to WHO-recommended HIV testing strategies by streamlining efforts to adopt a three-assay testing strategy and introduce dual HIV/syphilis RDTs in ANC.

5281982 | Development of the Regional Biosafety and Biosecurity Legal Framework for the African Union Member States

Noumedem Kenfack Jaurès Arnaud, **Talkmore Maruta**
African Society For Laboratory Medicine & Africa Centers For Diseases Control And Prevention, Nigeria

BACKGROUND: The World Health Organization (WHO) Joint External Evaluation (JEE) conducted between 2016-2019, the Global Health Security (GHS) Index and regional consultative meetings coordinated by Africa CDC, highlighted lack of, and where they exist, limited scope and disaggregation of Biosafety and Biosecurity (BSBS) legislation as a major factor for the reported limited BSBS capacity among African Union Member States (MS). Legislation empowers MS to enforce compliance with BSBS requirements

METHODS: The development of the BSBS legal framework followed an iterative regional consultative process of Africa Union (AU) MS utilizing the established five multi-sectorial and multi-expert Regional BSBS Technical Working Groups (RBB-TWG) established in the five AU regions and a team of regional BSBS expert group. The legal framework was submitted to the Africa Union Specialized Technical Committee (STCC) for Health and Social Affairs, who upon approval will submit to the AU STCC for Legal Affairs until adoption at the Heads of States and Government summit

RESULTS: The draft regional BSBS legal framework contains seven domains areas including requirement for a national lead agency, development of national standards, authority for biological risk assessment, regulating entities handling high consequence pathogens and toxins (HCAT), human resource training and development education, transfer, storage, and disposal of HCAT and prohibition of all activities towards production of biological weapons.

CONCLUSIONS: The regional framework provides a basis for AU MS who do not have legislative documents for BSBS to adopt and adapt, serve as benchmark for review and updating for AU MS that already have legislation. Existence of legislation empowers MS to enforce compliance to requirements of BSBS

5266578 | Assessment of Viral Load Suppression Rates Among Paediatric Patients Living with HIV in Western Nigeria

Saheed Usman
APIN Public Health Initiatives Abuja Nigeria, Nigeria

BACKGROUND: In resource-limited settings, where genotypic drug resistance testing is rarely performed and unsuppressed viral load outcome is a function of poor drug adherence, programmatic approaches in scaling up optimal adherence is essential. The aim of this study was to assess the viral load suppression rates among pediatric patients living with HIV using ART multi-month scripting model in south-western Nigeria.

METHODS: This study was a longitudinal study conducted on 283 paediatric patients living with HIV (136 males and 147 females) enrolled into antiretroviral therapy from a selected health facilities across Western Nigeria, during a 12-month observation period starting October 2019 till September 2020. Quantitative viral load analysis was done using Polymerase Chain Reaction, Roche Cobas Taqman 96 Analyzer. All data were statistically analyzed, using Statistical Package for the Social Sciences (SPSS), with multiple comparisons done using Post Hoc Bonferonni test.

RESULTS: Most of the respondent were within the age range of 6 – 9 years, with a mean age of 6.07 ± 2.08 years. 167 (59.0%) & 37 (13.1%) of the subjects had viral suppression of <1000 RNA copies per ml and <20 RNA copies per ml respectively. The unsuppressed subjects went through enhanced adherence counselling (EAC) for three months and viral load test repeated thereafter. 33 patients who had completed the three sessions of EAC and repeated viral load increased the entire suppression numbers to 200 (70.7%) & 60 (19.0%) <1000 RNA copies per ml and <20 RNA copies per ml respectively during the period of observation. ART adherence has significant effect on viral load outcome from the study hypothesis tested ($\chi^2 = 15.763$, df = 1, P = 0.001).

CONCLUSION: Current ART regimen & HIV treatment enhanced adherence counseling are key to the achieving viral suppression, thus, routine viral load monitoring will ultimately help in HIV/AIDS disease progression follow up.

5237301 | Strengthening Laboratory Capacity for Detection and Surveillance of Antimicrobial Resistance: Bungoma County Referral Hospital in Kenya

Joshua Odero[1], Josiah Njeru[1], Sheilla Chebore[1], Joan Wasike[2], David Wanikina[2], Susan Githii[3], Evelyn Wesangula[3], David Mungai[1], Anicet Dahourou[1], David Mutonga[1]
[1]Infectious Disease Detection And Surveillance, Kenya; [2]Bungoma County Referral Hospital, Kenya; [3]National Antimicrobial Stewardship Interagency Committee (NASIC), Kenya

BACKGROUND: Antimicrobial resistance (AMR) is a global public health emergency that threatens the safe delivery of modern health care. High-quality laboratory testing is critical for detection and monitoring of resistance trends, to guide prevention and control measures. In Kenya, very few public health laboratories have bacteriology tests accredited to guarantee quality and reliable AMR results. Bungoma County Referral Hospital Laboratory (BCRHL) attained ISO 15189:2012 accreditation for bacteriology tests in 2020. We describe the journey BCRHL took to have bacteriology tests accredited.

MATERIALS AND METHODS: A gap analysis using the Laboratory Assessment of Antibiotic Resistance Testing Capacity (LAARC) tool was conducted in July 2019 to objectively evaluate and quantitatively measure capacity to detect AMR and manage data. An improvement workplan integrating Quality Management Systems (QMS) was developed in November 2019 to address identified gaps and implemented throughout the period, November 2019 to September 2020. Some targeted interventions included reorganization of workflow, review of testing standard operating procedures, procurement plans development, supplies and equipment procurement, bacteriology reagents budget advocacy, clinician's sensitization, development of training materials, training, and staff mentorship. At the end of improvement process, the laboratory applied to Kenya Accreditation Service for inclusion of bacteriology tests in the accreditation scope.

RESULTS: Per the LAARC tool, bacteriology average performance was 48% and after interventions, there was improved quality assurance practices, reagents availability, knowledge, and skills of laboratory personnel in detection of AMR in bacterial pathogens. Bacteriology culture workload increased from 759 in 2019 to 1214 in 2020. Bacteriology tests were successfully included in ISO 15189:2012 laboratory accreditation scope in September 2020,

CONCLUSIONS: Integrating QMS approach into bacteriology laboratory practices resulted in accreditation. The low rate of bacterial culture examinations indicates weak systems for bacteriology examinations. The findings show that clinicians confidence resulted in more bacterial culture requests.

Wednesday, 17 November | 11:00 – 12:30
LABORATORY RESPONSE AND LESSONS LEARNT

ORAL SESSION 3500
STRENGTHENING LABORATORY SYSTEMS AND NETWORKS FOR ROUTINE AND EMERGENCY

CHAIRPERSONS:
Nadine Abiola; Shirley Lecher

5237182 | Operational Feasibility of Screening Blood Samples with a CD4 Count of 100–200 Cells/µl for Cryptococcal Antigen in an Established Reflex Programme in South Africa

Lindi Coetzee[1], Greg Green[2], Miriam Mwamba[2], Naseem Cassim[1], Nelesh Govender[3], Deborah Glencross[4]
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BACKGROUND: Early detection of cryptococcal antigenaemia in immune-suppressed HIV-seropositive patients can decrease mortality through timely therapy initiation. The World Health Organization extended cryptococcal antigen (CrAg) testing recommendations to include people with CD4 counts 100-200 cells/µl. Routine CrAg reflex testing in South Africa is currently performed through 47 CD4 laboratories on samples with a count <100 cells/µl (routine testing) (~10% of national CD4 tests). An additional 11% of CD4 samples have a count of 100-200 cells/µl (extended reflex testing). This study reports on the operational feasibility of extended CrAg screening.

METHODS: In November 2020, all CD4 samples with a count of ≤200 cells/µl (both routine and extended reflex testing) were tested for CrAg using the IMMY lateral flow assay. Data were extracted from the NHLS Corporate Data Warehouse and de-duplicated to sample level.

RESULTS: Nationally, 38 597 samples had a CD4 count of ≤200 cells/µl, of which 9.7% had a CD4 count <100 cells/µl and 9.9% a count of 100-200 cells/µl. CrAg positivity was 6.7% for routine testing vs. 2.4% for extended reflex testing, with the latter decreasing from 2.6% (CD4 count 100-149 cells/µl) to 1.8% at a CD4 count of 150-200 cells/µl. CrAg testing volumes were highest in the Gauteng Province, followed by KwaZulu-Natal (KZN) and Eastern Cape provinces. KZN had the highest CrAg positivity for both routine (8.7%) and extended reflex testing groups (2.7%), where positivity for the latter exceeded the provincial average in 6/11 districts.

CONCLUSIONS: CrAg test volumes were equally distributed in the routine and extended reflex testing groups, doubling test volumes per laboratory. CrAg positivity was however significantly lower in the extended group, decreasing with increasing CD4 count up to 200 cells/µl. An appropriate cut-off for extended reflex CrAg testing thus needs to be established, considering the impact on costs, laboratory operations and patient outcomes.

5236684 | Improving Antimicrobial Resistance Surveillance Through Linking Laboratory Information Management Software with Hospital Information Systems in Vietnam

Huong Lien Pham[1], To Nhu Nguyen[1], Si Tuan Ngo[1], Duc Kien Pham[1], Ngan Giang Vo[2], Tuan Truong Nguyen[2], Le Van Ngoc Truong[3]
[1]Path, Vietnam; [2]FHI360, Vietnam; [3]Medical Service Administration, Ministry of Health, Vietnam

BACKGROUND: In Vietnam's National Surveillance System on Antimicrobial Resistance (AMR), few hospitals have established links between the hospital information system (HIS) and laboratory information system (LIS). The disconnection prevents comprehensive understandings of laboratory and clinical evidence, thereby negating effective management and treatment.

To address this, hospitals must establish HIS-LIS connections and mechanisms for sustaining data linkages. Through the Fleming Fund (FF) country grant for Vietnam, FHI 360 and PATH worked with the Medical Services Administration (MSA) and 19 hospitals in Surveillance System to install or upgrade LIS, link clinical and laboratory data, and strengthen AMR surveillance through standardized data reporting and improved data use.

METHODS: The project assessed 19 hospitals using standardized and customized data management assessment tools. On-site interviews, observation, semi-structured questionnaires, and data review were conducted to evaluate hospital laboratories' AMR data reporting and management capacity. Based on these findings, the project installed, upgraded, or replaced LIS and established HIS-LIS connection to meet reporting requirements. To ensure sustainability, the project allowed hospitals to select LIS providers and extended project ownership to hospital leaders.

RESULTS: The assessment revealed that only two hospitals had effective data management. The rest reported substandard data or lacked LIS and HIS-LIS connection. The project collaborated with MSA and participating hospitals to standardize LIS technical requirements. Within 20 months, the project acquired official commitment from 18 hospitals, completed LIS upgrades at 12, and established HIS-LIS connections at ten. Hospitals with completed or upgraded LIS have begun reporting AMR data to the online national portal. All participating hospitals are required to commit budgets to maintain the systems after the project's conclusion.

CONCLUSIONS: The project improved data management and linkages for 18 hospitals—foundational for standardizing AMR surveillance for human health in Vietnam. Enabling factors for the project included sustainable support from the government and hospital leadership.

5236801 | Diagnosis of Tuberculosis Infection to Species Level Amongst Multidrug Resistant Tuberculosis Patients for Better Patient Management and Improved Treatment Outcome

Cornelius Gweba[1], Chinonso Mfoneddie[1], Divine Onwubuariri[2], Chijioke Anya[2], Anuli Emeka-Amadi[2], Precious Uzor[2], Chike Ezeanya[1], Meshak Panwal[1], Mosunmola Iwakun[1], Abdullahi Abubakar[1]
[1]Institute of Human Virology, Nigeria, Nigeria; [2]Southeast Zonal TB Reference Laboratory Abia State, Nigeria, Nigeria

BACKGROUND: Clinical laboratories in Nigeria and other low and middle income countries, employ Gene Xpert MTB/RIF assay, MTBDRplus and MTBDRsl series for rapid identification of tuberculosis (TB) and Multi-drug resistant tuberculosis (MDR-TB). These diagnostic tools detect TB infection caused by members of *Mycobacterium tuberculosis* complex (MTBC), but does not provide information on MTBC species causing the infection. The lack of routine identification of MTBC species implicated in causing TB infection by clinical laboratories, has created a knowledge gap. We believe that, routine diagnosis of TB infection to species level will help to identify the predominant species implicated in causing TB infection in a population, serve as a pointer for intrinsic drug resistance and inform on source of infection including best preventive approach to mitigate the spread of TB in a community.

METHOD: TB clinical isolates of MDR-TB patients from southeast Nigeria cultivated between January and December 2020, were retrospectively differentiated to species level using Hain Lifescience GenoType MTBC series. DNA material were extracted from liquid culture cultivated on BACTEC MGIT 960 instrument. Amplification and detection were performed using Hain Lifescience instruments according to manufacturer's instruction at Southeast Zonal TB Reference laboratory, Nigeria.

RESULT: A total of 96 isolates were characterized and differentiated to species level of which, 58.30% (n=56) were *M. tuberculosis/ M. canettii*, 11.45% (n=11) were *M. africanum* and 2.10% (n=2) were *M. bovis*. However, 11.45% (n=11) were high gram positive bacteria, 14.60% (n=14) were invalid, while 2.10% (n=2) had no evaluable pattern.

CONCLUSION: Findings from this study shows a high rate of *M. tuberculosis/M. canetti* infection amongst the study population. *M. canetti* has been known to have an inherent resistance to pyrazinamide with no evidence of human-to-human transmission. Therefore, providing clinicians with information on MTBC species implicated in causing TB, will enhance patient management and improve treatment outcome.

5261476 | The Use of InTray COLOREX Screen and ESBL for Bacterial Identification and ESBL–Detection from Blood and Urine Cultures in Harare, Zimbabwe

Mutsawashe R Chisenga[1], Forget Makoga[1], Gwendoline Chimhini[2], Beauty Makamure[1], Heidi Hopkins[3], Katharina Kranzer[4], Ioana Diana Olaru[4]
[1]Biomedical Research And Training Institute, Zimbabwe; [2]Child And Adolescent Health Unit, Faculty of Medicine And Health Sciences, University of Zimbabwe, Zimbabwe; [3]London School of Hygiene And Tropical Medicine, Zimbabwe; [4]Biomedical Research And Training Institute/ London School of Hygiene And Tropical Medicine, Zimbabwe

Novel strategies that can simplify laboratory procedures are urgently needed to expand testing capacity and improve antimicrobial resistance surveillance. We evaluated a novel chromogenic culture media for presumptive identification of Gram-negative bacteria and detection of antimicrobial resistance in isolates from blood and urine.

METHODS: This analysis included samples collected within two studies: blood cultures from neonates with suspected sepsis from a referral hospital and urine samples from patients with urinary tract symptoms from primary healthcare facilities in Harare. Positive blood cultures which were incubated using an automated system and urine samples were inoculated onto InTrays COLOREX Screen and ESBL and incubated at 37°C for 24 hours. Conventional microbiological methods were used as reference standard.

RESULTS: of 216 blood cultures, 54 were positive for Gram-negative organisms, all of which were extended-spectrum beta-lactamase (ESBL)-producing *Klebsiella pneumoniae* using reference methods. InTrays provided a correct identification and detected the presence of ESBLs in all isolates. Turnaround times to identification and detection of resistance from blood cultures could be reduced from 72h from sample collection using conventional methods to 48h using InTrays. of 414 urine samples, 83 were positive for *Enterobacterales* and 22/83 were ESBL-producing organisms. The sensitivities and specificities of InTrays were 89.2% (95%CI 80.4-94.9) and 98.2% (95%CI 96.1-99.3) for bacterial identification and 95.5% (95%CI 77.2-99.9) and 99.5% (95%CI 98.2-99.9%) for ESBL-detection. Turnaround times for urine cultures could be reduced from 48h (conventional methods) to 24h (InTrays).

CONCLUSION: Our results showed that the InTrays had an excellent performance for the identification of Gram-negative bacteria and ESBL-detection from urine and blood cultures and shorter turnaround times. These culture media are ready-made, easy to use and have a long shelf-life making them attractive solutions for use in lower-level laboratories thus having the potential for expanding laboratory capacity and for strengthening antimicrobial surveillance in low-resource settings.

5250745 | Increased Viral Load Testing Capacity with Installation of Solar Power Systems in Zambia

Lugard Sichalwe[1], Clement Phiri[1], Aaron Lunda Shibemba[2], **Christine Mfula**[1], Delhan Hamomba Milimo[1], Valery Kadima[1], Mary Chileshe-Lombe[1], Sarah Snyder[1], Noah Hull[1], George Mwakanandi[2]
[1]Association of Public Health Laboratories, Zambia; [2]Ministry of Health - Pathology And Laboratory Services, Zambia

BACKGROUND: Medical laboratory hubs for viral load (VL) can experience an erratic supply of electricity that prevents the use of test instruments and delays in test results. Solar power offers a feasible option to supplement inadequate electricity grid coverage.

METHODS: Site assessments based on power needs, target population, and geographical location from the testing laboratory were conducted in 12 hubs. As a result, a solar power system design was developed based on the equipment and operational needs of each laboratory with 50% additional power.

RESULTS: The assessments indicated that 5/12 (42%) hubs had no electricity while 7/12 (58%) hubs had power but experienced sporadic electrical outages of 4-10 hours in a 24 hour period. Solar power systems of varying capacities were designed and installed in the 12 sites. Subsequently, the VL hubs were capacity built with sample processing equipment such as refrigerators and centrifuges, while others had existing equipment interfaced with the mounted power supply. Four of the 12 hubs (25%) were now able to have Disalink, a remote Laboratory Information System (LIS) for sample registration and result return, installed in addition to the existing 4/12 facilities on the national grid, which already had the LIS. Pre and post-data analysis indicated an increase of 21.4% in VL test results recorded for the 12 facilities credited in part due to the stability of the power backup systems installed at these sites.

CONCLUSION: Solar power provides stable and consistent energy that allows for less reliance on grid systems, generators, and other alternative Uninterrupted Power Supply (UPS) systems that rely on the central grid to charge the batteries, which become less effective during prolonged power outages. With adequate analysis, thoughtful design, and competent installation, solar energy can provide sufficient electricity capacity to support critical laboratory testing services.

5239225 | Étude de la Cinétique des Anticorps Anti-RBD Et Anti-N Du SARS-COV2 Dans un Échantillon de la Population Tunisienne

Mariem Gdoura, Habib Halouani, Donia Sahli, Meriem Ben Hmida, Imen Abouda, Wafa Chamsa, Henda Triki
Laboratoire De Virologie Clinique, Institut Pasteur De Tunis, Tunisia, Tunisia

INTRODUCTION: L'interprétation des résultats de la sérologie anti-SARS CoV2 ne peut se faire sans une connaissance approfondie des différents profils cinétiques des anticorps suite à l'infection. Nous nous proposons d'évaluer la cinétique de la réponse humorale en IgM et IgG anti RBD et en anticorps totaux anti N.

MÉTHODES: Il s'agit d'une étude prospective descriptive menée au Laboratoire de Virologie de l'Institut Pasteur de Tunis qui s'étend du 18/05/2021 au 03/03/2021. Ont été inclus 1292 sérums de patients ayant contracté le SARS-CoV-2, prélevés à différents moments après l'infection (de 0 à 365 jours) confirmée par une RT-PCR positive sur un prélèvement nasopharyngé. Ces sérums ont été testés par 1 ou 2 automates qui sont Vidas® Biomérieux (IgM et IgG anti-RBD, ELFA) et Cobas®Roche® (anticorps totaux anti-N IgG+++, IgM et IgA, ELECSYS) Les résultats obtenus sont exprimés en index et répartis en 6 groupes : 0 à 10 jours, 10-20 jours, 20-30 jours, 1 à 3 mois, 3 à 6 mois, >6 mois.

RÉSULTATS: Les données obtenues ont permis de proposer un profil cinétique général des anticorps anti SARS-CoV2. Les premiers anticorps détectés sont les IgM anti RBD à partir de J 0, le pic est rapidement atteint entre le 11ème et le 20ème jour pour décroitre rapidement et se négativer à partir du 3ème mois. Les IgG anti RBD ont été détectés à partir de J2 de l'infection, le pic a été atteint entre J 21 et J 30, un déclin lent est noté à partir de 1er mois. Les anticorps anti N se sont positivés à partir de J3, ensuite, une augmentation continue des valeurs des index a été observée qui semble se poursuivre après 6 mois.

CONCLUSION: La recherche des anti-N représente le meilleur marqueur de contage avec le virus même après un an de l'infection.

ORAL SESSION 3510
WORKFORCE DEVELOPMENT AND THE LABORATORY PROFESSION

CHAIRPERSONS:
Nicolas Steenkeste; Suzanne Kiwanuka

5237326 | Implementation of the ASLM SARS-COV-2 Antigen RDT Training Package: Field Experiences from South Africa

Lynsey Stewart-Isherwood[1], Abel Makuraj[2], Anura David[2], Francinah Nonyane[3], Shazia Basseer[4], Sandra Maphumulo[4], Mashate Silver[5], Violet Gabashane[4], Pedro Da Silva[6], Wendy Stevens[2]
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BACKGROUND: SARS-CoV-2 antigen (Ag) rapid diagnostic tests (Ag-RDTs) revolutionised the COVID-19 response by providing accurate results in <20 minutes. Adequate training is vital to ensure quality testing and resulting. To ensure that this is met, the National Health Laboratory Service (NHLS) in collaboration with the Department of Molecular Medicine & Haematology, Wits Health Consortium (DMMH, WHC) adopted and rolled out the African Society for Laboratory Medicine (ASLM) training package for SARS-CoV-2 Ag-RDT with the objective to foster and cascade transfer of knowledge and skills to health service providers from national to health facility levels across the country. The training package consists of both theoretical and practical components.

METHODS: The adopted ASLM Ag-RDT training package aligned to WHO and South African COVID-19 response guidelines. Training cascaded over four-tiered levels across eight provinces of South Africa; Training of NHLS Master Trainers (MTs) at national level, Trainings of Trainers (ToTs) at Sub-regional level, trainers at provincial level and End-Users (testers) at facility level. The ToT is CPD accredited by Wits. Trained participants who passed the course competence assessment were certified by ASLM Academy to perform testing. The results of the Ag-RDTs performed are captured onto the NHLS electronic COVID-19 Surveillance Application (CSA).

RESULTS: ASLM trained 23 MTs in January 2021, of which five had capacity to conduct ToT training. Nine ToT and 25 end-user sessions were conducted between February and June 2021. 171/337 (50.7%) ToT trainers and 279/303 (92.1%) end-users were accredited. Over one million Ag-RDT tests over 140 public health testing sites were recorded on CSA.

CONCLUSIONS: Standardised training is important for maintaining quality across Africa and training should be kept relevant through continuous monitoring of the testing landscape. Inadequate resources for continuous supervision visits at facility-level, poor connectivity to support data management and limited access to clinical trainers, remain a challenge.

5237490 | Impact of the National Health Laboratory Service Extension for Community Healthcare Outcomes Programme on Teaching and Training of South African Laboratorians and Healthcare Workers During the COVID-19 Pandemic

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BACKGROUND: The COVID-19 pandemic required rapid training of laboratory and healthcare workers (HCWs) to aid South Africa's public health emergency response. The National Health Laboratory Service (NHLS) Extension for Community Healthcare Outcomes (ECHO) programme is an innovative, remote training solution that links experts to healthcare facilities, especially in medically under-served regions, enabling widespread, rapid dissemination of knowledge. The authors aim to demonstrate the impact of the ECHO programme on the development of South African laboratory and HCWs.

METHODS: ECHO was implemented in 2018 to enhance training in pathology disciplines, including didactic and clinical consultation sessions conducted via 85 NHLS ECHO sites with remote access equipment. In 2020, ECHO expanded to include training on COVID-19 and provided remote support for NHLS programmes affected by lockdown restrictions. Post-session evaluations were sent to attendees.

RESULTS: ECHO facilitated 368 sessions in 2020, which were presented by 179 experts to 2208 participants (average of 41 attendees per session), including students, laboratorians, and HCWs. Sessions included 21 case presentations, 204 skills development sessions, and 14 COVID-19 sessions (average COVID-19 session attendance, 93 participants). The post-session evaluation response rate was 51%: 57% of respondents were very satisfied with the quality of the session, 70% rated the session as above average, 54% agreed that the information provided was relevant to their profession, and 55% felt very confident in their ability to apply the skills they had learned.

CONCLUSION: The positive response received from students, laboratorians, and HCWs indicates the success and impact of ECHO. External departments, such as the Department of Education, have requested ECHO sessions, and ECHO will be expanded to additional remote NHLS facilities to serve more laboratories and HCWs as the COVID-19 pandemic continues.

5330258 | Situational Analysis of the Response to HIV Viral Load Results Requiring Attention in PEPFAR/CDC Supported Primary Healthcare Facilities in South Africa

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Healthcare workers (HCWs) response to abnormal HIV viral load (VL) results, including fidelity to procedures and timeliness, can impact goals of providing optimal patient care and reaching UNAIDS 95% viral suppression. A quality improvement project involving a situational analysis was conducted, reviewing VL procedures at PEPFAR/CDC-supported facilities, South Africa.

During April–June 2021, nine virtual zoom training sessions were conducted for CDC-funded partner staff supporting primary healthcare facilities, on a system alerting HCWs to abnormal VL results requiring attention: invalid results/rejected specimens requiring repeat blood draws and unsuppressed results requiring enhanced adherence counselling. During sessions, participants were asked nine questions assessing typical procedure and timeframe for actioning VL results. Self-reported, free-text responses were deidentified and analyzed to identify gaps for strengthening.

Among 120 participants across 11 districts, staff actioning VL results include: Enrolled-Nurse, Professional-Nurse, Case-Facilitator, Adherence-officer, Lay-Counsellor and Linkage-officer. VL results action is typically performed by several staff members and varies by facility. Ninety-six percent of respondents reported VL results are checked daily. Similarly, 96% reported attempt to contact patients for repeat blood draws or adherence counselling within 7 days; 77% within 2 days from receiving results. Ninety percent reported providing adherence counselling within 1 month; 78% within 2 weeks of receiving results. For patients not initially reached, 98% reported recontacting patients or referring for home tracing. After VL testing, 97% reported patients are provided their next appointment date within 1 month.

Fast action on abnormal VL results is critical for optimal patient care. Several staff are involved, potentially leading to gaps in continuity and delayed patient care; standardization within facilities and across districts could be a strategy to improve response to abnormal VL results. While a large percentage reported fast action, results are self-reported and possibly subject to bias: true percentages may be lower adding further motivation for standardization.

5265935 | Use of Precise Duty Rosters to Reduce Staff Work-Over Load: A Quality Improvement Intervention

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INTRODUCTION: Laboratory services are very critical in HIV service provision. TASO Gulu receives substantial test requests from both facility and community drug distribution points. However, the demand for quality laboratory tests versus increased number of tests presents a big human resource challenge given the thin number of technical laboratory staff. In this study, we demonstrated how precise duty roasters lead to optimized workload for laboratory staff.

METHOD: We constituted work improvement team (WIT) led by the laboratory manager that harmonized/streamlined the duty roaster to task specific stations; Work-over load was analyzed using fish-born tool and prioritized by multi-voting. Few laboratory staff, unclear duty roasters and absenteeism were the identified root-causes. Improvement changes developed and tested were: classification of task stations according to test menu (reception/phlebotomy, serology, parasitology/microscopy, biochemistry/hematology, results recording, validation and dispatch to clinicians/sample referral packages), allocation of staff per station with strict supervision and proper delegation of duties. We used the interactive cycle of improvement to implement the changes.

RESULTS: Overall, we recorded a substantial decrease in work load for laboratory staff with 98% (240/245) of the test results reviewed in June, 99.6% (282/283) results reviewed in July and 100% (231/231) in August; which was sustained at 100% in September 2019.

DISCUSSION: The use of roasters has resulted in increased compliance to work schedules and reduced staff work-over load leading to 100% review of test results which improved overall quality of results produced. An improved turn-around time for laboratory tests was recorded which drastically reduced client waiting time hence client satisfaction.

CONCLUSION: Task classification, specific task allocation and proper delegation proved very effective in reducing staff work-over load, improving turn-around time for laboratory tests, curbing absenteeism and reducing overall client waiting time. We recommend replication of this intervention in settings with similar challenges.

5227945 | Converting a Highly Interactive Laboratory Accreditation Curriculum to On-line Learning in Resource-Limited Settings: A Study of Effectiveness, Feasibility, and Costs for Multi-Country Implementation

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BACKGROUND: Illuminating the Path to ISO15189 Accreditation (SLMTA 3) is a curriculum that helps laboratories implement a Quality Management System to fulfill ISO15189 requirements in resource-limited settings. To minimize impact from the COVID-19 pandemic, we converted the 2-week classroom-based training to 15-week on-line learning. This study evaluates the effectiveness, feasibility, and costs of the new course in multi-country implementation from February to May 2021.

METHOD: The on-line course employed a blended learning approach using 185 pre-recorded videos, 20+ hours of homework, weekly live webinars and office hours, and peer support via WhatsApp and on-line forum. A course scorecard monitored webinar attendance and punctuality by the participants, timeliness of homework submission, and participant attention during on-line sessions. Weekly surveys solicited participant feedback for continual improvement throughout the course. An exit survey measured participants' perceived effectiveness and preference of on-line vs. any previous classroom training. Training delivery costs for both models were compared.

RESULTS: The course enrolled 27 participants from 19 countries; 26 (96%) fulfilled the requirements for course certificates. Participants rated both models equally effective on the didactics, ease of asking questions, and immediate laboratory improvement, while classroom was rated better at facilitating teamwork and interactions. Given the options, most participants (65%) would choose face-to-face learning. This on-line course cost US $100,000 less than its classroom equivalent and reached previously hard-to-reach participants.

CONCLUSIONS: The blended learning approach is feasible for training of this duration in low-and-middle income countries despite challenges such as unstable internet connections and struggles to balance the coursework with a full-time job. Most participants were able to overcome challenges with commitment, advance planning, and effective time management. The new model has the potential to be a cost-saving alternative to traditional classroom training even after the pandemic. Further studies will inform proper interventions to increase preference for on-line learning.

5260785 | Antimicrobial Resistance Surveillance Curriculum Development: A Kenyan Experience

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INTRODUCTION: Antimicrobial resistance (AMR) is an increasingly severe threat to global public health that requires action across different sectors. Introduction of antimicrobials revolutionized the ability to treat infectious diseases. However, selection of appropriate antimicrobials is becoming increasingly a global challenge due to the emergence of drug resistance. The Ministry of Health (MOH) and the Ministry of Agriculture, Livestock, Fisheries and Cooperatives (MALFC) developed the AMR policy and National Action Plan (NAP) in 2017. A technical working group on AMR surveillance has been supporting the implementation process. However, lack of a holistic in-service health workers AMR Surveillance training curriculum has slowed down the implementation of the surveillance component of NAP. A curriculum targeting all AMR stakeholders was proposed.

METHOD/PROCESS: An initial draft of AMR curriculum was developed with support of One Health stakeholders, which was then shared to a team of experts for review. Infectious Disease Detection and Surveillance (IDDS) project organized a 1-day stakeholders meeting for further inputs before another 5-days workshop to develop the curriculum, facilitator, and participants manuals. Finally, a validation workshop was held to finalize the documents for formal approval.

RESULTS: A multisectoral AMR surveillance training curriculum, facilitator and trainee manuals were developed and endorsed by MOH and MALFC. The documents were officially launched in November 2020 and used to train 25 Trainer of Trainers at national level, sensitized 200 human and animal health workers and trained 15 participants from on data analysis and use from 5 IDDS counties.

CONCLUSION: A multi-disciplinary training curriculum was developed to standardize training for AMR detection and surveillance. This is a timely tool to guide systematic strengthening of knowledge and skills development for AMR prevention and containment using a One Health approach. The curriculum is now available on an e-learning platform for self-paced learning.

KEY WORDS: AMR, Surveillance, Curriculum, Training,

ORAL SESSION 3520
SCIENCE AND TECHNOLOGY TO SUPPORT COST-EFFECTIVE AND INTEGRATED LABORATORY NETWORKS

CHAIRPERSONS:
Paolo Maggiore; Anafi Mataka

5237287 | Independent Evaluation of the WHO Prequalified M-PIMA HIV-1/2 Viral Load Assay

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BACKGROUND: Point of care testing for viral load (VL) can be used for priority populations and remote areas that conventional VL testing is unable to reach. The Abbott m-PIMA™ HIV-1/2 VL assay received World Health Organization (WHO) prequalification in April 2019. Operational and performance characteristics of this test were independently evaluated to ensure a quality product for use in countries supported by the President's Emergency Plan for AIDS Relief (PEPFAR).

METHODS: The limit of detection (LOD), cross-contamination, precision, error rate, and linearity for five major HIV-1 subtypes and HIV-2 Group A and B were evaluated. HIV-negative plasma was spiked with virus culture or the WHO third International HIV-1 RNA Standard, or the WHO first HIV-2 RNA Standard for this analytical evaluation.

RESULTS: Using PROBIT analysis, the LOD was calculated to be 884.6 copies/mL for HIV-1 and 283.6 copies/mL HIV-2 with a 95% confidence interval of 550.9-2,275 copies/mL and 201.9-714.5 copies/mL, respectively. No cross-contamination was detected. Linearity assessment of HIV-1 subtypes A, CRF02-AG, B, C, and D showed *R2* values greater than 0.98 and for HIV-2 groups A and B greater than 0.99. The average error rate was >10%. Error code analysis resulted in Abbott refining the m-PIMA™ analyser and updating assay software lowering the final error rate to 2%.

CONCLUSIONS: This evaluation revealed high error rates due to the premature release of products. Although this assay was WHO prequalified before this evaluation, the findings of this evaluation led to modifications to the instructions for use, software, hardware, and overall performance of the assay and manufacturer-managed updates to previously deployed instruments. These findings affirmed the excellent performance of HIV-2 VL quantification. As the only commercial VL assay for monitoring HIV-2 patients on treatment, this assay may be particularly valuable in settings such as West Africa, where HIV-2 infection is common.

5237665 | Variable Performance of Chromogenic Agars When Screening for Multi-Drug Resistant Organism (MDRO) Colonization in the Antibiotic Resistance in Hospitals and Communities (ARCH) Study in Kenya

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BACKGROUND: Colonization screening is critical to contain the spread of MDRO in healthcare settings. Chromogenic agars are an option, but performance in clinical settings is not well-established in resource-limited settings. We examined chromogenic agar screening performance for methicillin-resistant *Staphylococcus aureus* (MRSA), carbapenem-resistant Enterobacterales (CRE), and extended-spectrum cephalosporin resistant Enterobacterales (ESCrE) in Kenya.

METHODS: Nasal swabs and stools were plated on HardyChrom™ MRSA, CRE, and ESBL plates imported from the U.S. Pigmented colonies underwent identification and antibiotic susceptibility testing (AST) using Vitek 2®. Concordance was defined as growth on chromogenic agar plus expected AST phenotype: resistant to oxacillin or cefoxitin (MRSA); not susceptible (NS) to ertapenem, meropenem, or imipenem (CRE); and carbapenem-susceptible plus ceftriaxone NS (ESCrE). Quality Control (QC) records were reviewed.

RESULTS: of 349 *Staphylococcus aureus* isolated from MRSA agar, 52 (15%) confirmed as MRSA by AST. CRE plates yielded 415 Enterobacterales; 145 (35%) confirmed as CRE. Concordance for CRE E. coli (43%) was significantly higher than *K. pneumoniae* (13%), *E. cloacae* (28%) and other Enterobacterales (41%) (P<.0001). ESBL plates yielded 2158 Enterobacterales; 2050 (95%) confirmed as ESCrE. Concordance among ESCrE *E. coli* (97%) and *K. pneumoniae* (95%), was significantly higher than among E. cloacae (78%) and other Enterobacterales (75%) (P<.0001). One study site used plates expired 1 - 45 days alongside in-date plates. Weekly QC records showed no failures, yet concordance for in-date CRE plates (38%) was significantly higher than expired CRE plates (19%) (P=0.002).

CONCLUSIONS: Chromogenic agar effectively screened for ESCrE, but not CRE or MRSA. Expired media could not fully explain susceptible breakthrough. False positive screening results may cause erroneous infection prevention measures, such as improper patient cohorting. Laboratories implementing chromogenic agars for MDRO screening should be aware that routine QC may not detect media deterioration and should perform thorough verification studies to ensure reliable performance.

5216247 | ELABS: Innovative Digital Tool for Strengthening the Clinic-laboratory Interface: Results From a Scaled-Up Programme in South Africa

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BACKGROUND: eLABS is a digital health solution designed for strengthening the clinic-laboratory value chain through electronic monitoring of pre-analytical, analytical and post-analytical processes, thereby continuously improving the visibility of bottlenecks for quicker mitigation, leading to shorter results turnaround times (TAT). Mobile smart devices track HIV-VL and COVID-19 specimens and deliver real-time results from the Laboratory Information System, directly to healthcare workers (HCWs) for immediate action. Programme performance is monitored through business intelligent analytic dashboards.

METHODS: Implementation involved training of HCWs and drivers, site assessments, system configuration, change-management, and competency assessments. Provision of standard operating procedures, job aides and monitoring tools for continuous site support followed. Pilot implementation (24 facilities) occurred in 2018. Scale-up to 500 facilities (2019) was a collaborative effort by eLABS trainers and PEPFAR partners. Ministry of Health HCWs were trained as implementers to strengthen ownership and sustainability. This allowed for further scale-up to 2535 facilities in 2020/2021. Indicators for measuring program performance include TAT, specimen rejections, results acknowledged, device activity and specimens scanned and delivered.

RESULTS: Currently, 1789/2535 facilities are live on eLABS with 16271 HCWs and 287 drivers registered as users. Over a 28-month period, result TAT reduced from 108.3 to 70.4 hours, specimen rejection rates reduced from 2.6% to 2.0%. The median results for action acknowledged before COVID-19 (15 months) was 80% and after is 76% (13 months). Active facilities on eLABS are 99% (1789/1803).

CONCLUSIONS: Delayed HIV-VL results TAT is a significant barrier to timely clinical decision making for patients and threatens the success of the HIV treatment and care program. eLABS has improved operational efficiency through reduced TAT and specimen rejection rates by improved accountability, quicker service responsiveness and optimized workflows. This solution successfully transitioned from a pilot to a scaled program within 33 months. Future developments are to include other priority tests.

5205993 | Evaluation of the Abbott Alinity M HIV-1 Assay for Viral Load Testing Using Plasma and Dried Blood Spots

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BACKGROUND: The Abbott Alinity m is a high-throughput, multiplex, fully automated, continuous, and random-access system that can process up to 1,100 samples in a 24-hour timeframe. In this independent evaluation of the Abbott Alinity m HIV-1 Assay, both plasma and dried blood spots (DBS) sample types were assessed to verify the manufacturer's claims for consideration for use in countries supported by PEPFAR.

METHODS: HIV-1 negative plasma and whole blood were spiked with either cultured virus or using the WHO HIV-1 RNA fourth International Standard for this evaluation. The limit of detection (LOD) was calculated using PROBIT analysis. The precision of measurement, cross-contamination, error rates, and linearity for subtypes A, B, C, D and CRF02-AG were also determined.

RESULTS: The LODs were estimated to be 19.9 copies/mL (95% CI 13.6-53.0) for plasma and 305.36 copies/mL (95% CI 221.06-715.25) for DBS. No cross-contamination was detected with either sample type. Standard deviation within run ranged from 0.06-0.10 log10 copies/mL and 0.07-0.11 log10 copies/mL for plasma and DBS, respectively. The standard deviation between runs ranged from 0.10-0.16 log10 copies/mL and 0.07-0.13 log10 copies/mL for plasma and DBS, respectively. Linearity assessment of the main subtypes showed R2 values of >0.97 for plasma and DBS. Initially, the overall average error rate for plasma was 12% (0-30.1%), which was much higher than manufacturer's claims of <5% . Abbott adjusted their instructions for use, calibration and software and the error rate decreased to 1.2% for plasma and 1.9% for DBS.

CONCLUSIONS: Findings of the Abbott Alinity m evaluation led to modifications in software and instructions for use, resulting in decreased error rates. Our findings of this HIV-1 assay confirm the manufacturer's claims using both plasma and DBS. These results have led to the approval of the Abbott Alinity m instrument and assay for DBS and plasma in PEPFAR-supported countries.

5211793 | Evaluation of the HIV-1 Viral Load Assay on the Cobas® 4800 Platform for Early Infant Diagnosis

Katrina Sleeman, Demetrius Mathis, Guoqing Zhang, Heather Alexander, Clement Zeh
Centers For Disease Control And Prevention, United States

BACKGROUND: Roche Molecular Diagnostics recently added the claim of HIV early infant diagnosis (EID) testing using dried blood spots (DBS) to its cobas® HIV-1 test on the cobas® 4800 (c4800) platform. The HIV-1 test on the c4800 was independently evaluated for EID testing using DBS as an alternative to EID-specific reagents commonly used on the Roche COBAS AmpliPrep/COBAS TaqMan in countries supported by the President's Emergency Plan for AIDS Relief (PEPFAR).

METHODS: An analytical evaluation of the cobas® HIV-1 test using DBS created from HIV-negative whole blood spiked with cultured virus or using the fourth HIV-1 RNA International WHO Standard was conducted. Prepared DBS were stored at -80°C and thawed on day of testing. Testing was performed using the c4800 HIV-1 DBS Qual workflow and the cobas® HIV-1 test reagent kit. The limit of detection (LOD) was calculated using PROBIT analysis. The reproducibility, cross-contamination, error rate, and subtype detection for HIV-1 A, B, C, D and CRF02-AG were also determined.

RESULTS: The LOD was calculated to be 619.4 copies/mL with a 95% confidence interval of 447.7 – 997.0 copies/mL. No cross-contamination was detected, and no errors were observed in 450 tests performed for this evaluation. The five major HIV-1 subtypes evaluated were all detected.

CONCLUSIONS: The c4800 HIV-1 qualitative DBS workflow met accepted standards for reproducibility, cross-contamination, error rate, and LOD. The Roche c4800 HIV-1 viral load assay, pending final WHO prequalification, demonstrated excellent performance, and confirmed dual claim for EID using DBS. This finding can assist in combatting the supply chain challenges for EID amplified by COVID-19 pandemic-related disruptions that many countries continue to face, however the clinical performance should be verified.

5266597 | Introduction of a Viral Load Data Management System in Ghana

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[1]Association of Public Health Laboratories (APHL), Ghana; [2]National AIDS Control Program And The Policy, Planning Monitoring, Ghana

BACKGROUND: PEPFAR[1] has supported HIV prevention and control efforts in Ghana since 2008. Despite considerable progress over a decade, challenges remain with timely and complete knowledge of HIV infections among PLHIV (58% aware of HIV status), reach and enrollment of antiretroviral therapy (ART) (77% on ART), and sustained viral suppression among those on ART (68% are virally suppressed) [2]. This knowledge relies on accurate and efficient laboratory testing and reporting; however, HIV testing laboratories in Ghana lack robust, standardized and interoperable data management systems.

METHODS: To address data management limitations, APHL collaborated with the National AIDS Control Program and the Policy, Planning Monitoring and Evaluation Division of the Ghana Health Service to develop and deploy the Viral Load Data Management System (VLDMS). VLDMS serves as a holistic solution by impacting every stage of the testing and reporting cycle; from integration with Etracker to receiving test requests from ART clinics, management of data within the laboratory, interfacing with VL/EID analyzers for automated data capture and electronic reporting of results back to care providers through interoperability with Etracker.

RESULTS: The VLDMS was piloted at one HIV VL laboratory and 5 ART clinic sites to confirm the interoperability between VLDMS and ETracker for ART clinics to electronically submit test requests and receive results. The VLDMS analyzer interface minimized manual entry for the laboratory and decreased transcription error.

CONCLUSION: To increase efficiency and reduce turnaround time (TOT) of VL and EID results in Ghana, VLDMS implementations must be scaled-up, specimen identification numbers, data collection, and indicators need to be standardized. These efforts, combined with training health care workers and laboratory staff to use the VLDMS and eTracker integration, will shorten TOT for patient results and improve knowledge of critical VL testing data.

[1] U.S. President's Emergency Plan for AIDS Relief

[2] Ghana AIDS Commission Report 2019

ORAL SESSION 3530
PATHOGEN GENOMICS TO CONTROL DISEASES

CHAIRPERSONS:
Sikhulile Moyo; Gerald Mboowa

5237542 | Human Coronavirus Circulation Prior to Sars-Cov-2 Epidemic in Zambia: 2019-2020

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BACKGROUND: Human coronavirus (hCoV) types 229E, NL63, HKU1 and OC43 are the four main endemic human coronavirus strains known to cause upper and lower respiratory tract infections in both adults and children. The initial SARS-CoV-2 epidemic in Zambia was less severe than predicted, raising the possibility of some degree of pre-existing immune protection in the population. Some studies have suggested prior hCoV exposure might impart partial protection against SARS-CoV-2. We sought to determine if a previous outbreak of hCoV) preceded onset of the Covid-19 epidemic in Zambia.

METHOD: A retrospective study was conducted using samples collected through routine sentinel site surveillance for influenza like illness (ILI) and severe acute respiratory illness (SARI) between January 2019 and March 2020, before the first case of Covid-19 was detected in Zambia. 560 samples from patients with ILI and SARI were selected and analyzed by real time polymerase chain reaction (RT-PCR) using US CDC single-plex assay for the four main common human coronaviruses.
RESULTS: of 560 specimens tested, 14 (3%) were positive for hCoV including 10 (2%) HCoV-NL63 and 4 (1%) HCoV-HKU1. Five (36%) of the specimens were from patients aged <5 years. Most of the positive samples were collected in July (29%) and December (43%) which corresponds to winter and rainy seasons in Zambia.

CONCLUSION: Although there were human coronavirus in circulation in the period leading up to the SARS-CoV-2 epidemic in Zambia, there was no widespread outbreak that could explain some deglree of pre-existing SARS-CoV-2 protection in the population. ILI/SARI surveillance is a useful platform to investigate trends prevalence of respiratory viruses. Continued hCoV surveillance might help clarify the prevalence and circulation trends of hCoV in Zambia to determine if pre-exposure to hCoV might be associated with protection from SARS-CoV-2. Immunological studies would be necessary to corroborate any such findings.

5263904 | SARS-CoV-2 Lineages Among Clinical and Community Surveillance Samples Submitted to an Academic Virology Laboratory, Gauteng, South Africa, March 2020-February 2021

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BACKGROUND: Since the first wave of SARS-CoV-2 in South Africa, B.1.1.54, B.1.1.56, and C1 lineages were identified. The C1 lineage includes the signature amino acid variation S(spike):D614G. Late in 2020, the first SARS-CoV-2 variant (N501Y.V2 from B.1.351 lineage) of epidemiological concern was identified in South Africa. We aimed to identify additional mutations in SARS-CoV-2 viruses among samples from March 2020 to January 2021, received at the National Health Laboratory Service, Gauteng, South Africa.

METHODS: SARS-CoV-2 was detected in respiratory specimens received at Virology, National Health Laboratory Service, Charlotte Maxeke Johannesburg Academic hospital, using the TaqPath COVID-19 and nCoV-19 Allplex assays. Residual SARS-CoV-2 positive specimens were sequenced using and amplicon-based approach with the ARCTIC V3 primers pools and the NextSeq system.

RESULTS: A total of 269 samples were sequenced from in-patients, out-patients and community surveillance. of the 90 samples sequences from March-July 2020, 17 lineages were identified, including B.1.1.448 (31.1%; 28/90) characterised by S:D614G, S:T95I, S:V70F, N(nucleocapsid):R203K, N:G204R, M (membrane):S212R, M_H125P, and M:S212R mutations, and C1 (15.6%; 14/90) characterised by S:D614G, N:R203K and N:G204R. From November to December 2020 four lineages dominated including B.1.237 (N:S194L and S:D614G mutations), and B.1 (S:D614G, S:D215G, S:244del, S:242del, S:L452R, S:A701V, S:E484K, E:P71L, N:S194L, N:T205I), with the majority being B.1.351 (87.2%; 109/125). In January to February 2021 only the B.1.351 (83.3%; 45/54) lineage was identified. Among the B.1.351 lineage we identified S:N501Y, S:L18F, S:L822F, S:D215G, S:K417N, S:E484K, E:P71L, and N:T205I amino acid substitutions.

CONCLUSION: Additional mutations observed from our data include S:L18F, N: R203K, N:G204R may play a role in increasing infectivity and antibody immune escape. A distinct displacement in lineages from March 2020 through February 2021 was evident. However, limited sequence data are available from Gauteng which may impact our understanding of future evolutionary changes of Sars-CoV-2 which may exert further pressure on the vaccine roll-out.

5240427 | Molecular Characterization of Plasmids Encoding CTX-M Extended Spectrum β-lactamases Among Escherichia Coli Clinical Isolates in Ethiopia

Abebe Aseffa Negeri
Ethiopian Public Health Institute, Ethiopia

BACKGROUND: CTX-Ms are the most widely distributed extended spectrum β-lactamases (ESBL), and are the most important resistance mechanism to oxyimino-cephalosporins in *Enterobacteriaceae*. In most countries their dissemination is associated with resistance plasmids and international successful pandemic clones. This might also be true for Ethiopia, but very little is known about these associations. To address this knowledge gap, we took advantage of an established Ethiopian collection of CTX-M producing *E. coli* clinical isolates, several of which were international pandemic clones, and performed a molecular characterization of antimicrobial resistance plasmid carriage for the purpose of understanding the molecular basis for the rapid antibiotic resistance spread among bacterial populations in Ethiopia

METHODS: 100 CTX-M positive *E. coli* analyzed. The antimicrobial susceptibility test and ESBL phenotypic characterization were performed according to the Clinical and Laboratory Standards institute guideline. CTX-Ms production was analyzed using PCR-sequencing. Plasmids were transferred either by conjugation or by transformation. Transformability of CTX-M genes, plasmids incompatibility groups and addiction systems and *ISEcp*1 were identified by PCR.

RESULTS: of the 100 CTX-M producing *E. coli* isolates investigated, 75% carried transmissible plasmids encoding b*laCTX*-M genes: CTX-M-15 (n=51), other group 1 CTX-Ms (n=17), CTX-M-14 (n=1), and CTX-M-27 (n=6). Single IncF plasmids with the combination of F-FIA-FIB (n=17) carried the bulk of *bla*CTX-M-15 genes (n=40, 78.4%). IncF plasmids were also the most predominant plasmid type harbouring the genes for other group 1 CTX-Ms and group 9 CTX-Ms. In addition, IncF plasmids were associated with multiple addiction systems, *ISEcp*1 and various resistance phenotypes for non-cephalosporin antibiotics. Moreover, IncF plasmid carriage associated with the international pandemic E. coli clone ST131. The CTX-M plasmids were associated partly with serum survival of the strains, but not associated with biofilm formation.

CONCLUSION: Both horizontal gene transfer and clonal expansion contribute to the widespread distribution of CTX-M encoding genes in Ethiopia

5266354 | First Laboratory Confirmation and Sequencing of Zaire Ebolavirus in Uganda After Introduction of Cases from the 10th Ebola Outbreak in the Democratic Republic of the Congo, June 2019

Luke Nyakarahuka, Sophia Mulei, Jackson Kyondo, Alex Tumusiime, Baluku Jimmy, Stephen Balinandi, Julius Lutwama
Uganda Virus Research Institute, Uganda

BACKGROUND: Uganda established a domestic Viral Hemorrhagic Fever (VHF) testing capacity in 2010 in response to the increasing occurrence of filovirus outbreaks. In July 2018, the neighboring Democratic Republic of Congo (DRC) experienced its 10th Ebola Virus Disease (EVD) outbreak and for the duration of the outbreak, the Ugandan Ministry of Health (MOH) initiated a national EVD preparedness stance. Almost one year later, on 10th June 2019, three family members who had contracted EVD in the DRC crossed into Uganda to seek medical treatment.

METHODS: Samples were submitted for VHF diagnostic testing at UVRI. All samples were initially tested by RT-PCR for ebolaviruses, marburgviruses, Rift Valley fever (RVF) virus and Crimean-Congo hemorrhagic fever (CCHF) virus. The VHF laboratory at UVRI also performed Next Generation Sequencing (NGS) and phylogenetic analysis of the EVD confirmed samples for the first time in Uganda.

RESULTS: During this DRC EVD preparedness and enhanced surveillance period (August 2018 – December 2019), the VHF lab tested 1,098 suspect VHF samples, four of which were positive for EVD, eighteen were positive for CCHF and ten were positive for RVF. The first case was detected at Kagando hospital in Kasese district neighboring DRC. Three more cases were detected and treated at the Ebola Treatment unit (ETU) at Bwera hospital located in Kasese District making a total of 4 cases, three of which were one family cluster and the fourth was independently identified later in August 2019.

CONCLUSION: This is demonstration of the long-established VHF surveillance system in Uganda, and its near real-time detection and response capacity. This rapid response by the MoH, UVRI and partners led to the control of the outbreak and prevention of secondary virus transmission. The continuation of enhanced VHF surveillance and molecular diagnostics also detected a number of additional VHF cases during the same period.

5266700 | Strategie de Surveillance Génomique du SARS-CoV-2 au Gabon

Samira Zoa Assoumou[1], Armel Mintsa[2], Benedicte Ndeboko[3], Ludovic Mewono[4], Rodrigue Bikangui[5], Marien Juliet Verald Magossou[5], Georgelin Nguema Ondo[5], Joel Fleury Djoba Siawaya[3], Jean Bruno Lekana-Ndouki[6], Ayola Akim Adegnika[5]
[1]Uss, Gabon; [2]Laboratoire National De Sante Publique, Gabon; [3]Chumeje, Gabon; [4]Lpdg, Gabon; [5]Cermel, Gabon; [6]Cirmf, Gabon

INTRODUCTION : Depuis l'apparition du SRAS-CoV-2 fin 2019 à Wuhan, en Chine, des variants ont émergés dans le monde. La diffusion du SRAS-CoV-2 liée par les voyageurs alimente la pandémie mondiale et la propagation de variants. Ainsi, la surveillance génomique du SARS-CoV-2 permettrait de retracer l'émergence et la propagation des variants pour mieux comprendre et anticiper leur impact sur la santé publique. La surveillance génomique du SRAS-CoV-2 en Afrique a été décrite comme un défi. Néanmoins, le Gabon a relevé le défi de mettre en place et de mettre en œuvre la surveillance génomique du SARS-CoV-2.

METHODES : La surveillance génomique du SARS-CoV-2 au Gabon s'appuie sur un réseau des laboratoires COVID-19 du Gabon qui regroupe 15 laboratoires répartis dans neuf (9) régions sanitaires sur les dix que compte le pays et deux instituts de recherche, le CIRMF à Franceville et le CERMEL, à Lambaréné. Ces laboratoires de recherche utilisent les plateformes MinION et ABI 3500 Genetic Analyzer de Applied Biosystems pour la recherche des variants.

RESULTATS : Ainsi, depuis le début des activités de veille génomique au Gabon, 733 échantillons SARS-CoV-2 positifs ont été séquencés. La distribution des variants retrouvés est la suivante : variants préoccupants : Variant alpha (anglais, B.1.1.7) : 32,9% ; Variant Beta (Sud-africain, B.1.351) : 1,0% Variant Kappa, B.1.617.1: 0,9%. Concernant les variants d'intérêt (à suivre) : Variant B.1.525: 10,5% ; Variant B.1.1.318: 7,3% et Variant B.1.620 : 1,7%. Variant en cours d'évaluation : (B.1, B.1.1, B.1.400, B.1.1.409, A.21): 7%.

CONCLUSION : Cette initiative nationale en complémentarité avec les initiatives internationales et régionales permettra d'enrichir la base factuelle concernant la transmission et l'évolution du virus SARS-CoV2 au Gabon afin de guider au mieux les actions de santé publique visant à mieux contrôler la pandémie.

5239530 | Carbapenemase-Producing Enterobacteriaceae in Malawi: Genomic Composition and Features of Plasmids Encoding Carbapenemases

Geoffrey Kumwenda[1], Yo Sugawala[2], Watipaso Kasambala[1], Yukihiro Akeda[2], Kazunori Tomono[3], Shigeyuki Hamada[2]
[1]National Reference Laboratory, Ministry of Health, Malawi, Malawi; [2]Research Institute For Microbial Diseases, Osaka University, Japan; [3]Department of Infection Prevention And Control, Osaka University Hospital, Japan

BACKGROUND: Carbapenemase-producing *Enterobacteriaceae* (CPE) are a global health problem. Dissecting the genetic constitution of CPE is important in order to understand transmission events and curtail spread. This study described the advent and genetic characterization of CPE and plasmids encoding carbapenemases in Malawi.

METHODS: We investigated the presence of carbapenemases among 200 ceftriaxone-nonsusceptible *Enterobacteriaceae* from Malawi, January 2016 - December 2017. We employed phenotypic/genotypic tests and WGS using Illumina MiSeq and Oxford Nanopore platforms to genetically characterize CPE. Transmissibility of plasmids was assessed by filter-mating assay and stability of plasmids was evaluated under nonselective growth condition.

RESULTS: We detected 16 (8%) multidrug-resistant CPE from one referral hospital. These comprised seven *bla*KPC-2-positive *Klebsiella pneumoniae* ST340/CC258, two *bla*NDM-5-positive *Escherichia coli* ST636 (phylogroup B2), *six E. coli* ST617 (phylogroup A) and one *Klebsiella variicola* carrying *bla*OXA-48. Isolates of same strain-type displayed clonality despite originating from different wards, suggesting acquisition during admission and intra-hospital spread. *bla*KPC-2 was located on a mobile IncQ1 plasmid within a non-Tn*4401* (NTEKPC-IId) element. In *E. coli* ST617 *bla*OXA-48 was located within a Tn*1999.2* transposon on a self-transmissible IncL/M(pOXA-48) plasmid. In *K. variicola*, *bla*OXA-48 was encoded on an IncL/M(pOXA-48) plasmid-type that had acquired an extra genetic segment previously described in China. This region encoded *qnrS1* which was integrated into an inverted Tn*1999.2*, giving rise to a novel Tn*1999* variant (designated Tn*1999.6*). Additionally, this plasmid had *traH* and *traI* conjugation genes deleted, hence lost the ability to self-transfer. *bla*NDM-5 was located on a conjugative IncX3 plasmid previously described in Indian and China. Whilst IncQ1 and IncX3 plasmids exhibited high stability, IncL/M(pOXA-48) plasmids were rapidly lost in the absence of antibiotic selective pressure.

CONCLUSION: The study highlights the existence of genetically diverse multidrug-resistant CPE harbouring carbapenemase-encoding transferable and/or highly stable plasmids that are potential vehicles for the spread carbapenemases in Malawi.

Thursday, 18 November | 11:00 – 12:30
OWNERSHIP, PARTNERSHIP AND INNOVATION

ORAL SESSION 4500
RESEARCH FOR BETTER LABORATORY SYSTEMS AND NETWORKS

CHAIRPERSONS:
Linda Oskam; Collins Odhiambo

5228417 | Field Evaluation of the Asanté HIV-1 Recency Assay for HIV Diagnosis and Recent Classification Using Samples from the Nigeria HIV/AIDS Indicator and Impact Survey

Ernest Yufenyuy, Mervi Detorio, Jeni Vuong, Amy Zheng, Olumide Okunoye, Mcpaul Okoye, Bharat Parekh
Centers For Disease Control And Prevention, United States

BACKGROUND: Asanté HIV-1 Recency Assay, a rapid test for recent infection, diagnoses HIV infection and distinguishes HIV-1 recent from long-term infection. A field evaluation was performed using remnant samples from the Nigeria HIV/AIDS Indicator and Impact Survey (NAIIS -2018) to assess the performance and accuracy of Asanté for diagnosis and recent characterization.

METHODS: Plasma samples consisting of all HIV-positive (n=2,772), -indeterminate (n=172), and a subset of negative specimens (n=7,061) from NAIIS, were tested on the Asantéand results were read both visually and by use of a reader. Using the national HIV testing algorithm samples were classified as HIV positive or negative. HIV-1-positive samples were classified as recent or long-term. Data were analyzed using latent class analysis (LCA) and 2x2 tables. LCA was used to evaluate Asanté against each of the following: the national HIV testing algorithm, Geenius, and Western Blot. 2x2 tables were used to compare visual and reader interpretations and Limiting-antigen avidity and Asanté recency results.

RESULTS: Sensitivity and specificity of Asanté was 98.2% and 98.9%, respectively. Sensitivity and specificity using LCA was 99.0% (range 98.7 – 99.9%) and 98.8% (range 98.2 – 99.7%), respectively, compared to each of the 3 tests. Visual interpretation of results and the use of a reader were comparable for both verification and long-term lines (99.8% and 93.5% agreement, respectively). Asanté showed good agreement (93.5%) with the LAg for recent infection classification.

CONCLUSION: Results demonstrate that Asanté may be used for HIV diagnosis and recent infection classification. The performance of the reader was comparable to visual interpretation. Overall, the sensitivity and specificity of the Asanté showed good agreement with final NAIIS results and met WHO prequalification criteria. Asanté's ability to provide rapid diagnosis and identification of recent infections could enable real-time public health response that could accelerate the epidemic control.

5228079 | Dried Tube Specimens for Quality Assurance in the Implementation of Rapid Tests for Recent HIV-1 Infection

Keisha Jackson, Mervi Detorio, Jeni Vuong, Latasha Williams, Bharat Parekh, Ernest Yufenyuy
Centers For Disease Control And Prevention, United States

BACKGROUND: Rapid tests for recent infection (RTRI) distinguish recent (<12 months) from long-term (>12 months) HIV-1 infection are being implemented globally to interrupt HIV transmission. Efforts to improve the accuracy of RTRIs in the field rely on quality assurance measures including quality control (QC) and proficiency testing. We explored dried tube specimen (DTS)-based panels for RTRI QC, which does not require cold-chain for transportation.

METHODS: DTS were prepared using three plasma QC samples (HIV negative, HIV-1 recent, and HIV-1 long-term (LT), stored at different temperatures (-20°C, 4°C, 25°C, 37°C, and 45°C) for 28 weeks and tested weekly using Asante RTRI by two testers. Samples stored at -20°C were tested monthly. The stability of the DTS eluate was tested over 7 days at similar temperatures and over five freeze/thaw cycles. All results were interpreted visually and with the reader.

RESULTS: Visual and reader classifications of the recent sample were maintained up to 11 weeks at 4°C, 2 weeks at 25°C, and <1 week at 37°C. For LT samples, the positive verification line was maintained at all temperatures during the study, and the LT line was maintained for 28 weeks at 4°C, 3 weeks at 25°C, and steadily declined in signal and intensity at 37°C. Similar results were observed at higher temperatures. Storage at -20°C maintained both visual and reader interpretations during the study (>1 year). DTS eluate was stable over 7 days stored at all temperatures with minimal decline and across five freeze/thaw cycles.

CONCLUSION: Our results suggest that once prepared, DTS specimens can be stored should be stored at -20°C until shipment and testing the samples immediately upon receipt would improve accuracy and quality of RTRI.

5265071 | Approaches for Improving the Turnaround Time for Viral Load Testing Services in the Eastern Province of Zambia

Lugard Sichalwe[1], Gideon Zulu[2], George Mwakanandi[3], Wessy Miyanda[3], Martin Mwanza[4], Cletus Kabwe[3], Charles Shumba[2], Goodsons Mukosa Mpumba[2], Clement Phiri[1], Ranjit Warrier[4]
[1]Association of Public Health Laboratories, Zambia; [2]Ministry of Health - Clinical Care Services, Zambia; [3]Ministry of Health - Pathology And Laboratory Services, Zambia; [4]The Centre For Infectious Disease Research In Zambia - Lab Innovation For Excellence, Zambia

BACKGROUND: The Eastern Provincial Health office experienced viral load (VL) backlogs with a high turnaround time (TAT) of average 119 days beyond the national established guildelines of 14 days. This caused a delay in test results and a potential reduction in the VL testing numbers, with prospects of affecting provision of timely healthcare.

METHODS: Strategies and potential outcomes of mitigating the high TAT were evaluated and implemented from January 2018 to December 2019, focusing on the available laboratory testing space, capacity of the testing platform, the number of VL hubs and location from the testing laboratory, adequacy of sample preparation equipment, and the existing courier system.

RESULTS: A new molecular testing laboratory was refurbished at Chipata Central Hospital with the installation of a higher throughput VL testing machine, the Cobas 4800, and specimen storage refrigerators. Zonal mapping of 10 VL hubs was completed, and where capacity was built with equipment such as refrigerators and centrifuges. Eight Laboratory hubs and 69 health facilities had Disalink and e-labs, the remote Laboratory Information Systems (LIS) for sample registration and result return installed and interfaced with the LIS, Disalab, at the testing laboratory. The Laboratory hubs were also provided with data capturing registers, thermometers, and onsite mentorship. In addition, ten motorbikes and one vehicle were procured to support the existing intra- and inter-district courier system. Subsequently, the molecular laboratory cleared the 15,324 VL backlog with the provincial pre and post-data analysis illustrating TAT improvement from 119 days to within 14 days. Viral load tests equally increased by 63.5%, attributed in part to the improved laboratory diagnostic services implemented.

CONCLUSION: Capacity building of laboratory systems with critical infrastructure and equipment is key to the improvement of diagnostic services. It is thus, cardinal that programs are evaluated and supported to attain the intended outcome.

5225238 | LabBook 3.0, an Opensource LIS Developed to Facilitate Data Exportation to DHIS2 and WHONET

Anja Mampianina Ramilson[1], Mafoudji Kande[1], Oumar Kanté[2], Alexandre Charles[3], Philippe Meurier[3], Philippe Brun[3], Aicha Marceline Sarr[1], Laurent Raskine[1], François-Xavier Babin[1], **Nicolas Steenkeste**[1]
[1]Fondation Merieux, Madagascar; [2]Centre Hospitalier Régional De Ziguinchor, Senegal; [3]Aegle, France

BACKGROUND: The Mérieux Foundation is committed to fighting, in the field, the infectious diseases that affect developing countries by building capacities, particularly in clinical laboratories. Its mission is to improve the access to diagnostics in developing countries.

One of the objectives was to develop a Laboratory Information System (LIS) to help and guide laboratories moving from paper-based laboratory workbooks to a software solution that is easy to use and maintain. As a result LabBook was created in 2010 co-funded by AFD and Mérieux Foundation. The software is available on the LabBook website: https://www.lab-book.org/. Three releases of the software have been released by Epiconcept (LabBook 1.0, 2.0 and 2.5). A survey was then conducted to better understand the use of the software which led to the release of LabBook 3.0 by AEGLE.

METHODS: A survey of 100 direct users (laboratory staff) and indirect users (MoH) from 8 countries (Benin, Burkina Faso, Guinea, Madagascar, Mali, Niger, Senegal, Togo) was conducted with 33 questions.

RESULTS: 64/100 users of this survey were direct users of LabBook in the daily routine of their lab work and 36/100 were indirect users. The most noted aspect of LabBook were its ease of use and its data analysis capability.

The most requested improvements were to increase the software celerity, the data analysis capability, the flexibility of the analysis results report layout, and above all the export antimicrobial resistance (AMR) data to WHONET.

CONCLUSIONS: Based on this survey a new version of LabBook was developed: LabBook 3.0. It can be downloaded freely from the project website. This new release is faster as the framework has been completely redeveloped (MySQL, Python, Podman). As an Opensource solution, the code is available on Github.

To reinforce the data analysis capability, LabBook 3.0 is now able to export to DHIS2 and WHONET. Moreover, the quality management interface has been improved and now integrates a stock management solution directly in LabBook 3.0.

5266585 | Peut-On Utiliser L'Antithrombine À la Place du Facteur v dans L'évaluation de L'insuffisance Hépatocellulaire Chez les Patients Cirrhotiques ?

Mohamed El Horri[1], Abdelkrim Chikh Khelifa[1], Ibrahim Khachaa[1], Malika Baghdadi[1], Fatima Seghier[2]
[1]Military University Hospital of Oran, Algeria; [2]Hospital University Center of Oran, Algeria

INTRODUCTION : L'insuffisance hépatocellulaire (IHC) retrouvée dans la cirrhose est associée à des manifestations cliniques et biologiques, secondaires à l'altération des fonctions hépatiques telle la perturbation de la synthèse des facteurs de la coagulation. Notre Objectif était d'évaluer les performances du FV et de l'AT dans le diagnostic de l'insuffisance hépatocellulaire associée à la cirrhose du foie.

PATIENTS ET MÉTHODES : Il s'agit d'une étude descriptive prospective portant sur 110 patients cirrhotiques. Les dosages du Facteur V et de l'Antithrombine ont été fait par methodes chronométrique et chromogénique.

RÉSULTATS : L'âge moyen de nos patients était de 65 ans. Le sex-ratio était de 1,2 avec une prédominance masculine. Les étiologies étaient majoritairement virales (HCV et HBV) avec 43% de fréquence . La cirrhose était compensée dans 28% des cas. Les décompensations liées à une insuffisance hépato-cellulaire étaient présentes chez 63% des patients. 38,1% des patients avaient un score Child Pugh A, le reste était reparti entre le Child Pugh B et C.

Par rapport aux patients compensés, les patients présentant des décompensations liées à une insuffisance hépatocellulaire, nous avons constaté une différence statistiquement significative dans les taux du facteur V et de l'Antithrombine ; le FV (respectivement 73 et 47%, p=0.000), l'AT (respectivement 77% et 47%, p=0.000). Cette association était plus forte que le TP et l'INR. Les valeurs du facteur V et de l'Antithrombine étaient d'autant plus diminuées que la maladie s'aggrave (selon le score Child Pugh). (p= 0,007). De plus nous avons observé qu'il y'avait une excellente corrélation linéaire entre les taux du facteur V et de l'Antithrombine (r = 0,916).

CONCLUSION : La corrélation positive nous a permis de conclure que les deux ont les mêmes performances diagnostiques. Donc il est possible d'utiliser l'Antithrombine comme marqueur d'évaluation de l'insuffisance hépatocellulaire au même titre que le facteur V.

5239491 | Performance Evaluation of the Panbio ™ Covid-19 Antigen Rapid Test Device Compared to a PCR-Based Point of Care Test

Bonolo Mashishi, Bhaveshan Reddy, Nonhlanhla Mbenenge, Kathleen Subramoney, Florette Treurnicht
Virology, National Health Laboratory Service-Charlotte Maxeke Johannesburg Academic Hosp / Univ of Witwatersrand, Johannesburg, South Africa

BACKGROUND: The gold standard for severe acute respiratory distress syndrome-2 (SARS-CoV-2) diagnosis is detection of the virus gene fragments by real-time revere transcription polymerase chain reaction (rt-RT PCR) which can be expensive and laborious. Decentralised point-of-care rapid antigen testing is a feasible and cost-efficient alternative in response to growing demands for disease diagnosis in outbreak and pandemic settings.

METHODS: A total of 114 (64 positive and 50 negative) respiratory samples that were either freshly collected or retrieved from storage were included. Each sample was tested with the Panbio ™ COVID-19 Ag rapid test device (Abbott Rapid Diagnostic Jena GmbH, Jena, Germany) and the Xpert ® Xpress SARS-CoV-2 point of care rRT-PCR assay (Cepheid, Sunnyvale, CA, USA) as a reference. Fresh samples were collected with the Panbio™ rapid antigen swab and sample buffer whereas for stored samples a Panbio ™ swab sample was generated in the laboratory.

RESULTS: The overall performance of the Panbio™ had a sensitivity of 46.88% 95%CI (34.28-59.77%) and a specificity of 100% 95%CI (92.89-100%). For samples testing positive on the Xpert ® assay with cycle threshold values ≤35 the Panbio™ COVID-19 Ag rapid test had a sensitivity of 68.18%; 95%CI (52.42-81.39) and a specificity of 100%; 95%CI (92.89-100%), the Cohen's Kappa value was 0.70; 95%CI (0.566 to 0.84). The rapid antigen test did not detect SARS-CoV-2 in samples that were positive with ct values greater than 35 (n=19) on the Xpert ® assay.

CONCLUSION: Consensus agreement is that further viral transmission is only of concern in persons who test positive by PCR with ct values less than 35. Therefore, despite low assay sensitivity the Panbio ™ rapid antigen test was found acceptable for point of care diagnosis of SARS-CoV-2. However, where clinical suspicion is high for COVID-19 in cases that test negative by rapid antigen assay a sample must be submitted for SARS-CoV-2

ORAL SESSION 4550
PARTNERSHIP, POLICY AND REGULATION TO IMPROVE ACCESS AND EQUITY OF DIAGNOSTIC TOOLS

CHAIRPERSONS:
Francesco Marinucci; Anafi Mataka

5237213 | Assessing the Costs of Extending Cryptococcal Antigen (CrAg) Reflex Testing in South Africa up to a CD4 Count of 200cells/µl

Lindi Coetzee[1], **Naseem Cassim**[1], Deborah Glencross[2]
[1]National Health Laboratory Service (NHLS), Johannesburg, South Africa;, South Africa; [2]Department of Molecular Medicine And Haematology, University of The Witwatersrand, Johannesburg, South Africa, South Africa

BACKGROUND: The routine national reflexed CrAg program tests all CD4 patient samples with a count <100cells/µl through a network of 47 CD4 laboratories, using the IMMY lateral flow assay (LFA). Changes in CrAg testing guidelines include samples with a CD4 count of 100-200cells/µl; representing 11% of annual testing, with a CrAg positivity rate of 2.4%, compared to 6.7% positivity for routine CrAg testing.

AIM: The study assessed the cost impact of extended CrAg reflex testing.

METHODS: An exchange rate of R14.518/$1, error rate of 1% and annual discount of 4% was used. The outcomes reported cost-per-result, annual equivalent costs (AEC) and the cost per CrAg positive result for a CD4 count <100, 100-200 (with four 25cells/µl increments) and <200cells/µl. Laboratory CrAg test volumes and positivity rates were used. Calculated costs included laboratory equipment, staff and reagents. The percentage full time equivalent (FTE) was calculated from nett working minutes/annum, multiplied by annual salary costs for an AEC per staff category.

RESULTS: The cost-per-result was similar for samples with a CD4 <100 and 100-200cells/µl. A cost-per-result of $6.88 was reported, where laboratory equipment, staff and reagents contributed 0.05%, 34.7% and 65.3% respectively. The AEC was $2 090 604 for the CD4 100-200cells/µl group ($1 983 183 for CD4<100cells/µl) and $4 073 788 for the total CD4 <200cells/µl category. The cost of finding a single CrAg positive sample with a CD4<100cells/µl was $91.52, with a 3.5-fold increase to $320.30 in the 100-200cells/µl category.

CONCLUSION: The cost-per-result was equivalent for samples with a count <100 vs. 100-200cells/µl, but the addition of the 100-200cells/µl samples, will effectively double the AEC for the national programme. CrAg positivity rates of <2% resulted in significantly higher costs per positive CrAg outcome than positivity rates >5%. A full cost-effectiveness study is needed to assess the impact on patient outcomes.

5237045 | Cartographie des Laboratoires au Mali

Ousmane Traoré[1], Adama Sangaré[2], Souleymane Ongoiba[2], Sekou Traoré[1], Boubacar Doumbia[3], Samba Diallo[4], Ashenafi Aytenew[4], Seydou Fomba[2], Sere Keita[4], Yaya Coulibaly[1]
[1]DPM, Mali; [2]IDDS, Mali; [3]INSP, Mali; [4]ASLM, Burkina Faso

INTRODUCTION: La complétude des données sur la capacité des laboratoires de la plupart des pays africains est insuffisante et pose de nombreux défis dans leur amélioration. Afin de combler ces lacunes, la Société Africaine de Médecine de Laboratoire a développé un outil pour la cartographie des laboratoires, qui a été utilisé dans plusieurs pays d'Afrique subsahariens. Le Mali a bénéficié de cette expertise et a procédé à la cartographie des laboratoires à Bamako et dans 4 régions, pour les besoins de renforcement et les prises de décisions.

MÉTHODES: vingt-trois agents des laboratoires ont été formés sur la collecte des données sur l'outil de collecte «ODK COLLECT» et la plate-forme de stockage de données «ONA». La collecte a été effectuée en utilisant un questionnaire préétabli dans une tablette. Les structures concernées étaient les laboratoires de tous les niveaux des structures sanitaires publiques, privées, confessionnelles, de la santé animale, de l'agriculture et de l'environnement. La collecte a été réalisée de décembre 2020 à avril 2021.

RÉSULTATS: 282 laboratoires ont été cartographiés 95 à Bamako, 34 à Kayes, 63 à Koulikoro, 47 à Sikasso et 43 à Ségou. Les laboratoires de 1er niveau étaient les plus représentés avec 72,34%, le 2ème niveau 18,8%, le 3ème niveau composé des structures centrales et hôpitaux 8,90%. La charge virale et le diagnostic précoce du VIH chez les enfants étaient réalisés au niveau central respectivement dans 36% et 27% des laboratoires cartographiés. Seul 10% des laboratoires cartographiés réalisaient la culture bactérienne et 4% les tests de résistance antimicrobienne. Seulement 30% des laboratoires respectaient les bonnes pratiques de laboratoire.

CONCLUSION: Cette cartographie a permis d'avoir la situation réelle des laboratoires visités. Ces résultats aideront pour les prises de décisions en vue du renforcement des capacités et l'organisation du système de laboratoire.

MOTS CLÉS: laboratoire, cartographie, Mali.

5265966 | Impact of COVID-19 Pandemic Mitigation Strategies on Viral Load Coverage, Viral Suppression and Continuity of Treatment in PEPFAR Supported Facilities in the Hhohho and Shiselweni Region at Eswatini

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BACKGROUND: Despite achieving global 95-95-95 HIV-targets in 2020, Eswatini was hard-hit by the COVID-19 pandemic resulting in disruption of health service provision due to lockdown restrictions and supply chain interruptions. The Ministry of Health therefore, introduced a set of strategies to mitigate the negative impact of COVID-19 pandemic on patient outcomes.

METHOD: Various client-centered strategies were implemented in 65 PEPFAR-supported health facilities in the Hhohho and Shiselweni regions of Eswatini to mitigate a possible negative impact on health outcomes of people living with HIV and to ensure continuity of treatment to achieve viral suppression. The implemented strategies included community ART drug-distribution, multi-month dispensing, integration of viral load (VL) monitoring during community commodity distribution, scale-up of dried-blood-spot VL and quality improvement approaches. To determine the effect of these strategies, we analysed data on VL testing coverage, VL suppression and retention at 12months. Pre COVID-19 period (April, 2019 to March, 2020) and during COVID-19 period (April, 2020 to March, 2021) performance were compared.

RESULTS: Mean quarterly VL coverage was 83% (80% among <15yrs; 83% among ≥15yrs; 95% CI=79.71%-86.41%) during pre-COVID-19 period and 91.09% (83% among <15yrs; 92% among ≥15yrs; 95% CI=82.95% - 99.22%) in the COVID-19 period. Mean quarterly VL suppression was 97% (93% among <15yrs; 97% among ≥15yrs; 95% CI=95.28%-98.72%) during pre-COVID-19 period and was maintained at 97.25% (92% among <15yrs; 97% among ≥15yrs; 95% CI=95.36%-99.14%) during COVID-19 period. The 12-month retention was 74% (67% among <15yrs; 74% among ≥15yrs) during pre-COVID-19 period and 91% (100% among <15yrs; 91% among ≥15yrs) during COVID-19 period.

CONCLUSION: Deliberate efforts to implement patient-centered strategies proved effective in improving VL coverage, sustaining VL suppression and maintaining continuity of treatment during the COVID-19 era. However, the extent to which each specific intervention contributed to improved outcomes requires further evaluation.

5265948 | Public-Private Collaborative Approach to Strengthening Clinical Laboratory Capacity in Routine and Emergency Diagnostics Services: Lessons from Nigeria

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BACKGROUND: Access to quality diagnostics services is critical to achieving Universal Health Care (UHC) in resource-limited countries. In Nigeria, only seven of the more than 5,000 medical laboratories are internationally accredited, a benchmark of quality laboratory services. Public-private collaboration can accelerate the provision of quality laboratory services to the population. Consequently, the United States Pharmacopeia, Inc., (USP) engaged a privately owned and operated Access to Basic Medical Care laboratory (ABC), in Ibadan, Nigeria, towards international accreditation.

METHOD: Traditional SLMTA approach has helped public health laboratories to strengthen quality systems; but the progress is slow, averaging three-years to achieve accreditation. USP developed rapid-integrated-collaborative-approach (RICA) to fast-track journey to accreditation.

RICA begins with high-level management commitment through a memorandum of understanding (MoU); agreed-upon implementation plan; and allocate resources. From the the results of rapid assessment of quality management systems, laboratory improvement work plan is developed and signed off. The lab then develops standard procedures, hands-on testing and quality control, equipment maintenance plan, quality manual, biosafety/biosecurity, and internal process audits according to quality management systems standards towards accreditations.

RESULTS: In just one year of technical oversight by USP (from April 2020 to June 2021), the ABC laboratory was accredited by the Nigeria National Accreditation System (NiNAS) according to ISO 15189:2012. Today, the lab has over 100 SOPs, a quality manual, and other essential quality system documents; well-trained staff; strong management reviews; and functional equipment.

CONCLUSIONS: With USP's technical oversight, using RICA, ABC laboratory (a privately owned/operated) achieved international accreditation status as per ISO 15189: 2012 within one year of implementation. This accreditation signals that ABC now produces consistent, reliable, and valid data that can be trusted for medical decisions. With strong private sector collaboration, countries like Nigeria can accelerate access to basic care services towards UHC goals.

5264009 | Development of An All-In-One Transportable Clinical Bacteriology Laboratory: Feedback from Testing the Mini-Lab Prototype in Haiti

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BACKGROUND: MSF projects often operate in settings where patients are treated for invasive bacterial infections. However, these projects often lack laboratory capacity to diagnose pathogens and their antibiotic susceptibility. Next-generation diagnostics adapted to low-resource settings (LRS) are unlikely to become available within the near future, therefore MSF is currently working develop a stand-alone, transportable laboratory ("Mini-Lab") by adapting existing diagnostics and antibiotic susceptibility testing (AST) of bloodstream infections.

METHODS: The first Mini-Lab prototype was deployed in the MSF Burn Centre (Drouillard) in Port au Prince, Haiti from July 2019 to April 2020. The overall usability and ease-of-use of the analytical components were evaluated using a self-administered user experience questionnaire, with Osgood scale/Likert-type scale. Adherence to compliance was monitored using checklist and direct observation. Performance of analytical results was evaluated against standard methods in a reference laboratory in Europe (Bacteriology-Hygiene unit, Assistance Publique - Hôpitaux de Paris, Bicêtre Hospital, Le Kremlin-Bicêtre, France).

RESULTS: Even non-expert lab technicians found the Mini-Lab components easy to use (overall score: 96% maximum user-friendliness) and that their competencies improved in a short period of time (after training: 68%; 4 months: 91%). The agreement of full identification of Gram-negative organisms was 100% at genus and 98.3% at species level, while for Gram-positives was 100% and 88.6%, respectively. Categorical agreement of AST was >90% on the majority of antibiotic/organism combinations.

CONCLUSION: Overall, the experience in Haiti showed no major flaws and good adaptability of the Mini-Lab to field settings, encouraging further testing at field-level. The evaluations confirmed the high quality of performance, ensuring robustness of microbiology diagnostics in field conditions. Our results provide critical information to enhance the second prototype that will be deployed as the next step for fully integrated patient care in an MSF supported district pediatric hospital at Central African Republic.

5223605 | An Effective Implementation of Antigen Rapid Diagnostic Test (Ag – RDT) for COVID-19: A Program to Increase Testing Capacity in the African Region

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BACKGROUND: Despite significant progress in the adoption of COVID-19 RT-PCR testing across Africa, testing remains a challenge in many African countries. In December 2020, Africa CDC, in collaboration with partners,introduced the Ag- RDT for COVID-19 testing as part of a critical tool for scaling up testing in the fight against COVID-19. The goal is to expand COVID-19 testing capacity, increase testing access in decentralized settings, and eventually meet testing demand in all Member States. The purpose of the study is to examine the implementation of Ag-RDT testing as well as progress of scaling up Ag testing for COVID-19 diagnosis.

METHOD: The Africa CDC Ag- RDT for COVID-19 testing data given by Member States was examined. Trends in Ag testing, as well as the percentage of all tests and training data, were analyzed from April to June,2021

RESULT: As of June 30, 2021, 54 countries have reported over 52 million PCR tests with an average of 10% positivity rate (range 0.5-67.5%). Only 8(15%) of countries have a positivity rate of less than 5%. Since the Ag testing was launched, the Africa CDC has distributed over 6 million Ag testing kits to the 54 Member States, with overall increases in the proportion of Ag testing from 15 % in May 2020 to 41% of the total testing in March 2021. Nearly 4 million Ag –RDT tests were conducted in 12 countries with a positivity rate of mean 4.8%. Over 14,500 people were trained and Ag testing sites have increased from 120 to 450 sites from June 2020 to May 2021.

CONCLUSION/IMPLICATIONS: The results suggest that increasing testing for COVID-19 through deployment of rapid antigen tests will be effective to increase testing capacity. Partner coordination mechanism established by Africa CDC has allowed quick mobilization of resources, technical assistance and created synergy among.

ORAL SESSION 4575
HARNESSING THE POWER OF COMMUNITY

CHAIRPERSONS:
Helen Etyaale; Suzanne Kiwanuka

5236713 | Reaching the Unreached for HIV Viral Load Testing During the COVID-19 Pandemic: A Community-Led Camp Approach in Northeastern India

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BACKGROUND: The COVID-19 pandemic amplified the challenges of ensuring access to HIV viral load (VL) testing, in northeastern India, which has limited access to services owing to difficult terrain, suspension of testing, and travel restrictions. Community-based camps could help increase VL testing access which is critical for ART outcome, through systematic client mobilization and efficient laboratory workflow.

METHODS: The community-led camp approach focusing on key populations (KP) and children living with HIV (CLHIV) was a multi-partner initiative implemented in Nagaland, Manipur, and Mizoram states, at locations where large clusters of eligible individuals on ART for more than 6 months, unable to access VL testing. The implementation process included demand generation initiatives, community mobilization, sample collection and handling, transportation, testing, reporting, report utilization, and monitoring. Descriptive statistics and McNemar chisquare test were done. P-value less than 0.05 was considered statistically significant.

RESULTS: Of the 3,836 whole blood samples collected through 112 camps (April 2020–March 2021), most were from Manipur (61%), followed by Nagaland (20%) and Mizoram (19%). KP and CLHIV constituted 22% and 2% of the samples respectively. of the total VL testing through Roche and Abbott platforms in Manipur (7,654), Mizoram (5,786), and Nagaland (5,726), camps contributed 31% (2,342), 12% (717), and 14% (777) respectively. Around 70% (542) of those tested at camps in Nagaland were first-time clients, followed by 65% (464) in Mizoram and 19% (444) in Manipur. The pre-analysis sample rejection rate was 1.6% in camps. The camp approach, coupled with other strategies, significantly increased VL coverage from 24% to 66% in Nagaland, 38% to 67% in Mizoram, and 24% to 56% in Manipur from December 2020 to March 2021 ($p<0.001$).

CONCLUSIONS: The community-led camp approach effectively improved access to VL testing, especially among those who were never tested in hard-to-reach areas, ensuring the provision of services.

5262192 | Routine Viral Load Testing: Community-Led Campaigns to Increase Demand for the Test that Counts

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BACKGROUND: Routine viral load testing (RVLT) is essential to effective HIV treatment monitoring among people living with HIV (PLHIV). Scaling up RVLT is a key contributor to the goal of achieving viral suppression among people on antiretroviral treatment. However, uptake of RVLT among PLHIV remains low, hindered by a mix of demand and supply-side barriers; a significant barrier is the lack of awareness of the need for and importance of RVLT. Innovative, community-led approaches are needed to generate demand.

METHODS: The International Treatment Preparedness Coalition (ITPC) and six community organisations implemented a stepwise process for generating demand in the Democratic Republic of Congo (DRC), Malawi, Kenya, Sierra Leone, South Sudan and Zimbabwe. Multistakeholder teams jointly identified context-specific barriers to RVLT and affected populations. Country-specific multimedia communication campaigns, including tracking metrics, were developed and rolled out by communities between November 2020 - January 2021.

RESULTS: Overall, communication campaigns targeted adults, youth, expectant mothers, key populations, healthcare personnel, religious leaders and health ministry representatives. Carefully crafted messaging was disseminated across social & mass media, mobile, online, print and in-person platforms. Adults (Zimbabwe), youth (Kenya, South Sudan), and women and expectant women (DRC, Malawi) were most reached. Meanwhile, website (DRC), Twitter (Kenya), WhatsApp (Malawi) and radio (South Sudan, Zimbabwe) were most accessed. In-person meetings addressed queries and clarified messaging. Greater awareness led some individuals to seek RVLT testing. However, access to viral load tests was impacted negatively by COVID-19 and non-functioning machines, particularly in Sierra Leone.

CONCLUSIONS: Context-specific communication campaigns are effective tools for reaching and creating awareness about RVLT among PLHIV. Longer, more targeted campaigns hold the potential for reaching more people, increasing knowledge and effecting behaviour change – even more so when informed and adapted to local realities. However, systemic barriers to access should be addressed to ensure demand creation leads to RVLT access.

5262097 | Description of Women Attending First Antenatal Care Visits at Saboti Sub County Hospital from March to December 2020

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Saboti Sub County Hospital, Kenya

INTRODUCTION: Antenatal care (ANC) is a key strategy to improve maternal and infant health. The World Health Organization (W.H.O) recommends a 'Focused' ANC, consisting of (at least) four visits to a health facility during an uncomplicated pregnancy to be initiated within the first trimester of gestation. In sub-Saharan Africa women initiate ANC after the first trimester. The study was to describe socio demographics, assess teenage pregnancy, assess HIV and Syphilis positivity, characterize 1st visits by trimester and gravidity and conduct Data Quality Audit (DQA)

METHODS: The Study area was Saboti Sub County Hospital and all women who attended first ANC March – December 2020 (n=509)were included. This was a retrospective data review from ANC Register (MOH 405). The Data abstracted from MOH 405 and descriptive data analysis and DQA done on Excel.

RESULTS: The mean age of women was 25 with SD of 7 years and 23.4 % were teenagers. Women of 20-24 age group were 34% and 67.4% started ANC in their 2nd trimester. Married women and 1st time mothers were 78.4% and 37.7% respectively with HIV and Syphilis positivity of 0.6 % and 0.4 % respectively and 4 % of women received ITNs

CONCLUSION: Intended pregnancies is directly proportional to seeking ANC and 12.4% initiating ANC Care at 1st trimester was lower than western region of 20% (KDHS 2014). Syphilis screening is a key in prevention of poor pregnancy outcomes and possibly the two previous lost pregnancies were due to latent syphilis infection. ITNs had been out of stock and the 23.4% of teenage pregnant women was higher than, Lamu, Garissa and Wajir at 10% but lower than Narok at 40%. Recommendations; Community Directed interventions, Strengthen PMTCT, aPNS and Laboratory Testing and Maintain consistent supply of ITNs

5266674 | Maximizing the Benefits of Laboratory Tests During COVID-19 Pandemic by Systematically Engaging Community Networks and Leadership Structures in COVID-19 Suspect Identification (Alerts Approach)

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BACKGROUND: COVID-19 pandemic in Lesotho is part of the on-going worldwide pandemic of COVID-19 caused by SARS-CoV-2. The virus was confirmed to have reached Lesotho on 13 May 2020 with a traveller from South Africa. Many Lesotho citizens are employed in South Africa, most on temporary contracts in the mines or urban industries and they are frequently travelling back home. This made it difficult to the country to control COVID-19 transmission from these kinds of travellers since many of them are used to illegal crossing in and out of this neighbouring country while COVID-19 testing shows high cases among them. This challenge was minimized by designing a system that involved communities strictures which can identifies new travellers, so that they can be tested with COVID-19 RDT in a nearby Health facility before they interact with other community members.

METHODS: Master trainers Identification: National Reference Laboratory staff and its co facilitators and The National COVID-19 Secretariat, Its responsibility was to design a system approach.

Capacitation of district response teams

Training of Health Facilities on COVID-19 RDT antigen testing and community structures on case definition organized by Health Facilities Committees

RESULTS: 298 COVID-19 testing sites activated within a month, compared to 3 regional facilities which were used. COVID-19 test yield for travellers increased by 48%, an indicative that there were travellers that were coming in communities without being screen for COVID-19.

CONCLUSIONS: Where responsibility is well transferred to the community, the impact of public health initiative is improved. It was observed that communities implemented this strategy experience no COVID-19 outbreaks and deaths. This approach can be fruitful in Nations where its majority of population are located rurally.

5266149 | Assessing the Feasibility of Use of a Digital Health Solution to Support Antigen RDT (AgRDT) Screening (Professional Collection and Testing) at Taxi Ranks in Johannesburg, South Africa

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BACKGROUND: Previous studies in South Africa suggested that public transport, especially minibus taxis, are amongst the drivers of airborne transmission of disease. This study utilizes digital tools in conjunction with Rapid Antigen diagnostic tests to deliver COVID-19 testing to commuters, drivers, and vendors frequenting high-volume taxi ranks in Johannesburg.

METHODS: Prior to the intervention, a random survey was conducted within these ranks to determine knowledge, attitudes, and practices around COVID-19 testing. Testing points were established in well-ventilated areas of the taxi ranks. Consenting individuals completed a digital screening questionnaire on COVID-19 risks, which used a simple algorithm to determine who should be tested. Testing was conducted by trained nurses, with results sent to participants' phones. Positive cases were provided with information on health facilities to attend if needed, and followed up for two weeks by SMS and WhatsApp to encourage self-reporting of symptom severity through an online portal. All data was captured in the digital platform in real-time and submitted to the national dashboard.

RESULTS: There was high demand for testing: 78% of 1,591 individuals surveyed had never been tested, but 84% responded that they would get tested in the rank if available. In the first month of the intervention, 3,924 individuals were screened, with 10.1% identified as moderate risk and 24.3% as high risk. 1,187 Ag-RDT tests were completed. Positivity rate was 16% (190/1,187) overall, and higher among individuals identified through the digital algorithm as high-risk (19%), compared to those classified as moderate risk (8%).

CONCLUSIONS: Preliminary data suggests that point of care testing can be delivered in transport hubs, in conjunction with digital tools to support data capture and transmission, remote monitoring of the intervention and patient follow-up. This approach could be considered for expansion of testing beyond traditional health facility settings.

5266087 | Evidence of Reduced Academic Performance Among School Children with Helminthic Infection in Spite of Nutritional Status

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BACKGROUND: Soil transmitted helminths (STH) pose a formidable health risk to school-age children in resource-limited settings. Unfortunately, mass deworming campaigns have been derailed since the onset of the COVID-19 pandemic. The present study assessed the cross-sectional associations between intestinal helminthic infections, nutritional status and academic performance of school children in the Banda District of Ghana.

METHODS: School children (5–16 years) (n=275) were recruited through household visits by community health workers using a multi-stage cluster sampling technique. Data were collected through interviewer administered questionnaire. Anthropometric measurements of weight and height, stool microscopy and blood analyses for malaria, zinc and copper were performed. Multiple linear regression analyses were used to evaluate associations between academic performance and independent variables with significance accepted at $P< 0.05$.

RESULTS: Prevalence of STH was 49.5% (95% CI: 43.5%-55.4%). Commonly detected helminths were *Taenia sp., Entamoeba spp., Schistosoma spp., Strongyloides spp.*, and *Ascaris sp.* Children with helminth infection (53.7±11.5) had lower mean academic scores compared to uninfected children (59.6±16.9) (p=0.034). Undernourished children (67.4±17.5) had higher mean academic scores compared to children of normal weight-for-height (54.5±13.0) (p=<0.001). Children from wealthy households (59.6±15.0) had higher mean academic scores compared to children from poor households (52.5±12.9) (p=0.009). In multiple regression, helminthic status and z-scores for weight-for-age showed a collective significant effect on academic score ($F(1,117) =8.169$, $p<0.001$, $R2=.125$). Both helminth status (t= -2.026, p=0.045) and z-scores for weight-for-age (t= -3.321, p=0.001) were significant predictors of the academic score. The relationship between helminth status (t= -1.648, p=0.102) and academic scores was undermined when household income was added to the model ($F(2,117) =7.408$, $p<0.001$, $R2=.164$).

CONCLUSION: School children with helminth infection had poorer academic performance compared to uninfected children, in spite of their nutritional status. In addition to school-feeding programmes, mass deworming campaigns are critical for improving learning outcomes in young school children.

ORAL SESSION 4580
THE ONE HEALTH APPROACH TO SHAPE NEW LABORATORY SYSTEMS

CHAIRPERSONS:
Renuka Gadde; Beatrice van der Puije

5237350 | A Holistic Health System Strengthening Approach in Building AMR Diagnostics Networks: Lessons from Kenya

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BACKGROUND: The effect of antimicrobial resistance (AMR) is projected to be harsher in developing countries. Bacteriology diagnostics, often neglected, provide the much-needed evidence for informed patient's management and AMR surveillance. USAID's IDDS project, in partnership with MOH Kenya, has been strengthening AMR detection and surveillance systems in 5 laboratories since May 2019 in a holistic health system strengthening approach.

METHODS: The approach entailed baseline assessments, joint work planning between IDDS and supported counties, in-depth trainings in microbiology and AMR data management, AMR stewardship, quarterly mentorship support visits, implementation of bacteriology-specific competency procedures, support with commodities to complement counties initiatives, strengthening of information systems, and sensitization of clinicians for demand creation.

RESULTS: After six months into project interventions, one of the laboratories restarted offering bacteriology services. No service interruptions have been reported unlike before. The uptake of bacteriology tests has been on steady rise although volumes are still below target, partly due to COVID-19 pandemic. A total of 4544 culture tests have been conducted from across the 5 laboratories, yielding 1170 antimicrobial susceptibility results, a positivity rate of 25.7%. of these, 872 (19.1%) have been uploaded to the national AMR surveillance database. Significant data quality improvement has been noted spurring interests in use of AMR data locally. Two of the supported laboratories managed to successfully get bacteriology tests ISO15189 accredited.

CONCLUSION: Capacity built in the five laboratories has enabled them to efficiently serve as testing hubs thus increasing access to quality bacteriology services. Joint action plans resulted to ownership, commitment to allocation of resources for bacteriology, and overall appreciation of the role of laboratory in efforts to prevent and contain AMR. Good progress has been registered. However, unlike other diagnostic networks, AMR diagnostics networks require more attention and investment to build, sustain, and further decentralize, due to technical complexities of bacteriology cultures.

5266359 | Antimicrobial Resistance Genes of Escherichia Coli Isolated from Household Water in Municipal Ibadan, Oyo State Nigeria

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BACKGROUND: Fecally contaminated water is a potential reservoir for enteric bacteria carrying antimicrobial resistance genes that can be transmitted to pathogens. In this study, we characterized resistance gene repertoires of 82 *Escherichia coli* isolates obtained from household water samples in municipal Ibadan.

METHOD: Eighty two (82) *E. coli* strains obtained from 49 contaminated household water samples obtained from mapped locations in Ibadan were whole-genome sequenced using Illumina technology. Genomes were quality assured and assembled using SPAdes. Reads were mapped, called variants, and a phylogenetic tree was built using publicly available Nextflow pipelines. Multi-Locus Sequence Types (MLST), antimicrobial resistance genotypes and plasmid replicons were determined using ARIBA analysis.

RESULT: Thirty-seven (37) different antibiotic resistance genes (ARGs) belonging to 9 antibiotic classes were detected among the 82 isolates. Twenty-two (42.3%) and 10 (33%) of the isolates from dry and wet season household water respectively were multi-drug resistant (MDR). Twenty-one and 19 different Sequence Types (ST) were detected in dry and wet seasons respectively, with ST-10, ST-155, ST-165, ST-1011, ST-3696, ST-5523 and ST-6732 observed in both seasons. Seventeen STs detected more than once had identical or near identical (±1 gene) resistance gene profiles. Six of these MDR clones, and all eight clones with <2ARGs, were isolated in only one local government area. However MDR ST-1132 (10 strains, 10 ARGs, 3-4 plasmid replicons) and ST-8746 (3 strains, 11 ARGs, 3 plasmid replicons) clones were isolated across two separate Local Government Areas.

CONCLUSION: Household water in municipal Ibadan harbours MDR E. *coli*, which are more commonly recovered in the dry season. Resistant clones could be recovered from multiple sources, sometimes from disparate locations. Household water is an important vehicle for disseminating resistant enteric bacteria and a potentially under-appreciated resistance gene reservoir.

5266041 | Identification of Aedes Vectors in Arbovial Diseases Transmission Areas in Darfur, Western Sudan

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BACKGROUND: Arboviral infections are emerging public health threats worldwide particularly in Africa. Aedes mosquitoes are responsible for transmission of dengue, yellow fever, Zika, and chikungunya. Recently, a novel outbreak of dengue occurred in the Darfur area, western Sudan and appropriate surveillance systems are needed for tackling arboviruses in endemic setting. We aimed to identify Aedes vectors involved in the outbreak and determine their origin in two distinguished ecological regions in Western Sudan.

METHODS: Between 2018 and 2020, a cross sectional study was carried out in Zalingei (Central) and AlFasher (North) Darfur and mosquito larvae were collected from 18 locations. Larvae were reared to adults and morphologically identified using standard morphological keys. DNA extraction was performed from 30 samples/sites. Aedes species was confirmed by PCR and DNA sequencing Cytochrome oxidase 1 mitochondrial marker was performed.

RESULTS: At otal of 766 samples were morphologically identified including 573 (74.8%) A*e. aegypti* n=573 (74.8%), *Ae. simpsoni* 167 (21.8%) and *Ae. vittatus26* (3.4%). Results of PCR for the 60 samples including morphologically unidentified samples (65%; n= 39) revealed the presence of *Ae. aegypti* 21 (35%) and CO1 marker for four samples from unidentified, three samples confirm *Ae. aegypti* (98.3) and one sample as *Ae. metallcus* (1.7%). Phylogenetic analysis showed Zalingei and Al Fasher share same haplotype and were compratibely genetically close to isolates from Kenya, Cote d'Ivoire and Cape verde.

CONCLUSION: The high percentage (74.8%) of *Ae. aegypti* compared to other species, suggests its high distribution in Darfur region. The fact that genetically Al Fasher and Zalingei share same ancestoral origin indicates their gene flow or migration in Darfur region and thus acting potential foci for emerging and reemerging of arboviruses in Western Sudan.

5182344 | Occurrence of Multidrug Resistant Escherichia Coli in Contaminated Wells in Ile-Ife, South West, Nigeria: A Public Health Concern

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BACKGROUND: The emergence and rapid dissemination of multidrug-resistant bacteria is a major risk to public safety. The use of water that contains resistant bacteria could increase the risk of spreading antimicrobial resistance in the community. This study determined the quality of well water and the characteristics of antibiotic-resistant *Escherichia coli* in Ile-Ife, South-Western Nigeria.

METHODS: A total of 143 wells were assessed for safety using the most probable number method. The isolates were characterized by the MicrobactTM identification kit and their susceptibility patterns were determined by the Kirby-Bauer disc diffusion technique. All isolates were screened for extended-spectrum beta-lactamase (ESBL) production by the combination disk method. ESBL genes, plasmid-mediated quinolone resistance genes and Integrons were detected by polymerase chain reaction.

RESULTS: One hundred and ten (76.9%) wells were contaminated by coliform bacteria. of these, 94 (84.45%) wells yielded 202 *E. coli* strains. The isolates were commonly resistant to ampicillin (60.9%) but were all susceptible to meropenem and ceftazidime. Seventy-seven (38.1%) isolates were multi-drug resistant. Two isolates harbored *blaCTX-M* and *blaTEM* separately while four (19%) ciprofloxacin-resistant isolates carried the *oqxAB/aac-Ib-cr* gene. All the isolates with resistance genes harbored class 1 and/or 2 Integrons.

CONCLUSIONS: Most wells in Ile-Ife had coliform counts far above the standard limit set by the world health organization and are not safe for drinking. The presence of multidrug resistant isolates in well water portends grave danger for the consumers as this could lead to outbreaks of untreatable water-borne diseases. The detection of resistance genes and mobile elements necessitates the need for enhanced surveillance programs that can provide essential knowledge on the persistence and mobility of resistance traits between the community and hospital environments.

5264212 | A Multisectoral Collaboration to Develop Laboratory Leaders and Support a One Health Approach to Laboratory System Building

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BACKGROUND: Across the globe, health laboratories fill a critical role in the diagnosis, monitoring, control and prevention of human and animal diseases. They are also engaged in the ongoing detection of pathogens, harmful chemicals and residues affecting human and animal health. These laboratories will depend on effective and collaborative actions and leadership for success as they address the need for a One Health approach to disease prevention and control in humans, animals, and the environment. However, laboratory-specific leadership learning opportunities and multisectoral collaborations are often lacking, affecting the stability and function of health systems.

METHODS: Six organizations came together to address these critical gaps. The Global Laboratory Leadership Programme (GLLP) collaboration is a multi-year alliance between the Association of Public Health Laboratories (APHL), the Centers for Disease Control and Prevention (CDC), the European Centre for Disease Prevention and Control (ECDC), the Food and Agriculture Organization of the United Nations (FAO), the World Organisation for Animal Health (OIE) and the World Health Organization (WHO). Representatives from each organization formed working groups to create the *Laboratory Leadership Competency Framework* and the programme learning package. Each partner mobilized subject matter expertise, adapted learning materials, drafted new content, and edited materials to create a One Health learning programme addressing the nine leadership competencies across 43 subject areas.

RESULTS: In-country validations of the programme are on-going in eleven countries. Lessons learned through implementation are shared to improve the programme's quality. Although in the early stages of implementation, the GLLP provides opportunities for improved and expanded multisectoral communication and collaboration.

CONCLUSIONS: Transformation of laboratory systems to a One Health approach will require leadership and collaboration. Implementing GLLP provides a unique opportunity for countries to develop laboratory leaders who understand the One Health approach, will promote and support multisectoral coordination, and will lead collaborative laboratory systems.

OUTBREAKS, EMERGING PATHOGENS AND DISEASE BURDEN

5225280 | Impact of the Covid-19 Pandemic on Severe Childhood Malaria at the University Hospital of Brazzaville

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BACKGROUND: Malaria management has been a source of concern for health systems since the advent of the Covid-19 pandemic. We conducted this study to assess the impact of the Covid-19 pandemic on severe childhood malaria in Brazzaville.

MATERIAL AND METHOD: A quasi-experimental intervention/non-intervention study was carried out between March and October 2020 in the pediatric departments of the Brazzaville University Hospital. Children aged three months to 15 years hospitalized were the target population. Two groups were formed: the "intervention" group, that of children hospitalized between March and October 2020 and the "control" group that of those hospitalized between January and August 2015. The study variables were epidemiological, clinical, biological and therapeutic. Chi-square and T-Student tests were used. The impact of the intervention was assessed by the absolute risk difference.

RESULTS: of 1392 children hospitalized, 199 (14.6%) had severe malaria with an average age of 6.94 years. These were children under 5 years old n = 95 (47.7%) of low socioeconomic level n = 145 (72.9%) seen on average after 4.6 +/? 2.4 days. Repeated convulsions (56.8%) and anemia (20.1%) were the main reasons for hospitalization. These were isolated forms (n = 146; 73.4%) of which n = 84 (42.2%) neurological and n = 62 (31.2%) anemic. The lethality was 13.1%. Delayed consultation, fever, repeated convulsions, pallor, respiratory distress, sickle cell anemia, thrombocytopenia and hypoglycemia are associated with death. The risk difference for signs of severity between the two periods was 16.6 for repeated convulsions; 14.3 for severe anemia. The relative risk between the two studies was 1.8.

CONCLUSIONS: The increase in morbidity and mortality in severe malaria since the beginning of the Covid-19 pandemic encourages the maintenance of the balance between the management of the Covid-19 pandemic and that of other worrying health problems.

5225310 | High SARS-CoV-2 IgG/IGM Seroprevalence in Asymptomatic Congolese in Brazzaville, the Republic of Congo

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BACKGROUND: The Republic of the Congo detected its first case of COVID-19 on March 14, 2020, and within several weeks, the country had introduced necessary protective. Over the course of time, the progression in the number of clinical cases has appeared to be lower than expected, although RT-PCR testing has been somewhat limited. In order to evaluate the incidence of SARS-CoV-2 within the Congolese population, a seroprevalence study was conducted on healthy individuals from different districts of Brazzaville who were willing to know their COVID-19 infection status.

METHODS: Oropharyngeal swab and blood samples were collected from 754 healthy volunteers between April 2020 and July 2020. The samples were analyzed for SARS-CoV-2 using a qualitative RT-PCR assay, and IgG and IgM antibodies were detected using two different rapid tests.

RESULTS: A total of 56 participants (7.4%) tested positive for SARS-CoV-2. The remaining 698 participants (92.6%) had negative RT-PCR results; of these, 117 were found to have anti-SARS-CoV-2 antibodies using serological tests. For these RT-PCR-negative subjects, the seroprevalence of IgG and IgM was found to increase over time: from 1.7% and 2.5% in April, up to 14.2% and 17.6% in July, respectively. In April 2020, 5% of the women were found to have IgG or IgM antibodies, whereas the antibodies were not detected in any of the men. The seroprevalence in RT-PCR negative subjects was significantly higher in women within IgG (P = 0.012) and IgM (P = 0.045) over the first three months.

CONCLUSIONS: The proportion of the population who seroconvert over time is an important data to predict the risk of future COVID-19 waves and this will facilitate the efficient use of limited resources in a low income country like the Republic of the Congo.

5226455 | Studies on Microbial Contamination of Cut and Exposed Onions

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BACKGROUND: Onions (Allium cepa), a vegetable plant is consumed globally for its culinary and medicinal importance. Despite the various health benefits ascribed to it, rumours have it that it has the ability to act as a sponge absorbing microorganisms from the atmosphere once cut open and left exposed. This research work involved the exposure of the half portions of onions at different sites, while culturing the other halves immediately without exposure, to serve as a control.

METHODS: Thirty (30) fresh onion samples were exposed, and the sites of exposure include: living rooms, public conveniences, kitchens, fridge, freezer, and bole joints (roasted plantain eatery). They were inoculated in culture media for the isolation and identification of different microorganisms.

RESULTS: *Pseudomonas sp., Bacillus cereus, Escherichia coli, Staphylococcus sp., Klebsiella sp., Enterobacter sp., yeast* and *Aspergillus sp.*, were isolated with *Klebsiella sp., Pseudomonas sp.* and *Staphylococcus sp.* having the highest number of occurrence of 40% having been isolated from twelve test samples each. B. cereus had a percentage occurrence of 30%, having been isolated from nine test samples. E. coli had a 10% occurrence having been isolated from three test samples, while *Enterobacter sp.* had the lowest rate of occurrence having been isolated in just one test sample. For the fungi isolates, *Aspergillus sp* had a percentage occurrence of 76.6% having been isolated in twenty three test samples, while *yeast* had a percentage occurrence of 66.6%, having been isolated in twenty test samples.

CONCLUSIONS: The isolated organisms were all pathogenic organisms, and some such as *Staphylococcus sp.* and *Bacillus sp.* have been implicated in causing food poisoning. Some other organisms isolated have also been implicated in the spoilage of onions. It is therefore recommended that users of onions should reduce to the barest minimum the tendency to consume raw cut and exposed onion.

5237063 | Dengue Serotypes 2 and 4 Detected in Suspected Malaria Patients Attending Some Selected Health Centers in Jos, Nigeria

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BACKGROUND: Dengue infection is of public health importance but less investigated by clinicians and rarely considered in the differential diagnosis of febrile illnesses in Nigeria. There is paucity of data on circulating dengue serotypes in Nigeria. The objectives of the study was to detect the presence of Dengue IgG and/or IgM antibodies, dengue serotypes and Plasmodium species in the blood of febrile patients.

METHODS: One hundred and eighty-eight (188) consenting febrile patients suspected of malaria who met the inclusion criteria, participated in a cross sectional study. ELISA technique was used to detect Dengue IgM and/or IgG, and Viral RNA extracted from the positive samples. DNA was also extracted from all samples. Real Time Polymerase chain reaction was carried out on the extracted RNA and DNA to detect the presence of dengue serotypes and Plasmodium species respectively.

RESULTS: The prevalence of dengue antibodies was found to be 33.5% (63/188) with the mean age of 29.9±1.2. The prevalence dengue antibodies according to sex were 36.4% (16/44) and 32.6% (47/144) for Male and Female respectively. Dengue serotypes 2 and 4 were detected in the dengue antibodies positive samples as 15.9% (10/63) and 7.9% (5/63) respectively. The prevalence of malaria was 11.7% (22/188), with the highest prevalence of 12.5% (18/144) among the female group. Co-infection of Dengue and Malaria was recorded to be 2.6% (5/188). An association was statistically determined between Dengue and Malaria.

CONCLUSIONS: We detected dengue antibodies and its circulating serotypes in our study population. As compared to malaria infection in the study population, dengue prevalence was found to be higher. There is an indication for dengue diagnosis in febrile illnesses and a continuous surveillance of dengue infection to detect any possible outbreak.

5237580 | Environmental Surveillance of Crimean-Congo Hemorrhagic Fever Virus in Ixodid Ticks Infesting Livestock in Uganda: Findings from a Prospective Nationally Representative Survey

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BACKGROUND: Outbreaks caused by Crimean-Congo Hemorrhagic Fever virus (CCHFV) have been recorded in Uganda since 1958, yet its epidemiology in the country remains less defined. To gain an improved understanding of its presence in the environment, we collected ticks infesting livestock from several parts of the country and investigated them for the presence of CCHFV RNA.

METHODS: This was a prospective study design in which the first and second round of sample collection were performed in 2017 and between 2020-2021, respectively. The study areas included all districts of Uganda that border with neighboring countries, as well as all districts that lie within the Ugandan 'Cattle Corridor'. Ixodid ticks infesting cattle, goats and sheep were picked from randomly selected farms in the study areas, before they were identified morphologically at Uganda Virus Research Institute, Entebbe, Uganda. RT-PCR investigations for CCHFV were performed on pooled tick homogenates.

RESULTS: A total of 1,012 and 401 tick samples were collected in 2017 and 2020-21 study rounds, respectively. Ticks belonging to 17 species were obtained with the most predominant ones being *Rhipicephalus appendiculatus* (29.9%), *Amblyomma variegatum* (19.2%), *Rhipicephalus evertsi evertsi* (18.9%) and *Rhipicephalus decoloratus* (6.4%). Preliminary analysis has detected CCHFV presence in pools belonging to *Amblyomma variegatum* (n=3) and *Rhipicephalus appendiculatus* (n=1). Findings from the genomic sequencing of the positive CCHF samples is ongoing and will be presented at the workshop.

CONCLUSION: These data, help describe that apart from *Hyalomma* species that are known to transmit CCHF in many areas, other tick species like *Amblyomma variegatum* and *Rhipicephalus appendiculatus* may be involved in CCHFV transmission in Uganda.

5237707 | Urinary Schistosomiasis Among Children Under Ten Years in Tudun Wada Area of Kaduna South Local Government, Kaduna State, Nigeria

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BACKGROUND: Schistosomiasis is a chronic parasitic disease caused by blood flukes. (1) These blood flukes (trematode worms) are prime examples of complex multicellular pathogens that flourish in human hosts despite the presence of immune responses mounted against them. (2) Urinary Schistosomiasis is an increasing health burden among African children in Nigeria. The study was aimed at assessing the prevalence of urinary Schistosomiasis among children below 10 years in Tudun wada in Kaduna south local government, Kaduna state, Nigeria.

METHODS: A total of 505 children below 10 years voluntarily participated in the study after consent was gotten from their parents. Ten milliliter of urine sample was collected from each child. The urine samples were examined microscopically for *Schistosoma haematobium* eggs while count/10ml of urine was recorded. Data collected was analyzed using IBM SPSS version 21 at P=0.05.

RESULTS: Overall prevalence of urinary Schistosomiasis was 12.27%. There was a significantly higher occurrence of the infestation in females compared to males (females = 15.53%, n=251; males = 9.06%, n=254). This is lower compared to 79.4% among children of Ezza North local government of Ebonyi state (Uneke et al,. 2009), 41,5% in Benue (Houmsou et al., 2012), 78.4% in Lagos (Oluwasogo and Fagbemi, 2013) and 34.1% in Enugu (Ossai et al., 2014). Mean intensity in the female children (4.18 ±1.202 eggs/10ml) was significantly higher (P≤0.05) compared to 1.22±0.500 eggs/10ml in the male children.

CONCLUSION: There was no awareness of Schistosomiasis among the study population. From this study, the female children were more infected with urinary Schistosomiasis than the male children in Tudun wada area of Kaduna south local government of Kaduna state, Nigeria. Awareness should be done about the implications of urinary Schistosomiasis in females especially because it is a major cause of anaemia.

5237849 | Reported Reactions Post Covid-19 Vaccination

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BACKGROUND: In light of the peaking outbreak of COVID-19, UK authorities decided to vaccinate a large number of people with high risk in the shortest possible time. However, there have been varying reports of different symptoms that are somewhat fatal among person vaccinated.

METHOD: A total of 154 persons that received the COVID-19 at the Obio Cottage hospital and the University of Port Harcourt Teaching Hospital in Rivers state, Nigeria was interviewed using a structured PROFORMA data collection sheet.

RESULTS: The mean age of the respondents was 47.6±15.6. The age distribution showed that 28 (18.2%) were between 20 – 29 years. 21 (13.6%) were between 30 – 39 years, 33 (21.4%) were between 40 – 49 years, 31 (20.1%) were between 50 – 59 years, and 41 (26.6%) were at least 60 years old. There were 89 (57.8%) males and 65 (42.2%) females. The results also showed that 107 (69.5%) had symptoms after first dose vaccination while only 72 (46.8%) reported having symptoms after second dose vaccination. The symptoms reported after first dose vaccination was fever (40.3%), headache (16.2%), Pains (7.1%), weakness (2.6%) and dizziness (1.9%). Symptoms after 1st dose were mostly common in the 20 – 29-year age groups, followed by the 60 and above age groups, while symptoms after the second dose was mostly common among the 60 and above age group. There was no statistically significant ($p>0.05$) in the distribution of symptoms by age groups or gender after first and second dose.

CONCLUSION: The study showed a relatively high occurrence of symptoms after first dose which was reduced after the second dose vaccination.

5262081 | Impact of COVID-19 on HIV Viral Load for PEPFAR Countries

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CDC and the U.S. President's Emergency Plan for AIDS Relief (PEPFAR) are committed to maintaining an international response to the HIV epidemic even as countries face the challenge of controlling the COVID-19 pandemic. Recent COVID-19–related stay at-home orders and travel restrictions have affected essential HIV services particularly in sub-Saharan Africa. In the face of these challenges, CDC and PEPFAR are committed to sustaining the momentum necessary to achieve the target goal of facilitating testing and viral load (VL) suppression among 95% of persons with HIV. VL testing coverage for all PEPFAR-supported countries was stable at 78% pre-COVID-19 pandemic during September–December 2019. However, viral load testing coverage decreased to 71% during January–March 2020 as the pandemic began to interrupt essential HIV services including laboratory testing and supply chain shortages developed in many countries . After routine services were reinstated (April–June 2020), VL testing coverage increased to 75% and has varied between 75-77% through March 2021. VL suppression remained level from 91-92% September-December 2019 pre-COVID-19 pandemic to April-June 2020 during mitigation measures to control the pandemic with a gradual increase in VL suppression this year to 94% between January-March 2021. Innovative approaches are needed to sustain the global progress made in recent years in response to the HIV epidemic. Access to VL testing could be facilitated by community outreach for specimen collection and using point-of-care technology for special populations who need expedited testing. Despite the challenges of controlling the COVID-19 pandemic, countries should continue advancing toward the 95-95-95 by 2030 goals with expansion of VL testing for all persons with HIV infection who are receiving ART.

5265424 | Prevalence of Hepatitis B, Its Associated Factors and The Level of Knowledge in the Buea Regional Hospital

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BACKGROUND: Hepatitis B is the inflammation of the liver caused by the Hepatitis B virus. This infection causes the death of liver cells and can lead to complications like liver fibrosis, liver cirrhosis, and hepatocellular carcinoma. This study was designed to assess the prevalence of Hepatitis B, its most commonly associated risk factors, and to test the level of knowledge of patients on this infection at the Buea Regional Hospital.

METHODS: The participants signed a consent form and provided us with data by filling out our questionnaires. Blood samples were also collected and processed in the Serology lab of the Buea Regional Hospital. The data was analysed using SPSS 17.

RESULTS: The prevalence of hepatitis was 8.4% with 10 positive cases out of 120 participants. A greater proportion of the participants had adequate knowledge of Hepatitis B. Having had more than one sexual partner in the last 6 months and having visited a dentist for a dental procedure in the past was significantly associated with positivity for Hepatitis in the bivariate analysis ($p \leq 0.05$).

CONCLUSION: The prevalence of Hepatitis B in the Buea Regional Hospital is still relatively high. Health practitioners at the Buea Regional Hospital need to enforce measures to educate the patients and encourage them to take the vaccine.

5265514 | Sero-Epidemiology of HIV-1 Among the People Living in Rural Communities of Federal Capital Territory Abuja, Nigeria; An Outreach Experience

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BACKGROUND: Nigeria has the second largest HIV epidemic in the world with mixed HIV epidemic and high HIV prevalence among key population members and low prevalence in the general population. A greater knowledge of the burden of HIV in rural areas is important for interventions at primary health care level.

METHODS: We conducted a cross-sectional HIV sero-prevalence survey through outreach in rural communities of Federal Capital Territory, Abuja Nigeria. Percentage prevalence was calculated for both the male and females and across different age ranges for comparison. Using age-sex stratified non-randomized sampling of people from ages 15 and above, a total of 1,146 rural residents were tested which comprised of 697(60.82%) males and 449(39.18%) females.

RESULTS: Two hundred and thirty eight (20.77%) were tested HIV positive. Eighty two (7.16%) were males while 156 (13.61%) were females. On disaggregation by age, the highest prevalence was found among the people within the range of 25-29 years. Upon age-sex stratification, HIV prevalence was highest among the people within the age range of 35-39 (1.57%) and 25-29 years (4.19%) among females.

CONCLUSIONS: The result indicated that the prevalence of HIV is high among the rural residence of Federal Capital Territory, Abuja. This also showed that heterosexual transmission of HIV, is the major mode of transmission. This therefore called for reinvigorated prevention activities to reduce the menace of this infection among the rural dwellers of the Federal Capital Territory Abuja.

5265981 | Systematic Testing with COVID-19 Antigen Rapid Diagnostic Tests on Inpatient Admission Increases COVID-19 Case Detection in Homa Bay (Kenya)

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BACKGROUND: WHO recommends testing individuals that meet the COVID-19 case definition (WHO 2021). Those who may be infected but present with atypical COVID-19 symptoms or who are asymptomatic are often undiagnosed. This is problematic in inpatient settings such as Homa Bay county hospital, where the HIV prevalence in the population is 17% (NHIPS 2020), 38% of adult medical inpatients are HIV positive. MSF OCP in Homa Bay aimed to test all patients meeting admission criteria.

METHOD: We carried out a retrospective data analysis of COVID-19 testing of adult medical patients admitted at the Homabay county hospital from March to June 2021.

RESULTS: 982 patients and HCW were screened between 29/3-20/6 2021. 80% (769/982 were tested with Ag RDT (78.3%); the remainder (213 individuals) had at least one PCR.

49% (481/982) reported symptoms meeting the clinical case definition and 53 were contacts, thus a total of 534 individuals met the criteria for COVID-19 testing as per Kenyan national guidance.

141 (26.4%) were positive on RDT and 223 /534 (41.8%) were negative. The remainder (170) had a PCR test and of these 75/170 (31.8%) were positive. Overall, 235/534 (40.5%) were positive.

Those who did not meet the case definition for testing, 81/448(18.1%) were positive on rapid testing, 324 (72.3%) negative, and 43 (9.6%) had a PCR; of these 21/43 (48.8%) were positive. Overall, in this group, 102/448 (22.8%) were positive.

CONCLUSION: In inpatient settings with high rates of HIV, TB, and chronic conditions, differentiating symptoms of COVID-19 from other morbidities can be difficult. In this context, more than one in five individuals who did not meet the case definition tested positive for COVID-19.

SARS CoV-2 Ag RDT testing of patients on admission is feasible, results in faster detection, isolation, and management of patients with COVID-19, thereby reduces exposure of vulnerable non-infected patients.

5266112 | Characterization of Shiga Toxin-producing Escherichia Coli in Raw Beef from Informal and Commercial Abattoirs

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BACKGROUND: Shiga toxin-producing *Escherichia coli* are foodborne pathogens that are mostly associated with beef products and have been implicated in human illness. *E.coli*-associated illness range from asymptomatic conditions of mild diarrhoea to haemorrhagic colitis which can progress into life threatening haemolytic uremic syndrome (HUS). Beef from cattle are regarded as the main reservoir of Shiga toxin-producing E. *coli* (STEC) pathogen. The aim of this study was to assess the level and sources of contamination of raw beef with STEC, and determine the incidences of STEC strains in raw beef from informal and commercial abattoirs in Windhoek, Namibia.

METHODS: A total of 204 raw beef samples, 37 equipment and 29 hand swabs were collected and tested for STEC. The meat samples were first enriched with pre-warmed buffered peptone water, cultured on Tryptone Bile X-Glucuronide and CHROMagar STEC, and then sub-cultured on nutrient agar. The presence o*f E.coli* in the samples was confirmed by using VITEK 2 *E.coli* identification cards and PCR.

RESULTS: The overall prevalence of STEC in the meat samples from both the abattoirs was 41.66% raw beef samples; 5.40% equipment swabs; and none of the hand swabs was STEC positive. From the STEC positive meat samples 29.41% contained one of the major STEC strains. Moreover, 52% of the 25 samples that contained the major STECs were characterised by *eae* and *stx1*, 8% characterised by *eae* and *stx2* while 40% were characterised by *eae, stx1* and *stx2* virulence genes.

CONCLUSION: This study has revealed the necessity for proper training on meat safety (for meat handlers) as well as the development, implementation and maintenance of effective sanitary dressing procedures at abattoirs to eliminate beef contamination by STECs thereby ensuring the production of wholesome meat, and to prevent the occurrences of STEC infections.

5266566 | Prevalence of Anaemia in Children Attending Yusuf Dantsoho Memorial Hospital, Tudun Wada, Kaduna South Local Government Area of Kaduna State, Nigeria

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BACKGROUND: Childhood anaemia is a condition where a child has an insufficient haemoglobin level to provide adequate oxygen to the body tissues. The World Health Organisation estimated that more than half of the children in the world have a haemoglobin level indicative of anaemia and the prevalence may be as high as 56 – 68% in developing countries causing between 20% – 40% of childhood mortality. (WHO, 2012). The study was therefore aimed at assessing the prevalence of anaemia in children attending Yusuf Dantsoho Memorial Hospital, Tudun Wada, Kaduna south local government area of Kaduna state, Nigeria.

METHODS: A total of 240 children below 10 years comprising 152 males and 88 females, were included in the study after consent was gotten from their parents. Three milliliter of blood was collected by venipuncture into anticoagulant containing 5ml containers. The Packed Cell Volume estimation was carried out according to the method by Monica Cheesbrough. The Packed Cell Volume was read and recorded. Data collected was analyzed using SPSS version 21 for percentages and correlations.

RESULTS: The prevalence of anaemia in this study was 61.7% which was higher than 24.5% Global prevalence of anaemia in children, 46.0% among settled rural school children in Cote D'ivoire (Assobayire et al., 2004) and 49.8% in Kazakhstan (Hashizume et al., 2006). This is lower when compared to 82.6% among certain children in Abia state, southeastern Nigeria (Animawo et al., 2010). The average PCV in the male children was 26.9% (15 – 39%) and in females was 23.5% (11 – 44%).

CONCLUSION: There was significantly low haemoglobin level among the study population. Adequate measures should be put in place to save the children. Children should be brought to the hospital early for treatment. Supplements should be given to children to boost their blood levels.

5266589 | COVID-19 Case Management and Co-Morbid Illness; Outcome in a Low Resource Setting in Western Nigeria

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BACKGROUND: The severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) is a novel strain of coronavirus, which causes the current coronavirus disease 2019 (COVID-19) pandemic. The aim is to assess the co-morbidity and case management outcome of hospitalized COVID-19 patients in Ondo State, Southwestern Nigeria.

METHODS: A longitudinal study was carried out on randomly selected patients with COVID-19, confirmed by real-time reverse transcriptase-polymerase chain reaction (rRT-PCR), admitted to the Infectious Disease Hospital, Akure, from March to July 2020. Data obtained were analysed using the SPSS version 24.0 software and variables were compared using the Chi-square (χ^2) test and Odds ratio.

RESULTS: A total of 215 hospitalized COVID-19 patients were randomly recruited, with 103 males and 112 females, and a mean age of 37.24 ± 16.83 years. The commonest underlying health conditions were hypertension (4.7%) and diabetes mellitus (3.7%). The mean age ± SD of the co-morbid hypertensive patients was 58.10 ± 14.26 years; however, for the co-morbid diabetic patients, the mean age ± SD was 56.70 ± 12.41 years. Statistical analysis showed that diabetes mellitus [χ^2 = 7.76, OR 2.12 (95% CI: 0.31-8.69), p=0.005] and hypertension [χ^2=5.57, OR 1.66 (95% CI: 0.22-6.89), p=0.018] were underlying health conditions with a significant impact on the outcome of the patients.

CONCLUSION: This study showed that cardiovascular diseases such as hypertension and diabetes are major co-morbidities and risk factors for severity and mortality in COVID-19 infected patients; thus, their prevention or exhaustive management will be key to patient recovery and survival.

THE ROLE OF LABORATORIES IN OUTBREAK PREPAREDNESS AND RESPONSE

5228188 | Analysis of Laboratory Turnaround Time of the Positive Covid-19 Cases in Zambia-2020 to 2021

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BACKGROUND: Rapid turnaround time (TAT) of Covid-19 positive results is essential component for outbreak response and aids quick identification and isolation of positive cases to prevent further disease transmission. The World Health Organisation recommends 24 to 48hrs TAT for Covid -19 laboratory test results. We analysed the TAT for positive Covid-19 testing data in Zambia from March 2020 to January 2021.

METHODS: We conducted a retrospective analysis of TAT of Covid-19 positive test results maintained by the Zambia National Public Health Institute from March 2020 to January 2021. TAT is defined as the time taken to complete the process from specimen collection to result reporting. The analysis included polymerase chain reaction (PCR) results with complete specimen collection date and laboratory result date and excluded rapid tests results as they were limited and not widely used during period under review. We used R studio to calculate the median, interquartile range (IQR) and proportion of results with TAT within 48 hrs.

RESULTS: There were 38,207 positive test results for SARS-CoV-2 in Zambia from March 2020 to January 2021 and 18,404 were excluded due to insufficient data. The analysis includes 19,083 PCR results of which 38% (7315) were reported within 48hrs and 62% (11,768) after 48hrs. The national median TAT was 4 days (IQR 1-9)]. Lowest median TAT was in North-western Province [2days (IQR: 1 – 10)] while Eastern Province was highest at 10 days (IQR: 4 – 18).

CONCLUSION: With 62% positive SARS-CoV-2 results taking more than 48hrs, TAT was too long to interrupt transmission if persons did not adhere to quarantine while awaiting results. Delayed results might mean infected persons do not isolate, thus leading to further infections among contacts. TAT can be shortened through enhancing specimen transport system and increasing use of point-of-care testing strategies like antigen RDT.

5228408 | Panbio Rapid Antigen Test Not Useful in Hospitalised Paediatric Patients

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BACKGROUND: In order to curb the spread of COVID-19, widely available rapid detection and isolation of those infected with the SARS-CoV-2 is important. The use of inexpensive rapid antigen tests has become an important diagnostic tool in adult populations. We aim to determine the usefulness of the Panbio rapid antigen test (Panbio Ag) to diagnose COVID-19 in hospitalized paediatric patients.

METHODS: Routine diagnostic nasopharyngeal swabs (NPS) taken from paediatric patients admitted to the intensive care unit during the 2nd wave of the COVID-19 pandemic were sent to the Division of Medical Virology, Tygerberg National Health Laboratory Service, for SARS-CoV-2 testing by the Panbio Ag and either one of the established Reverse transcriptase Real-Time Polymerase chain reaction (RT-qPCR) assays: Allplex 2019-nCoV PCR (Seegene) and Xpress SARS-CoV-2 (Cepheid).

RESULTS: of the 15 children included, 10 (66.7%) were male, median age was 22 months (range 0-12 years) and 5 (33.3%) had underlying co-morbidities. In total 5 (33.3%) children presented with neurological, 3 (20.0%) with respiratory and 3 with gastro-intestinal symptoms. of the 15 NPS samples, seven (46.7%) tested positive by PCR, of which 3 (42.8%) had a Ct value of <32 i.e. presumably a high viral load. In contrast, no sample tested positive by the Panbio Ag.

CONCLUSION: Our sample size was small as recruitment was halted after none of 15 patients tested Panbio Ag positive. The Panbio Ag is known to be insensitive with low viral loads (Ct value > 32). Disappointingly, in this small study of hospitalized children it did not even detect three samples with high viral loads. Although screening with a Panbio Ag may have value in adults or in a community setting, this suggests that in hospitalized children with suspected COVID-19, NPS should be directly screened with a rapid RT-qPCR as an antigen assay may have limited utility.

5266052 | Performance Evaluation of SARS-CoV-2 Antibody Test (Lateral Flow Method) at Bacteriology and Virology Laboratory, Aristide le Dantec Hospital, Dakar

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BACKGROUND: Progression of the pandemic caused by the SARS-COV-2 virus, numerous tests have been developed to strengthen diagnostic strategy in order to speed up patient care. As Real-Time PCR (RT-PCR) techniques are not available everywhere, there is a need for rapid diagnostic tools as an alternative with performances close to amplification tests and easy to use on a large scale. Serologic tests can identify previous infection with SARS-CoV-2 and help confirm the presence of a current infection. The objective of this study was to evaluate at local level, the performances of serological test, the SARS-CoV-2 Antibody (IgM / IgG) of the Wondfo® laboratories using as Gold Standard the amplification method by RT-PCR.

METHOD: A sampling of 150 including 40 samples from controls and 110 sera and plasma from patients admitted to the epidemic treatment center (CTE) of the Aristide Le Dantec hospital in Dakar had been used to evaluate the immunochromatographic assay for rapid, qualitative detection of SARS-CoV-2 IgG/IgM antibody.

RESULTS: Age of the patients was ranged from 19 to 90 years with a sex ratio of 1.2. The evaluation showed 100% of specificity and a sensitivity of 94.38% for plasma and 80.64% for sera, respectively. However, among the patients with COVID-19 and positive RT-PCR, eleven N = 11 (0.1%) came back negative for the serological test among which 55% were asymptomatic with benign clinic and 45% were symptomatic with moderate clinic and comorbidities including diabetis, arterial hypertension and chronic renal disease.

CONCLUSION: Results obtained on the performance of the serological test show that these tests can play an important role in a mass screening strategy in order to rule on the state of immunity of the general population or to detect an infection at an advanced stage when the virus can no longer be detected by RT-PCR.

5266197 | Detection of SARS-CoV-2 Infection by RT-PCR In North-Central Nigeria

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BACKGROUND: The outbreak of COVID-19 has had a significant impact on clinical laboratories globally in the past several months. Prompt interventions in terms of early detection and clinical management along with isolation of positive cases is of utmost importance. Early detection will not only help to limit the spread of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infections, but also the morbidity and mortality associated with it. This study aim to present the data on the prevalence of SARS-CoV-2 and also explore predictors of COVID-19 test outcome amongst exposed individual who received PCR based test in north central Nigeria.

METHODS: A total of 157,398 suspected COVID-19 samples were collected across north central Nigeria by trained healthcare personnel, who completed a detailed Case Investigation Form (CIF) and collected a minimum of one nasopharyngeal or nasal swab, and one oropharyngeal swab and transported to the laboratory. All nasopharyngeal and oropharyngeal swab samples collected in Viral Transport Medium (VTM) were tested using the Cobas®8800 system as per manufacturer's recommendations for the detection of the SARS-CoV-2 RNA in the swab samples by RT-PCR.

RESULT: The Cobas® 8800 System verification showed 100% sensitivity and 95.65% specificity. of the total samples assayed, 52% were female and 9% of the total participants had a positive RT-PCR outcome (with the age group 22-55 contributing the most to the positive outcome).

CONCLUSION: The RT-PCR test results should be carefully interpreted. Negative RT-PCR test results in cases with significant findings or history should be released with specific comments including the possibility of false negative results. Patients with suspected COVID-19, the diagnosis must rest not only on RT-PCR test results but also on the clinical presentation and on the findings from other tests, most notably chest CT.

5266385 | Process of Laboratory Setup and Quality Indicator Monitoring for SARS-CoV-2 Molecular Testing in Response to an Outbreak in a Resource-limited Setting in Kenya

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INTRODUCTION: Laboratory setup and preparedness to respond in diagnosis of infectious diseases as witnessed in SARS-CoV-2, is key in outbreak management. The need for rapid response while ensuring laboratory quality elements, can be challenging.

The Association of Public Health Laboratories (APHL) built capacity for seven Regional Laboratories in Kenya to respond to the demand for SARS-CoV-2 testing while ensuring quality assured results are released within 24 hours. Laboratory performance indicators were identified and implemented in laboratories through the help of an APHL mentor.

METHOD: Laboratory setup involved identification of one national and seven regional laboratories for molecular testing, infrastructure capacity building for PCR testing, equipment and consumables procurement, competency assessment of staff, and enrollment in an external quality assurance program to ensure quality SARS-CoV-2 testing through gap analysis using WHO checklist. Quality management system (QMS) was initiated in three of eight laboratories that were not ISO 15189:2012 accredited, with a focus on six quality indicator monitoring areas: performance of EQA, equipment serviceability state, reagents and consumables stock levels, result turnaround time, workload, and performance of internal quality control over a defined time period.

RESULTS: Laboratory gap analysis identified laboratory needs. Laboratory set-up was successfully done in six out of seven Regional Laboratories and molecular testing initiated. Six laboratories submit their results to the National COVID-19 Data Repository. Baseline assessment and QMS implementation in all non-ISO 15189:2012 accredited laboratories were initiated to have them accredited within 6 months. Quality indicator monitoring for the six indicators is in progress.

CONCLUSION: Rapid laboratory setup with quality assured standardized testing processes is possible in resource-limited settings by applying multiple strategies simultaneously, and establishing quality indicators of measure. This process has eased the demand for SARS-CoV-2 testing services by ensuring quality assured results are accessible when needed, thus relieving pressure from other referral testing laboratories.

THE THREAT OF ANTIMICROBIAL RESISTANCE

5199901 | Evaluating Fluoroquinolone Resistant and Susceptibility Pattern in Seven States at Seven Tertiary Health Facilities in North Western Nigeria

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BACKGROUND: Fluoroquinolones are broad- spectrum (BS) potent antibiotics used in medical practice for severe infections treatment since late 1980s. Antimicrobial resistant remains a global challenge justify need for update across countries.

OBJECTIVE: To evaluate pattern of Fluoroquinolone resistance and susceptibility profile among bacterial isolates from seven health facilities (HF) in North western (NW) Nigeria.

METHODS: A total of 1,000 Enterobacteriaceae and Gram positive bacteria consisting *Escherichia coli* 390, *Klebsiella pneumonia*-165, *Proteus spp*-67,*Pseudomonas aeruginosa*-48, *Staphylococcus aureus*-235, others-95. After ethical approval from Teaching Hospital (TH) and Federal Medical Center (FMC) isolates collected August 2017-December 2020 from Aminu Kano TH, Ahmadu Bello TH Kaduna, FMC (Zamfara, Kebbi, Katsina) States, Rasheed Shekoni TH Jigawa and Usman Danfodio TH Sokoto. All population included. Isolates identification carried out using Microbacterial Identification kit (24E). ESBL screening/ confirmation performed according to Clinical Laboratory Standards Institute Susceptibility/ synergy-testing. ESBLs performed on Mueller- Hinton agar. Following antibiotic tested (Oxoid) tested;Norfloxacin-(NOR), Ceftazidime (CAZ), Tigecycline (TGC), Imipenem-(IPM), Levofloxacin-(LEV), ofloxacin (OFX), Ciprofloxacin-(CIP), and Colistin-(CL). Reference strains were *E. coli* ATCC 25922 & *pneumoniae* ATCC 700603. Data presented in frequency and percentage. association of variables of interest explored by chi square test, significant level $p<0.05$.

RESULT: of 1,000 isolates Urine 401-(40.1%), Swabs-364 (36.4%), others-(23.5%). Male 515-(51.5%) median age 32years ranged <1 to 75years. Prevalence of Multi-Drug Resistance (MDR) in relation to States showed Sokoto highest 91/121/ (75.2%), Jigawa lowest 24/140-(17.1%). No significance difference between MDR and States ($p=0.34$). MDR prevalence in male 188/515-(36.5%) not significantly different with female 188 /485-(38.8%) ($p=0.461$). Susceptibility pattern of isolates resistance to LEV, CIP, OFX, NOR, CAZ.

CONCLUSION: *Enterobacteriaceae* showed high resistance to all Fluoroquinolones in seven HFs in NW but sensitive to CL, IPM and TGC antibiotics. Isolates showed high resistance to Fluoroquinolones and MDR showed no significant association with gender and States.

5237179 | Blood Culture Testing Outcomes Among Non-Malarial Febrile Children at Antimicrobial Resistance Surveillance Sites in Uganda, 2017–2018

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BACKGROUND: Blood culture (BC) processes are critical to the utility of diagnostic testing, bloodstream infection (BSI) management, and antimicrobial resistance (AMR) surveillance. While Uganda has established BC guidelines, often laboratory practice does not meet the desired standards. This compromises pathogen recovery, reliability of antimicrobial susceptibility testing, and diagnostic test utility. This study assessed laboratory BC process outcomes among non-malarial febrile children below five years of age at five AMR surveillance sites in Uganda between 2017 and 2018.

METHODS: A cross-sectional study was conducted at the five national AMR surveillance sites using secondary data from routine laboratory BCs from October 2017 to September 2018. BC testing data was reviewed against established standards.

RESULTS: Overall, 959 BC specimens were processed. of these, 91% were from female patients, neonates, infants, and young children (1–48 months). A total of 37 AMR priority pathogens were identified; Staphylococcus aureus was predominant (54%), followed by Escherichia coli (19%). The diagnostic yield was low (4.9%). Only 6.3% of isolates were identified. AST was performed on 70% (18/26) of identified AMR priority isolates, and only 40% of these tests adhered to recommended standards.

CONCLUSIONS: Interventions are needed to improve laboratory BC practices and data management for effective patient management through targeted antimicrobial therapy and AMR surveillance in Uganda. Further research on process documentation, diagnostic yield, and a review of patient outcomes for all hospitalized febrile patients is needed.

5237189 | Point Prevalence Survey of Antimicrobial Use at Three Rural District Hospitals in Rwanda

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BACKGROUND: Inappropriate use of antibiotics has increasingly become a challenge in global health with the posing danger of antimicrobial resistance (AMR). In Rwanda, AMR is not well documented due to the lack of adequate surveillance systems. Point prevalence surveys provide insight in prescribing patterns, inform quality indicators, and guide initiation of antimicrobial stewardship (AMS) and infection control programs.

METHODS: Through a point prevalence survey conducted at three rural district hospitals - Butaro (BDH), Kirehe (KDH) and Rwinkwavu (RDH), we assessed antimicrobial prescribing patterns among health care providers between March - April 2021. We used a standardized study tool adapted from the WHO Methodology. All admitted patients by 8am on the day of data collection and who were prescribed antimicrobials were included. Additionally, a survey was conducted with all prescribers to highlight prescribing patterns. Data was analyzed using Stata v.15.1.

RESULTS: 315 admitted patients who were prescribed antimicrobials were included – 147 from KDH, 95 from BDH and 73 from RDH. The prevalence of antibiotic use per facility was 57.2% for BDH, 72.8% for KDH and 73.7% for RDH. Antibiotics from the "Access and Watch" WHO categories were the most prescribed, with three ranking higher — ampicillin (27.7%), gentamicin (18.9%) and third generation cephalosporin such as cefotaxime (12.5%). From the prescribers' survey, only 25.5% of the prescribed antibiotics were based on microbiology reports. Common indications for antibiotic prescription in this sample were neonatal risk of infection, C-section risk of infection, and pneumonia.

CONCLUSION: The study findings show significant broad spectrum antibiotic prescribing rates against reported low rates of laboratory results. Prospective surveillance of antibiotic use over time and between different health facilities, promoting laboratory test guided prescription habits and developing site specific data driven antibiotic guidelines may improve rational prescribing practices which, in consequence, will support rational AMS in Rwanda.

5237435 | Phenotypic Profile and Antibiogram of Biofilm-Producing Bacteria Isolates from Diabetic Foot Ulcers in Zaria, Nigeria

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BACKGROUND: Diabetic foot ulcers (DFUs) present with high morbidity and reduce patient's quality of life. There is a gross paucity of data on biofilm-producing bacteria in DFU Infection in North-western Nigeria. The study sought to determine the biofilm-forming ability of bacteria isolates from DFUs and determine their antimicrobial susceptibility pattern in Zaria, North-Western Nigeria.

Materials and **METHODS:** This hospital-based cross-sectional study of patients with diabetic foot ulcers from June 2018 to February 2020. Consecutive biopsies were aseptically collected. These bacteria were isolated and identified using a Microgen kit. Biofilm forming ability and antibiogram of isolates were determined by microtitre plate and disk diffusion methods, respectively.

RESULTS: of the 225 participants enrolled, males constituted the majority, 144 (64.0%) with 88 (36.0%) females, median age of participants were 54 (48-60) years and the age range was 36-77 years. A total of 172 bacteria were isolated and 123(71.5%) were biofilm producers. *Staphylococcus aureus* (26.7%) was the highest biofilm producer, while C*itrobacter freundii* and St*enotrophomonas maltophilia* were the least biofilm producers, 1 (0.6%) each. A disproportionate resistance pattern was demonstrated among the biofilm and non-biofilm producers against the cephalosporins tested, Ceftazidime (68% versus 18%), Ceftriaxone (50% versus 8.0%) and Cefotaxime (21% versus 0.0%). About 46% and 68% of the biofilm producers were resistant to gentamycin and ciprofloxacin, respectively. While only 2% of the non-biofilm producers were resistant to imipenem, 11% of the biofilm producers were resistant to it.

CONCLUSION: These findings revealed a high proportion of biofilm-producing bacteria and were found to be more resistant compared to non-biofilm producers

5265102 | Bacteremia Isolates Before and During the COVID-19 Pandemic in Ibadan, South West Nigeria

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The COVID-19 pandemic has strained health systems and limited access to healthcare. This study assessed the impact of the pandemic on bacteremia isolate recovery in Ibadan, Nigeria.

Febrile patients were recruited for typhoid surveillance from University College Hospital (UCH), a tertiary healthcare facility, and Kola Daisi Foundation (KDF) primary healthcare facility, from August 2019 to March 2020 (pre-COVID-19) and from August 2020 to March 2021 (pandemic period). Blood culture was carried out using the BACTEC system, isolates were identified conventionally and their antimicrobial susceptibility determined by disc diffusion according to Clinical Laboratory Standard Institute guidelines. Antibiotic use at recruitment was inferred by testing urine from a fraction of patients for antibacterial substances using Urotest AB kit.

At UCH, 464 patients were blood cultured in the pre-COVID-19 period and 377 during the pandemic period, while at KDF, 133 and 105 were cultured in the pre-COVID-19 and pandemic periods, respectively. Pathogen yield was 35 (5.9%) pre-COVID-19, and 22 (4.6%) during the pandemic. *Staphylococcus aureus* 22 (38.6%) and *Salmonella* 14 (24.6%) – including eight *S.* Typhi - were the most commonly recovered pathogens, with *S. aureus* recovered more frequently pre-COVID-19 and Gram negative isolates predominating during the pandemic. Among the 441 (40.9%) patients from whom urine samples were tested for antimicrobial detection, reduced positivity was observed during the pandemic compared to the pre-COVID-19 period at UCH (37.3%: 57.1%) and KDF (31.6%: 46.8%), respectively. Nonetheless, median Gram negative inhibition zone diameters were lower during the pandemic, particularly for second- and third-generation cephalosporins, ciprofloxacin and azithromycin.

A Gram negative shift in pathogen recovery, and more pronounced antimicrobial resistance, was observed in Ibadan during the COVID-19 pandemic. The pandemic may be associated with lowered access to, or patient avoidance of, supervised care but the contribution, if any, from unsanctioned use outside health facilities remains unclear.

5266202 | Molecular Studies of Primary Drug-Resistance in Mycobacterium Tuberculosis Among Presumptive Tuberculosis Patients in North West, Nigeria

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BACKGROUND: Primary drug-resistant tuberculosis is a public health concern in underdeveloped nations and continues to be a burden. The study area lacks data on demographic features and other factors related with primary drug-resistant tuberculosis, spatial distribution, prevalence, illness pattern, and gene associated with resistance in identified *Mycobacterium tuberculosis*. The goal of the study was to determine current trends in primary drug resistant among presumptive patients, the illness pattern, and proven genes related with resistance in *Mycobacterium tuberculosis* strains found in the study area.

METHODS: The research included 384 sputum samples from consented/assented individuals in a cross-sectional, prospective investigation (from Kano, Jigawa, Zamfara and Kaduna State). Structured questionnaire was given out, on demographic information, as well as factors linked to tuberculosis resistant and the spatial distribution of tuberculosis in the study area, were gathered. The samples were examined using the PCR (Line Probes Assay) method, and the data was analyzed using Chi-Square and Arc GIS 13.1 software.

RESULTS: Male participants accounted for 231 (60.2%) of the total, while female participants accounted for 153 (39.8%). MTB positivity was found in 41 (10.7%) of the individuals. The transmission dynamics of medication resistance in *Mycobacterium tuberculosis* were found to be strongly influenced by marital status, HIV status, and contact with TB patients ($p<0.05$).

CONCLUSIONS: The occurrence of DR-TB was confirmed in the study population; thus, a sentinel survey under the NCDC is required, and the government should strengthen laboratory capacity and make these services available, affordable, and accessible to all presumptive TB patients.

5266208 | Implementation of a Bacteriology Laboratory in Rural Liberia: Early Reports on Bacterial Isolates and Their Antimicrobial Susceptibility Patterns at JJD Hospital

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BACKGROUND: Lack of or still limited laboratory capacity on infectious diseases surveillance is an area of significant weakness in many African national health systems1. Without these essential diagnostics and antimicrobial resistance data accessible through microbiology services, clinicians often manage and treat patients empirically, which may fuel inappropriate use of antimicrobials and emergence of resistant microbes.

METHODS: In order to mitigate this issue and along with the Liberian Ministry of Health, Health Focus GmbH worked with Partners In Health to implement a first-of-their-kind bacteriological laboratory at JJD Hospital, now serving the far South Eastern region of Liberia since October 2019. Clinical samples from patients treated at South East hospitals and JJD Hospital were cultured on standard microbiological media; bacterial isolates were identified and ASTs were performed following general bacteriology procedures as per Clinical Laboratory Standards Institute (CLSI). Data were collected and analyzed from samples processed between October 2019

RESULTS: A total of 784 specimens were processed, of which 308 (39.2%) were culture-positive from patients with a median age of 28 (less than 1 year- 84 years). of the positive cultures, 65% were from females. Most common specimens were urine 39.5% (310), swabs 32% (251), body fluids 11% (86), blood 14.3% (112) and stool 3.3% (26). Approximately 78% of the isolates were Gram-negative. Predominant isolates were *E. coli* 25.4%, *Klebsiella pneumoniae* 20.1%, *S. aureus* 14.9%, *P. aeruginosa* 12.4%, *Acinetobacter calcoaceticus* 7.5% and *P. mirabilis* 5.7%. Generally, the isolates exhibited a high level of resistance to commonly used antibiotics such as Ampicillin, Amoxicillin-Clavulanic acid, Erythromycin, Gentamicin, Tetracycline, co-trimoxazole and ceftriaxone.

CONCLUSION: Results from this report would contribute to increase knowledge of the local prevalence of bacterial organisms and their corresponding antibiotic resistance patterns, which are pivotal for a guided-antibiotic treatment rather than empirical, and potentially curb a high rise of antibiotic resistance found.

5266293 | Carbapenem Resistance from a One Health Perspective in Nigeria: A Scoping Review

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BACKGROUND: Increasing rates of carbapenem resistance (CR) are reported in humans, animals and the environment in Africa and these are driven primarily by misuse and overuse of antibiotics. Still, the extent of occurrence of CR in Nigeria is not comprehensively understood due to lack of effective CR surveillance system. This scoping review was conducted to describe the prevalence and geographical distribution of CR in Nigeria using One Health Approach.

METHODOLOGY: Peer-reviewed articles published in English language from January 01, 2000, to June 30, 2020 were retrieved from the MEDLINE and AJOL databases with reference to CR prevalence, diagnostic methods and geographical distribution in Nigeria. Using the PRISMA guideline for a scoping review with established inclusion and exclusion criteria, data from eligible studies were extracted in an Excel spreadsheet.

RESULTS: A total of 1361 articles were identified but 94 were eligible and included in the study. of these, 90(95.8%) employed cross-sectional study design and 57/94(60.6%) were published between 2015-2020. Clinical samples were used by 75(79.8%) of the studies, imipenem and meropenem antibiotics were mostly used for carbapenem antimicrobial susceptibility testing (AST). A significant proportion of the studies were from Southwestern Nigeria 38/94(40.4%) and the Northeastern Nigeria recorded the lowest number of CR study 6/94(6.4%). Although AST techniques vary, the disc diffusion susceptibility testing technique using the CLSI guideline was employed in 60/75(80.0%), 8/10(80.0%) and 5/7(71.4%) of the human, animal, and environmental studies respectively. CR prevalence was high; 5/75(6.7%) human studies reported complete bacteria resistance to carbapenem and CR prevalence among animals ranged between 3.7%-85.4% while 5.9%-84.4% CR prevalence was recorded in studies using environmental samples

CONCLUSION: CR varies widely but prevalent in the country. It is essential to establish a national CR surveillance system using standardized diagnostics and to design antimicrobial stewardship interventions across all the regions in the country.

5266377 | Molecular Studies of Primary Drug-Resistance in Mycobacterium Tuberculosis Among Presumptive Tuberculosis Patients in North West, Nigeria

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BACKGROUND: Primary drug-resistant tuberculosis is a public health concern in underdeveloped nations and continues to be a burden. The study area lacks data on demographic features and other factors related with primary drug-resistant tuberculosis, spatial distribution, prevalence, illness pattern, and gene associated with resistance in identified M*ycobacterium tuberculosis*. The goal of the study was to determine current trends in primary drug resistant among presumptive patients, the illness pattern, and proven genes related with resistance in *Mycobacterium tuberculosis* strains found in the study area.

METHODS: The research included 384 sputum samples from consented/assented individuals in a cross-sectional, prospective investigation (from Kano, Jigawa, Zamfara and Kaduna State). Structured questionnaire was given out, on demographic information, as well as factors linked to tuberculosis resistant and the spatial distribution of tuberculosis in the study area, were gathered. The samples were examined using the PCR (Line Probes Assay) method, and the data was analyzed using Chi-Square and Arc GIS 13.1 software.

RESULTS: Male participants accounted for 231 (60.2%) of the total, while female participants accounted for 153 (39.8%). MTB positivity was found in 41 (10.7%) of the individuals. The transmission dynamics of medication resistance in *Mycobacterium tuberculosis* were found to be strongly influenced by marital status, HIV status, and contact with TB patients ($p<0.05$).

CONCLUSIONS: The occurrence of DR-TB was confirmed in the study population; thus, a sentinel survey under the NCDC is required, and the government should strengthen laboratory capacity and make these services available, affordable, and accessible to all presumptive TB patients.

5266426 | Profile of Antimicrobial Resistance at Jinja Regional Referral Hospital Between January to July 2021

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INTRODUCTION: Antimicrobial resistance data in Africa is scarce since many countries have not been doing AMR surveillance but it is estimated that up to 8 million people die from AMR related infections per year. Jinja regional referral hospital laboratory is one of the laboratories that were activated in 2018 to participate in the Global antimicrobial resistance surveillance systems (GLASS) and the site has been implementing AMR surveillance by compiling data on bacterial profiles and antimicrobial susceptibility for proper patient care.

METHODS: This was a cross-sectional laboratory-based study design. Bacterial isolation was done using conventional identification methods. AST was carried out using the disk-diffusion method according to the CLSI guidelines. Quality control was carried out at every procedure involved in generation of the final result. Data obtained was entered into WHONET software for analysis.

RESULTS: The commonest isolated organisms were S.aureus 34 (17.6%), E.coli 32 (16.6%) other coliforms 31 (16.1%), candida Spp 15 (7.8),citrobacter spp 9 (4.7%), pseudomonas spp 8(4.1%), and K. pnuemonae 7(3.6%) The resistance pattern for gram positive cocci (N=35) were erythromycin 66%, penicilin G 83%, ciprofloxacin 51.4%, cefoxitin 40%, clindamycin 26%, chloramphenicol 5.7%, gentamicin 14.3%, cotrimoxazole 11.4%, and tetracycline 8.6%. The resistance pattern for enterobacteriaceae (N=99) was ampicillin 65%, ceftazidime 27.3%, cefotaxime 11.1%, ceftriaxone 30.3%, ciprofloxacin 42.4%, cotrimoxazole 16.2%, nitrofurantoin 4%, Amikacin 4%, chloramphenicol 33.3%, imipenem 0%, etrapenem 13.1%, tetracycline 8.1% and gentamicin 24.2%.

CONCLUSION: High levels of AMR to commonly-used antibiotics were reported, including upto 65% resistance to ampicillin and Penicilin(83%), emerging resistance to gentamicin (up to 24.3%) and relatively high levels of resistance to ceftriaxone (30.3%) among infections by Gram-negatives.

RECOMMENDATIONS: A bigger study should be done in all health facilities across the region to establish the drivers of resistance and general AMR picture since nothing about the two is currently known.

5266472 | Enhancing Human Capacity for Antimicrobial Resistance (AMR) Surveillance in Africa and Asia

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BACKGROUND: Antimicrobial resistance (AMR) is a major challenge in Africa due to ineffective AMR surveillance strategies, limited training of laboratory and epidemiological experts to detect and report on these pathogens of interest. To this end, the Fleming Fund project ''Qualifying the Workforce for AMR surveillance in Africa and Asia (QWARS)" seeks to bridge the current critical lack of adequate workforce for AMR surveillance under the One Health approach. QWARs seeks to train and qualify Microbiologists and Epidemiologists for AMR surveillance. We describe the early phase results of the QWARs roll out and implementation

METHODS: Trainees were nominated by their respective countries, with local experts delivering the curriculum consisting of 6 Epidemiology and 7 Microbiology modules developed by the project. Training delivery is a blend of e-Learning and face-to-face sessions, and a quiz is completed at the end of each Module. Progression to the next module is based on scoring 95% or above. Trainees who pass the final qualifying exam will be certified as experts to sustain the program in-country through cascading the trainings to sentinel sites.

RESULTS: Between 12 April and 9 August 2021, 333 trainees were enrolled for the QWArS training; 149 (45%) Epidemiology and 184 (55%) Microbiology. The first two modules were common to both groups and was successfully completed by 267/333 (80%) of the learners (n=115-Epidemiology and n= 152- Microbiology). Ninety-one (91%) Microbiology and 75 (65%) of Epidemiology trainees completed the subsequent modules. The aggregate rating of the course modules by the trainees is 8.9/10.

CONCLUSIONS: Performance results indicated significant levels of participation and knowledge transfer suggesting the capacity of Microbiologists and Epidemiologists will be enhanced for AMR surveillance in the continent.

5266487 | Antimicrobial Resistance Patterns of Bacterial Isolates from Blood Stream Infections at Jinja Regional Referral Hospital from January 2019 – June 2021

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BACKGROUND: There is currently no aggregated literature about the prevalence and antimicrobial susceptibility pattern of blood stream infections at Jinja regional referral hospital to monitor trends of resistance to antimicrobial agents. The objective of this study was to determine the main causative agents for blood stream infections and their antibiotic profiles.

METHODS: A retrospective analytical study was conducted among patients with positive blood cultures from January 2019 – June 2021. Blood samples were cultured using the BD BACTEC™ FX40. Conventional methods were used for the bacterial identification. Antibacterial susceptibility testing was performed using the Kirby–Bauer disk diffusion method following the CLSI -M100 guidelines. Data analysis was done using WHO-NET software considering only the first isolate per patient to generate antimicrobial profiles. Authority was sought from the research and ethics committee of Jinja regional referral hospital.

RESULTS: A total of 114 samples were positive. 68(59.6%) were gram positive bacteria mainly Staphylococcus aureus 40(35.1%) followed by Coagulase negative staphylococcus 20(17.5%) then Streptococcus species 8(7%). 43(37.7%) were Gram negative including E. coli 10(8.8%), other Coliforms 17(14.9%), Klebsiella species 5(4.4%), Acinetobacter species 4(3.5%), Pseudomonas aeruginosa 3(2.6%) then Salmonella species 2(1.8%). For S. aureus, percentage resistance was as follows: Penicillin G (100%), Cefoxitin (60%), Gentamicin (14.8%), Ciprofloxacin (20.7%), Erythromycin (52.2%), Clindamycin (13.6%), Tetracycline (20%), Chloramphenicol (33.3%). For E. coli, percentage resistance to Ampicillin, Ceftazidime, Gentamicin, Ciprofloxacin, Imipenem and Chloramphenicol were 100%, 100%, 42.9%, 33.3%, 0% and 20% respectively.

CONCLUSIONS: There is a high level of resistance to commonly used antibiotics and it is advised to routinely utilize microbiology services to guide antimicrobial use and monitor antimicrobial resistance trends to strengthen antimicrobial stewardship policies at the facility and region at large.

5266515 | Evaluation des Mesures de Biosecurite en Aulacodiculture : Cas du Sud-Ouest de la Region des Plateaux au Togo

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CONTEXTE : en réponse aux dangers biologiques existants et émergents, la biosécurité sert de rempart dans l'élevage. Pour autant, les perceptions et les approches de mise en œuvre sont diversifiées et peu explorées en aulacodiculture. La présente étude avait pour objectif de caractériser les pratiques de biosécurité dans l'élevage des aulacodes dans la partie Sud-Ouest de la Région des Plateaux au Togo.

MÉTHODES : une étude descriptive et transversale a été menée dans quatre préfectures sur la période d'août à octobre 2020. Une enquête utilisant des questionnaires structurés basés sur les cinq principes de biosécurité a été réalisée et des taux de conformité déterminés.

RÉSULTATS : globalement, la bio-exclusion (75,0 %) était mieux maîtrisée avec pour corollaire, une meilleure mise en œuvre des mesures de biosécurité externe (75,0 %) comparativement à celle interne (67,3 %). Le score moyen d'observance des mesures de biosécurité dans cette étude était de 70,0%. Les éleveurs avaient en effet collectivement moins de maîtrise des mesures en lien avec la bio-prévention et la bio-préservation, laissant entrevoir les possibilités de contamination et de persistance des dangers infectieux dans l'environnement. En plus de la métaphylaxie qui était appliquée, 100% des exploitants faisaient recours à la phytothérapie et la tétracycline était l'antibiotique le plus utilisé dans 50% des sites d'aulacodiculture.

CONCLUSION : ces données suggèrent la nécessité de mettre en place des actions de santé publique en vue de préserver la santé des éleveurs et celle de l'environnement. Enfin, une étude avec des outils standardisés, incluant un grand nombre de sites, devra permettre de déterminer si le déficit de maîtrise de la bio-préservation entrainant la persistance environnementale des microorganismes peut potentialiser les risques d'antibiorésistance dans cette filière.

5266614 | Phenotypic and Genotypic Characterization of Extended Spectrum Beta Lactamase and Carbapenemase Produced by Gram-negative Bacteria from Chicken Droppings, Fomites and Farm Workers in Lagos State

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BACKGROUND: The emergence of carbapenemase producing Gram-negative bacteria constitutes a public health threat in humans, animal husbandry, livestock management and animal medicine, as carbapenem antibiotics are considered the last resort for treatment of Extended-Spectrum Beta-lactamase (ESBL) producing bacteria.

METHODS: Gram negative bacteria were isolated from chicken droppings, fomites and farm workers in Lagos State. Disk diffusion method was used to determine the antimicrobial susceptibility of the bacteria against 10 antimicrobials including meropenem. Screening for ESBL and carbapenemase production was done using double disc synergy test and Modified Hodge's test respectively. Multiplex PCR was used to determine the presence of *bla*TEM, *bla*SHV, *bla*CTXM, *bla*KPC *bla*OXA, *bla*IMP and *bla*VIM.

RESULTS: *Escherichia coli* (67.8%, n=74) and *Proteus mirablis* (8.4%, n=9) were the most prevalent of 20 different species isolated. The majority of isolates were resistant to most tested antimicrobial agents except meropenem with the lowest resistance rate (3.6%, n=4). Resistance to three or more classes of antibiotics was observed in 98% (107) of the isolates. Genes encoding ESBL and carbapenemase were detected in 41.2% (33) and 55% (44) of the isolates respectively, with 3.1% (1) and 22.2% (8) harbouring more than one ESBL and carbapenemase gene respectively. The most prevalent genes were *bla*CTX-M and *bla*OXA, found predominantly in *E. coli*.

CONCLUSION: The detection of ESBL producing and carbapenem hydrolyzing isolates in poultry droppings is of great public health concern as these droppings are used as manure for agricultural purposes and evidence abounds of their transmission to humans.

5266650 | Prevalence and Molecular Assessment of Carbapenem Hydrolyzing Genes in Extended Spectrum Beta Lactamase Producing Gram-Negative Bacteria from Clinical Laboratories in Lagos State

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BACKGROUND: Antimicrobial resistance, especially in extended spectrum beta-lactamase (ESBL) producing Gram-negative pathogenic bacteria, is a great scourge on human health, exacerbated by the acquisition of resistance to carbapenems, the last resort treatment for infections caused by Extended Spectrum Beta Lactamase (ESBL) producing bacteria.

METHODS: Bacterial samples were obtained from urine, throat swabs, high vaginal swabs, wound swabs, sputum, semen and stool. Kirby Bauer disc diffusion method was employed in the determination of susceptibility of the isolates and results interpreted using CLSI standards. Double disc synergy test was used to detect ESBL production and multiplex PCR was used to ascertain the prevalence of *bla*TEM, *bla*SHV, *bla*CTX-M, *bla*KPC, *bla*IMP, *bla*OXA and *bla*VIM in isolates obtained.

RESULTS: *Escherichia coli* (40%, n=22) and *Klebsiella pneumoniae* (13%, n=7) were the most predominant of 14 different species isolated. Multidrug resistance was discovered in 34 (62%) of the isolates, mainly from urine, with 42 (76%) positive for ESBL production and 14 (26%) of the isolates not susceptible to meropenem. The ESBL genes *bla*TEM, *bla*SHV, and *bla*CTX-M, as well as carbapenemase genes *bla*KPC and *bla*VIM were detected in 23 (55%) and 11 (26%) of the 42 isolates respectively, with 8 (32%) harbouring 3 different resistance genes.

CONCLUSION: The detection of *bla*KPC and *bla*VIM in Gram-negative bacteria, particularly *K. pneumoniae* which readily transfers genes to other bacteria is disturbing, as carbapenems are the drugs of choice for treatment of infections caused by ESBL producing and multidrug resistant bacteria. Protocol to screen patients for genes encoding carbapenemase production is expedient in clinical laboratories for continuous epidemiological surveillance of the genes, in order to functionally prevent further dissemination and conserve of the efficacy of available drugs as there are no new ones in line for production.

5266688 | Coexistence of Multiple Bla Genes in Proteus and Serratia Species Isolated from Ready to Eat Foods and Cooking Utensils Samples in South West, Lagos State

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BACKGROUND: Extended spectrum beta-lactamase (ESBL) producing Enterobacteriaceae have become a huge burden globally. Antimicrobial resistance (AMR) pattern and virulence genes of extended-spectrum beta-lactamase producing *Proteus* and *Serratia spp.* from vendor foods, kitchen utensils and surfaces were evaluated.

METHODS: *Proteus* and *Serratia spp.* were isolated from food samples and swabs from kitchen utensils and surfaces were collected from various canteens and restaurants in Lagos state. Antibiotics susceptibility of the bacteria and the presence of genes encoding ESBL and carbapenemase were determined using Kirby Bauer disk diffusion method and multiplex PCR respectively.

RESULTS: The total heterotrophic bacteria count from each sample ranged from 1.2 x 104 CFU/g to 2.2 x 106 CFU/g. *Serratia* and *Proteus* spp. accounted for 17.4% of the total isolates and all displayed resistance to ciprofloxacin but susceptibility to meropenem. Higher resistance to all antibiotics tested was detected in *Proteus vulgaris* (70%) than *Serratia marcescens*, *S. plymuthica* and *S. liquefaciens* (30% each). The *bla*CTX-M and *bla*SHV were the most prevalent genes for ESBL production and were found only in *P. vulgaris*. Cohabitation of *bla*KPC, *bla*SHV, and *bla*VIM was detected in *Proteus vulgaris* isolated from vegetable soup and *bla*CTX-M an d*bla*VIM in *P. vulgaris* isolated from cooking table.

CONCLUSION: The coexistence of multiple *bla* genes encoding ESBL and carbapenemase production in *Serratia* and *Proteus* isolated from food observed in this study raises public health concerns about the dissemination of antibiotic resistance, particularly carbapenem resistance among consumers of ready-to-eat foods in Lagos state.

5266703 | Antimicrobial Susceptibility Profile and Molecular Characterization of Gram Negative Bacteria Isolated from Cafetarias in Lagos State, Nigeria

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BACKGROUND: Beta-lactamase harboring Gram negative bacteria are no longer exclusively linked to the health care system, therefore, investigating the possible threats to food safety and integrity posed by these bacteria has become increasingly important.

METHODS: A total of 159 samples were collected from cooked foods (spaghetti, fried and jollof rice, beans and vegetable soup) and swabs of fomites (spoons, forks, serving tables and cooking tables) from which Gram-negative bacteria were isolated and identified via Analytical Profile Index (API 20E). Antimicrobial resistance was observed against 10 antibiotics, using the Kirby Bauer disk diffusion method. Polymerase chain reaction analysis was used to determine the predominance of genes encoding beta-lactamases including extended spectrum beta lactamases (ESBL) and carbapenemases.

RESULTS: A total of 69 (47%) non duplicate isolates of Gram-negative bacteria were obtained with 43 (62.3%) from cooked foods and 26 (37.7%) from fomite swabs. The highest resistance was observed to ciprofloxacin (73.9%), and the lowest to meropenem (8.7%). Polymarase Chain Reaction analysis revealed that 23 (33.3%) isolates harbored genes encoding ESBL and/or carbapenamases of which 9 (13%) were from fomites and 14 (20.3%) from cooked foods. Cohabitation of *bla*SHV and *bla*KPC as observed in 10 (14.5%) of the isolates: *Klebsiella pneumoniae, Providencia alcalifaciens* and *Enterobacter cloaca* from spaghetti, two strains of *K. pneumoniae* from vegetable soup, one strain of K. *pneumoniae* from fried rice, and four strains of *K. pneumoniae* from spoons and serving tables.

CONCLUSION: The results indicated that people who patronize the food vendors are unwittingly exposing themselves to antimicrobial resisant microorganisms. It is imperative that good sanitation be maintained in food preparation and handling of cooked foods at all times to save consumers from the possible dangers of food-borne illnesses.

LABORATORY RESPONSE AND LESSONS LEARNT

STRENGTHENING LABORATORY SYSTEMS AND NETWORKS FOR ROUTINE AND EMERGENCY

5213267 | Improving Quality and Reliability of Malaria Laboratory Diagnosis in Endemic Countries is Fundamental in the Era of COVID-19

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BACKGROUND: Malaria is a major public health disease resulting to a million deaths globally with the highest in tropical and sub-tropical countries. World Health Organization (WHO) African region reported that *Plasmodium falciparum* account for majority of global cases of malaria infection with about 90% in Africa. COVID-19 pandemic is a respiratory infection reported as an additional deadly disease burden. Association between malaria and COVID-19 is still not completely understood but clinical presentation and misclassification of both diseases is common in malaria endemic settings.

OBJECTIVES: To highlight areas needing continuous quality improvement in Malaria Laboratory Diagnosis (MLD) in an endemic settings experiencing COVID-19 pandemic.

MATERIALS AND METHODS: This traditional review focus on how to improve quality and reliability of MLD through synthesis of available grey and peer reviewed literature across Africa. Articles published within 10 years on the quality and reliability of MLD were reviewed. Eight areas were reviewed namely; 1. policy and guidelines, 2. funding sources 3. proliferation of malaria rapid diagnostics (MRDTs) kit, 4. standardization of malaria microscopy.5 malaria staining and reading 6. Quality Assurance (QA)/External Quality Assurance/Proficiency Testing (EQA/PT) 7. Quality Management System (QMS) 8. MRDTs periodic validation.

RESULTS: Six countries (Tanzania, Mozambique, Kenya, Uganda, Mali and Nigeria) had outdated policy and guidelines. Funding is majorly from USA (35%), UK (16%), African countries combined (32%), Global Funds contribute 56% globally. Most national EQA/PT programs are not accredited. Overall, MRDTs combined with microscopy is not optimized in terms of coverage and quality.

CONCLUSION: Regular update of policies and guidelines, increased government funding, functional QMS encompassing MRDTs and microscopy, national EQA/PT across testing points layered with accredited provider are areas needing improvement to guarantee quality and reliability of MLD. These will go a long way to mitigate risk and consequences of misdiagnosing in this era of COVID-19 and malaria.

5216543 | Continuous Quality Evaluation of Asante Rapid Test for Recent Infection as Part of Kit Lot Quality Control

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BACKGROUND: Rapid tests for recent infection (RTRI) diagnose HIV-1 infections and characterize HIV-1 as recent or long-term via the positive verification line (PVL) and long-term line (LTL), respectively. Tracking with Recency Assays to Control the Epidemic (TRACE) uses RTRI for real-time infection surveillance. Successful implementation of TRACE requires high-quality test performance. The goal of this study is to ensure this through additional quality checks, beyond that of the manufacturer, before field use.

METHODS: Test kits are evaluated at the Centers for Disease Control (CDC) using a blinded, well-characterized panel of 133 samples by two testers. Linear regressions are conducted comparing PVL and LTL results against reference data from previous passed lots for consistency (slope=1.00 + 0.1; intercept close to 0; and R2≥0.9). LTL and PVL data between testers analyzed using linear regression (0.85≤slope≤1.15 and R2≥0.80). Inter-rater reliability is used to (Cohen's kappa cutoff=0.85) assess test validity. The Levey-Jennings plot is used to identify systematic errors and assess test kit performance over time.

RESULTS: With these evaluations, CDC failed 3 Asante kit lots (n=32) that initially met manufacturer's lot quality control criteria. Regression analyses demonstrate that test kits were performing as expected with consistent R2≥0.92 for both PVL and LTL. On average, inter-rator reliability kappa was 0.9, indicating a strong level of agreement.

CONCLUSION: Ongoing evaluation of new RTRI kit lots is important to ensure high quality results. Our results highlight the need to continue to work with manufacturers to ensure high-quality tests. Investing in effective quality-assurance measures, using both pre- and post-market surveillance, could help improve RTRI accuracy and outcomes of similar testing programs.

5222776 | Zambia Waste Management Strengthening Project Implementation for Public Health Facilities Supporting Conventional Viral Load and Early Infant Diagnostic Testing Services

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BACKGROUND: Concerns of the use of guanidinium thiocyanate routinely used for HIV viral load (VL) and HIV early infant diagnosis (EID) prompted a review of waste management (WM) procedures at public health laboratories. Zambia Ministry of Health (MOH) and US Centers for Disease Control and Prevention (CDC) initiated a review of WM that was carried out by the Association of Public Health Laboratories (APHL) and the Centre for Infectious Disease Research in Zambia (CIDRZ).

METHODS: A stakeholder meeting was convened to consider strategies, activities, and expected outcomes. A detailed survey document was used by an MOH, APHL, and Zambia Environmental Management Agency team to assess 21 facilities that support VL and EID testing. The assessments evaluated waste handling, personnel training, personal protective equipment (PPE), and waste treatment technologies.

RESULTS: The assessments identified several weaknesses in waste management practices including a) 81% of facilities not properly segregating waste, b) 90% of facilities had inadequate personal protective equipment, c) 81% of facilities lacked autoclaves, and 100% of facilities lacked properly operational incinerators. Based on evaluation of facility waste streams, incineration was identified as the best option for waste disposal and an improvement plan developed and implemented. 11/21 (52%) of facilities required incinerator replacement, and 10/21 required service and repair of the existing incinerators. Eight 70Kg/hr MacroBurns and three 50Kg/hr Inciner8 incinerators were installed in 11 facilities; ten incinerators of varying types were repaired at 10 sites and a 48 operators from the 21 sites were trained.

CONCLUSION: Engagement and empowerment of the laboratory and environmental health staff at the facilities is cardinal for the development of correct WM activities and sustainability.. Routine reporting of WM operations is essential to maintain safe and effective waste disposal and spread repair and replacement cost over many budget years to sustain sufficient operations.

5223404 | Hospital Based Epidemiology of Influenza in Ethiopia: Descriptive Analysis of Sever Acute Respiratory Illness (SARI) 2009-2019, Addis Ababa, Ethiopia

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BACKGROUND: Influenza is an acute viral respiratory tract disease classified as influenza types A, B and C. Subtypes of influenza A viruses H1N1, H2N2, and H3N2 have been associated with widespread epidemics in humans. In Ethiopia the index case of influenza A (H1N1) pdm2009 was detected in 2009. We determined influenza virus positivity rate and distribution of sever acute respiratory illness cases at Yekatit 12 Hospital medical college.

METHOD: Descriptive data analysis was employed for Yekatit 12 medical college Hospital influenza surveillance data from January 2009-December 2019.

RESULT: A total of 986 cases were registered on case-based database from January 2009-December 2019 and 835(85%) of them were tested for influenza. Among them 30(3.6%) cases were positive for influenza and of which 25(83.3%) were influenza A and 5(16.7%) were influenza B virus. From total 25 influenza A cases, 16(64%) of them were influenza A(H1N1)pdm2009 the rest 9(36%) were seasonal influenza A(H3N2) type. Among the total Influenza positive cases, 17(56.6%) were <2 years, followed by age group 5-14 years and 15-49 years by 5(16.7%) and 3(10%) respectively.

CONCLUSION: Seasonal influenza A (H3N2), (H1N1) pdm2009 and influenza B were found at Yekatit 12 medical college hospital from 2009-2019 surveillance period. Influenza positivity rate and number of sever acute respiratory illness cases were predominantly observed among age <5 years and occur in all months of the year. Increasing the number of influenza surveillance sites in Addis Ababa will be more representative and important to determine burden of respiratory infections for effective intervention.

5223626 | Geo-Spatial Mapping of Laboratory Testing Capacity and Networks Functions for Better Laboratory Programming

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BACKGROUND: By 2020, 15 countries had signed up to participate in the laboratory mapping initiative, which aims to develop a system for collecting, storing, and analyzing geospatial data on laboratory capacity, systems, and networks in order to improve laboratory services through evidence-based decision making. The purpose of this study is to describe the LabMap project's progress thus far, taking into account countries' collaboration and access to data sets, among other things.

METHODS: From April to May 2021, technical reports, project documentation, progress narratives, the LabMap database, and reusable tools were examined to assess number of portals, number of curated laboratory data and level and type of labs, test menu, number of countries mapped.

RESULT: During the LabMap project's implementation, 195 data collectors from 15 countries were trained. 2,131 labs were mapped using digital mapping tools. There are 1151 (54%) level 1 laboratories, 831 (39%) level 2 laboratories, and 149 (7%) level 3 laboratories mapped in 15 countries. Public laboratories account for 84 percent of the 2,131 labs, while private labs account for 8%, non-profit and religious labs 7%, and academic labs 1%. A public portal instance was developed for 11 countries (70 percent). Data was curated for 15 countries in a Google sheet using Google script and Open Refine tools, which was fully integrated with the ONA platform. 15 countries have access to their own LabMap data sets, and countries collaborate to upload real-time data to the Ona platform.

CONCLUSIONS: The LabMap project provides feasible and reusable and open source solutions to countries that are ready to inventory geo-located information on their laboratory systems, in support of evidence-based decision making. The LabMap project results will also be used to advocate for more funding from countries and donors to expand the LabMap project to the rest of African countries.

5224305 | Delays in HIV-1 Infant PCR Testing May Leave Children Without Confirmed Diagnoses

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BACKGROUND: The early diagnosis and confirmation of HIV infection in newborns is crucial for expedited antiretroviral therapy initiation. Confirmatory testing must be done for all children with a reactive HIV PCR result, and the results be released expedited for early initiation of antiretroviral therapy. There is currently no comprehensive data on confirmatory testing, turnaround time (TAT), and rejection of HIV PCR test requests at National Health Laboratory Service laboratories. We aim to assess relevant measures for routine infant HIV PCR testing: rate of rejected test requests, turnaround time, and rate of confirmatory testing.

METHOD: A retrospective review was performed on the laboratory-based data of all HIV PCR tests that were performed on children ≤24 months old (n=43,346), and data of rejected HIV PCR requests (n=1,479) over a 24-month period (2017-2019). These data were extracted from the laboratory information system. Data were analyzed from sample collection to release of results, assessing the TAT and follow-up patterns.

RESULTS: The proportion of HIV PCR requests that were rejected was 3.3%, of which 83.9% were rejected for various pre-analytical reasons. The majority of test results (89.2%) met the required 96-hour TAT. of the reactive initial test results, 53.5% had a follow-up sample sent, of which 93.1% were positive on follow-up. of the initial indeterminate results, 74.7% were negative on follow-up.

CONCLUSION: A significant proportion of HIV PCR requests were rejected for various pre-analytical reasons. The high number of initial reactive tests, without evidence of follow-up, may suggest that a shorter TAT would be required to allow confirmatory testing, before children are discharged.

5225112 | Stepwise Quality Improvement in 23 National Reference Laboratories for Tuberculosis in West and Central Africa During the COVID-19 Pandemic Using the SLIPTA Approach

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BACKGROUND: Since 2019, the Global Fund for HIV, Tuberculosis (TB) and Malaria funds the TB LAB project, led by the Supranational Reference Laboratory (SRL) for tuberculosis in Cotonou (Benin). The project aims to strengthen the capacity of 23 National Tuberculosis Reference Laboratories (NTRLs) in the West and Central Africa region, assisted by expert consultancy of the SRLs of Antwerp (Belgium) and Milan (Italy).

METHODS: Thanks to this project, an on-site baseline assessment of 23 NTRLs was conducted between July 2019 and January 2020, using the SLIPTA checklist. This was followed by an on-site follow-up assessment one year later, between October 2020 and January 2021. Each NTRL received the checklist at least two weeks prior to the assessment visit and was assessed by 1 or 2 auditors using this checklist. Between both assessments, on-site technical assistance was not possible due to the COVID-19 related travel ban but an 8-weeks online course was offered consisting of 12 theoretical webinars and 8 practical workshops in French, and 12 theoretical webinars and 8 practical workshops in English. This course was followed by 8 weeks of individual online coaching of the quality officers of the NTRLs by a team of 7 coaches from the 3 SRLs.

RESULTS: Among the 21 NTRLs assessed twice, 17 increased their SLIPTA score. This resulted in 4 NTRLs gaining 2 SLIPTA stars, 6 gaining 1 star and 11 remaining with the same number of stars. This progress was obtained despite an important impact of the COVID-19 pandemic on the functioning of the NTRLs and their difficulties in accessing a stable internet connection.

CONCLUSIONS: Despite the COVID-19 pandemic related travel ban in 2020 and the instability of internet connections, much has been achieved by supporting NTRLs online with the implementation and improvement of their quality management systems.

5225210 | Implementation of an External Quality Assessment Program for Xpert MTB/RIF and Microscopy in West and Central Africa

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BACKGROUND: Participation in an external quality control program as require by ISO 15189 standards, reflects the performance of a laboratory. As tuberculosis (TB) diagnosis is mainly based on microscopy and GeneXpert MTB/RIF in West and Central Africa, there was a need of implementing an EQA in the region. Within the framework of the TB LAB Project funded by the Global Funds for HIV, TB and Malaria and led by SRL Cotonou, an EQA program for both tests was implemented in a COVID-19 pandemic context at the National TB Reference laboratory (NTRL) of the region.

METHODS: A batch of 10 unstained microscopy slides for AFB detection and 5 dry tube samples for the detection of Mycobacterium tuberculosis and Rifampicin resistance status was shipped to the participating NTRLs. For Xpert, a satisfactory result was considered as 80 % of agreement for MTB detection and Rif resistance status. For microscopy, satisfactory result was considered by the absence of high false negative/positive (HFP/HFN) result and an overall agreement of 80%.

RESULTS: Among the 22 Labs of the network, 20 labs received the panels due to the absence of sample transportation company and all the participating labs submitted their results timely. For microscopy, 75% of labs met the requirements. At least 1 HFN result was reported by 25% of participating labs but no HFP was reported. Regarding Xpert, the requirements were met by 95% of the labs. Error rate, Invalid rate and No result rate was respectively: 2,5%; 0.4% and 0%. The rate of correct MTB Detection and Rifampicine resistance detection was established at 97% and 99% respectively

CONCLUSIONS: The quality of Xpert in the region was satisfactory whereas microscopy is still a challenge in some countries and need support by framework as TB-Lab project. Sample shipment also needs to be improved in the region

5225760 | Evaluating a Waste Management Method and Strategy for HIV Viral Load (Vl) and Early Infant Diagnosis (EID) Testing

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BACKGROUND: Laboratory waste generated from molecular tests for HIV viral load (VL) and early infant diagnosis (EID) often contains guanidine thiocyanate (GTC). GTC may release hydrogen cyanide gas (HCN) if exposed to common oxidizing cleaning agents such as bleach. Collection/disposal services for this effluent waste are often unavailable or expensive in PEPFAR-supported countries. GTC concentration in the effluent is unknown because the amount consumed is unspecified. Methods were developed to assess GTC concentration in the effluent and to remove the (cyanide-containing) thiocyanate ion via a precipitation method as cuprous thiocyanate - CuSCN.

METHODS: A titration analytical method was developed and evaluated vs 50.0 % w/w GTC standards and >100 VL/EID platform waste samples to determine the GTC concentration. The precipitation method utilized sodium thiosulfate and copper sulfate mixed with effluent to precipitate CuSCN. FTIR (Fourier-transform infrared) and ICP (Inductively Coupled Plasma) spectroscopy analysis for sulfur were used to determine composition of the precipitate. The titration and precipitation method were then evaluated in the field at the University Teaching Hospital (UTH) in Lusaka, Zambia on liquid waste from Roche CTM 48/96 platforms.

RESULTS: The titration analytical method showed 53.8% +/- 4.2% GTC on a series of 50.0 % w/w standards. Titration analysis of the UTH clinical waste showed 8.2% GTC before treatment and 0.0 g/l GTC after treatment. The thiocyanate molecule was precipitated from laboratory waste solutions as CuSCN. The supernatant was disposed to drain without risk of

5226817 | Significantly Decreased Viral Load Test Rejection Rates After Implementation of a Quality Improvement Project in 28 Healthcare Facilities in Zululand District, KwaZulu-Natal, South Africa

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BACKGROUND: Viral load (VL) test or specimen rejection in a laboratory threatens optimal VL coverage. A US President's Emergency Plan for AIDS Relief (PEPFAR) program review (August 2020) highlighted high VL test rejection rates in South Africa. We used VL test data from National Health Laboratory Service in Zululand district to investigate VL test rejection rates, and we report the progress of our quality improvement plan (QIP) in the 6 months after implementation.

METHOD: We identified 28 PEPFAR-supported facilities with high VL test rejection rates (>2% in 1 month). We conducted a root cause analysis for each facility and developed a QIP, mainly targeted training and mentoring, which was implemented from August 2020 onward. QIP implementation was managed by healthcare facility staff. A Laboratory Advisor from a PEPFAR implementing partner provided direct monthly oversight via in-person visits or virtual monitoring. Wilcoxon signed-rank test was used to measure difference in rejection rates at 6 months after QIP implementation. The rates are absolute values.

RESULTS: The identified causes of VL test rejections in order of importance include: heamolysis, electronic gate keeping cancellation, clotted blood, unsuitable blood tube etc. District VL test rejection rates decreased from 7.2% (August 2020) to 2.8% (February 2021). VL test rejection rates were significantly lower at 6 months after QIP implementation in the 28 facilities ($p<0.0001$). The reduction in VL test rejection rates ranged from 17.5% to 100.0% in the 28 facilities. VL test rejection rates were <2% in 11 of the healthcare facilities.

CONCLUSION: QIP implementation in these facilities significantly decreased VL rejection rates and associated wastes (specimen, time and cost), improved access to test results, and could eventually improve VL coverage and provision of timely care services such as adherence support and treatment regimen change to patients. QIP to be extended to other districts.

5227932 | The Mentorship Program to Strengthen and Improve the Quality Managment System of Medical Laboratories in TOGO

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BACKGROUND: Laboratory Quality Improvement Process Towards Accreditation (SLIPTA) is an assessment checklist proposed by World Health organization (WHO) for baseline assessment, supervision, monitoring and evaluation of medical laboratory progress towards accreditation. This checklist creates a stepwise assessment approach that emphasizes incremental improvements that impact the quality of medical laboratory services and patient care.

OBJECTIVE: Strengthen the quality management system (QMS) of the medical laboratories in health facilities across Togo.

METHODS: To prepare the implementation of the mentorship program, a pool of auditors and mentors were trained on the WHO SLIPTA and Laboratory Quality Stepwise Implementation tools. After baseline assessment in 86 labs, 35 of them with zero star were selected and supported by the mentorship program. The impact of the program was evaluated after 6 months (follow up I) and the sustainability was measured after 12 months (follow up II) and 18 months (follow up III).

RESULTS: Baseline scores ranged from 11-83% with an average of 32%. Over 90% of the labs had zero star and 1.2%, 2.3% and 5.1% got one star, two stars, and three stars respectively. A significant impact of the program was observed at the follow up I assessment by an increased average SLIPTA score from 27.8% to 53.4%. Among 35 labs mentored, 45.7% got one star and 8.6% got two stars. The sustainability of the program was showed by an increase of the score from 53.4% to 58.2% between follow up I and follow up II and a slight decrease from 58.2% to 56.1% between follow up II and follow up III.

CONCLUSION: This mentorship program remains an excellent approach used to helping Togo medical labs to improve their QMS

5236589 | Limitations of Polymerase Chain Reaction-Based Identification of Diarrhoeagenic Escherichia Coli in Nigeria

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BACKGROUND: Diarrhoeagenic E*scherichia coli* (DEC) are important intestinal pathogens. They are delineated by specific virulence genes commonly detected using polymerase chain reaction (PCR)-based protocols. We evaluated a popular published PCR protocol, hypothesizing that it would offer comparable precision to whole genome sequencing (WGS).

METHODS: DNA extracted from 1230 biochemically-confirmed *E. coli* isolated for a study of DEC in diarrhoea in Ibadan Nigeria. DNA was screened by multiplex PCR and WGS using *aatA* (CVD432) as target for enteroaggregative *E. coli* (EAEC), *sta* and ltcA for enterotoxigenic *E. coli* (ETEC), *bfp* and *eae* for enteropathogenic *E. coli* (EPEC), *stx1* and *stx2* for Shiga toxin-producing *E. coli* (STEC) and *ipaH* for enteroinvasive *E. coli* (EIEC). PCRs used genome-sequenced strains as controls. Sequence data was assembled using SPAdes, evaluated using QUAST and Virulencefinder was used to identify virulence targets.

RESULTS: PCR and WGS classified 568 and 432 strains as DEC respectively. PCR identified EAEC 99(21%), ETEC 150(31%), EPEC 43(9%), EIEC 33(7%) and STEC 46(10%) while WGS identified EAEC 137(29%), ETEC 19(4%), EPEC 23(5%) and EIEC 2(0.4%) and no STEC. The sensitivity of PCR compared to WGS was 77.8% for ETEC, 61.7% for EAEC, 45% for EPEC and 0% for both EIEC and STEC. The specificity of the PCR protocol for the different pathotypes ranged from 74.5% to 94.7%. Negative predictive values were 86.1% for EAEC and above 97.5% for other pathotypes but positive predictive values were 73.9% for EAEC and under 27% for other pathotypes.

CONCLUSIONS: Easily-implemented PCR protocols offer reasonable specificity for DEC in our setting. PCR is however too insensitive for clinical diagnosis and could lead to DEC burden underestimates. Predictive values may vary with strain genome so that PCR primers optimized for use in one part of the world may lack sensitivity in geographies where different pathogen lineages predominate.

5236706 | External Quality Assessment of Laboratory Testing in 48 Centers of Epidemiological Surveillance (CES) in West Africa

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BACKGROUND: This study is part of a World Bank Regional Disease Surveillance Systems Enhancement (REDISSE) project, involving Guinea Conakry, Guinea Bissau, Liberia, Sierra Leone and Togo, conducted from November 2017-March 2019. The objective was to evaluate the capacity of laboratories to identify microorganisms by microscopic examinations, using an international EQA program.

METHODS: The cross-sectional study was carried out in 48 district laboratories, which involved the microscopic detection and identification of acid-fast bacilli, plasmodium, trypanosomes, organized throughout under 3 programs, each consisting of 5 samples (labelled A, B, C, D, E, F) per program, 15 per laboratory. The samples consisted of blood smears stained with May-Grünwald Giemsa (2 programs); sputum smears or respiratory wash, stained using Ziehl-Nielsen coloration technique (1 program). The test event lasted 40 days. Laboratories performance was determined by an ISO/IEC 17043: 2010 accredited EQA provider. Performance criteria were established by the provider, based on the expected results for each sample and scored into three categories: *acceptable*, *unacceptable* and *not performed*.

RESULTS: Overall, the 48 laboratories recorded variable acceptable results according to the three programs: 82% (Mycobacterium spp), 59% (Plasmodiums spp) and 30% (Microfilaria-Trypanosoma-Plasmodium).

Successful identification also varied depending on the species : 72% (35/48) for *P. falciparum*, against 15% (7/48) for other plasmodial species (vivax and ovale); 79% (38/48) for *Mycobacterium tuberculosis* identification; 44% (21/48) for *Loa loa* ; 10% (5/48) for *Plasmodium ovale* and 36% (18/48) for *Trypanosma brucei*.

CONCLUSIONS: These results highlight the importance and value of laboratory participation in an EQA to measure their strengths and weaknesses in producing reliable and accurate results. The excellent performance on the identification of mycobacteria (TB program) should serve as a reference given the good laboratory skills to perform an accurate diagnosis.

5236868 | Resolution of Indeterminate Samples of Human Immunodeficiency Viruses Tested in the Serology Laboratory Between 2018 and 2021

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INTRODUCTION: Indeterminate results of rapid tests of the Human Immunodeficiency Virus are common, and the World Health Organization recommends retesting these samples. In Mozambique, the Human Immunodeficiency Virus rapid testing algorithm is serial and consists of a sequence of tests (determine and Unigold) for the detection of antibodies to Human Immunodeficiency Virus type 1/2. And this algorithm determines that undetermined results in the Health facilities must be sent to the reference laboratory for confirmation and in order to have the definitive diagnosis.

OBJECTIVE: Determine the resolution rate of indeterminate samples for Human Immunodeficiency Virus Rapid tests in the Serology Laboratory between 2018 and 2021.

METHODOLOGY: This is a retrospective study, where requests from the years 2018 to 2021 were analyzed, and the results presented in percentages.

RESULTS AND DISCUSSION: Between 2018 and 2021, a total of 205 requests were received for analysis. of these, 126 (61.4%) were female, 72 (35.1%) male and 7 (3.4%) without information. The median age was 39 and the majority were from Maputo Province (40.4%). of the 205 requests, 52 were from 2018, 68 were from 2019, 59 were from 2020 and 26 were from 2021. of the total requests, 43 were rejected (40 Inadequate and 3 requests without samples) and 162 were compliant (where 38 requests was from 2018, 55 from 2019, 51 from 2020 and 18 from 2021). Of the compliant requests, 47 (29%) had a definitive diagnosis in the Serology laboratory (31 positive and 16 negative) and 115 (70.9%) were referred for molecular diagnosis (31 positive, 78 negative and 6 without results). And the best resolution rate in the Serology Laboratory, according to the number of compliant requests received annually, was verified in 2019 to be 43.6%.

CONCLUSION: Between 2018 and 2021, 79% had compliant requests and the resolution rate was 43.6%.

5237345 | Near-Point-of-Care Viral Load Testing During Pregnancy in Relation to Viremia at Delivery: A Difference-in-Difference Study in Zimbabwe

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BACKGROUND: Viral suppression during pregnancy and at delivery dramatically reduces mother-to-child-transmission (MTCT) of HIV. We assessed whether near-point-of-care (POC) viral load (VL) testing at a woman's first antenatal care visit (ANC1) expedited clinical follow-up for women with unsuppressed VL (UVL), thereby increasing the proportion of women who are virally suppressed at delivery.

METHODS: A difference-in-difference study was conducted from August 2019-November 2020 across 20 public health facilities in Zimbabwe, with ten facilities providing ANC1 VL on near-POC devices and ten facilities providing at centralized laboratories. The baseline cohorts were from the same facilities, comprised of women delivering during the enrollment period. The study endpoints assessed were viral suppression at delivery and turnaround time from sample collection to result received and clinical action (if UVL).

RESULTS: 1782 women were included in the analysis of whom 54% presented at ANC1 in their third trimester. At baseline, only 28% of women received an ANC1VL, which increased to 86% at endline. In the endline cohort, women were more likely to receive VL results within 30 days of ANC1 sample collection with near-POC compared with centralized laboratory (51% versus 13%, RR: 4.07, 95% CI: 1.76-9.39), as well as receive clinical action among those with UVL (63% versus 8%, RR: 7.88; 95% CI: 1.53-40.47). However, we did not observe a significant change in risk of having an UVL at delivery with near-POC VL (RR: 1.02, 95% CI: 0.95-1.10).

CONCLUSIONS: Near-POC VL testing at ANC1 dramatically improved the timeliness of result receipt by patients as well as initiation of clinical action for those with an UVL. Although we did not observe a significant impact of provision of near-POC VL at ANC1 on re-suppression at delivery, potentially due to late presentation for ANC1, continued maternal near-POC VL testing during pregnancy may facilitate reducing UVL and MTCT risk.

5237751 | Evaluating the Suitability of BD Vacutainer Plasma Preparation Tube (PPT) to Improve Sample Collection and Testing for HIV Viral Load (Vl): Pilot Study from University of Uyo Teaching Hospital (Uuth), Akwa Ibom Nigeria

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BACKGROUND: Viral load test used in patients monitoring towards achieving undetectable results is a major measuring indicator in quality care services in HIV program service delivery. Improving VL results turnaround time through innovative approach at the pre-analytical and analytical phase workflow is essential to increasing efficiency and attaining VL coverage. PPT sample collection container provides a one step sample collection, plasma preparation and transportation of VL sample. Samples collected in PPT are used as primary testing tube, loaded directly on to the PCR machine for testing. A comparative analysis to evaluate suitability of PPT as an alternative as against samples collected in the EDTA tubes was carried out in UUTH PCR lab a USAID supported facility in South South Nigeria.

METHOD: A total 251 samples across 6 facilities from Cross Rivers were tested. Paired 5ml whole blood was collected into labeled PPT and vacutainer EDTA tubes from same client. The samples were processed through centrifugation, and sample from EDTA tubes were separated into Cryovials. All samples were stored frozen at -20 degree Celsius before transported to UUTH PCR lab. Both samples were tested on Abbott m2000 PCR machine, PPT was used as primary testing tube, while the plasma in the cryovials were transferred into a secondary testing tube.

RESULTS: Correlation analysis, paired student t test was used to assess suitability of both methods, and $p<0.05$ at 95 confident intervals (Cl) was considered significant. The analysis showed PPT mean VL log10 was 1.88±0.78 against EDTA-Plasma 1.88 ±0.86 (p=0.79,95% Cl: -0.044-0.0460). There was positive correlation between PPT and EDTA-Plasma VL Log 10 (r=0.91 p= <0.001). Observed higher failed assay 22/251 (8.8%) in Plasma EDTA compared to PPT 6/251 (2.3%).

CONCLUSION: PPT is a suitable alternative for Viral load testing and offer additional advantages, reduces pre-analytical TAT of testing process and number of failed assays. However more study

5239289 | Evaluation and Comparison of 4 WHO Approved RT-PCR Assays for the Detection of SARS-CoV2 Virus RNA

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INTRODUCTION: Molecular testing is the angular stone to prevent and control SARS-CoV2 virus circulation. In this study, we aimed to evaluate and to compare 4 WHO approved protocols by testing clinical specimens in order to decrypt the origins and the consequences of the diverging results.

METHODS: 260 nasopharyngeal samples were randomly selected then tested by 4 WHO approved RT-PCR protocols: Charité-Berlin (monoplex E/monoplex RdRp), Hong-Kong University (monoplex N/monoplex Orf1), CDC China (commercial test DAAN Gene ®, triplex N/OrF/internl control) and triplex IPP (tiplex IP2(nsp8 et 9)/IP4(RdRp)/internal control). RT-PCR results were evaluated and compared.

RESULTS: For positive samples, Ct for both targets of CDC China and Charité-Berlin were different (p<0,0001), mean of difference was 1,5+-2 and 2,3+-2, respectively. However, HKU and IPP gave similar CT for both targets (p>0,001). The protocol that gave the most discordant results, i.e positive for one target but negative for the other, is IPP (16,9%). For inconclusive results, Ct values of the positive target are high (mean of ct value >33,5) except for the IPP (mean of ct value=25,2). All protocols gave the same results for 184 samples, 70,8% (72 negative and 112 positive for at least one target per protocol), however, 76 samples (29,2%) gave discordant results. Obtained Ct values were high for the discordant cases, oppositely, ct values were much lower (p<0,001) for the concordant ones. CDC China is the most diverging protocol; for 43 cases it gives at least one positive target however all other results are negative. Agreement between Charité-Berlin, IPP and HKU, two by two is very good (k>0,8).

CONCLUSION: Due to serious discordant cases, our results outline the need to continually evaluate the performances of RT-PCR protocols and underscore the need of targeting at least two independent genomic targets for reliable detection.

5263894 | African Union-Africa Centres for Disease Prevention and Control (AU-A.CDC) Support to Strengthening Laboratory Response in Sierra Leone

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BACKGROUND: The first case of coronavirus in Sierra Leone was confirmed on the 31st of March 2020. At that point of confirmation of the first case there were five (5) public health laboratory but out of these five (5) laboratories there were only three CoVID-19 testing laboratories; Connaught Laboratory, Military 34 and China P3 Laboratory.

There was a need to increase and expand the testing capacity both within the Western Area and in the provinces, to be able to handle the increased cases.

In May 2020 A.CDC supported the Central Public Health Reference Laboratory (CPHRL) with a rapid responder to help with technical expertise so as to be able to respond quickly and efficiently.

METHODS: At the CPHRL testing and trainings are done using molecular diagnostic platforms and real time reverse transcriptase polymerase chain reaction (RT-PCR) assays.

To scale up the testing capacity to handle the workload, we transitioned from manual extraction to automated extraction using MagMax Express 96 and also initiated pooled amplification testing. This helped to reduce the turnaround time massively.

RESULTS:

CoVID-19 Testing
Out of a total of 71,537 samples (May 2020-Week 30 2021) analyzed so far. 3,920 were recoveries, 21,833 were surge/new, 24,371 arrivals and 21,413 departures samples.

Sequencing
A.CDC has also supported with the shipment and analysis of 70 samples at the Noguchi Memorial Institute for Medical Research.

In summary, there were NO variants of concern (i.e., B.1.1.7, B.1.351 and P.1) or variants of interest (i.e., B.1.427, B.1.429 and B.1.526) in the bath of samples sequenced.

CONCLUSION: The fight against the deadly SARS-CoV 2 virus is still ongoing in Sierra Leone but the support of A.CDC through technical expertise, reagents, consumables/supplies and vaccines has helped us to be able to contain the first, second and third waves that threatened the nation.

5264997 | Key Discussion Outcomes from ASLM's Laboratory System Strengthening Community of Practice (LabCoP) COVID-19 Virtual Sessions

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BACKGROUND: The Laboratory System Community of Practice (LabCoP) contributed to the COVID-19 response by mobilising diagnostics experts, frontline workers, policymakers, and manufacturers to discuss key SARS-COV-2 testing topics. Knowledge sharing and quick uptake of best practices are key to controlling the pandemic and other diseases. Opinions, interests, and experiences gathered in discussions constitute unique sources of user experience that moves the field forward. We analysed discussions and key questions posed during LabCoP COVID-19 sessions to understand main interests and challenges of the laboratory community.

METHODS: Comments and questions from sessions hosted between March and August 2020 were extracted from Zoom chat records and collated into Microsoft Excel files. Two independent scientists retrospectively categorised the questions by thematic analysis. Where overlaps occurred, the final theme grouping was obtained by consensus within the ASLM LabCoP core team. The number of questions in each theme was expressed as a proportion of the total analysed. Themes with higher percentages were assumed more important to the laboratory community.

RESULTS: Twenty-one sessions were conducted, with a median of 590 participants (IQR; 446, 808) from 126 countries. Presenters included experts, country representatives, manufacturers and covered topics on diagnostic landscape, country experiences, data and quality management. of 663 questions gathered, major themes were: test systems (30.7 %); procurement (16%); test performance (14.4%); sample management (9.3%); biosafety (7.5%) and result reporting (5.5%). Other themes (waste management, quality assurance, surveillance, e.t.c) had <5% each and collectively accounted for 16.3% of the questions. Some questions were cross-cutting (5.6%) and could not be categorised. Participants found sessions useful, with 98% (2013/2065) rating them as good, very good or excellent.

CONCLUSIONS: The community focused more on testing technicalities than supporting systems like quality management. Therefore, in an emergency, we need more support for implementing testing in the laboratory whilst raising more awareness that supporting systems are equally important.

5265002 | Improvement of Viral Load Coverage Amongst HIV Clients Accessing Anti Retro Viral Therapy (ART) at Taso Mbale During Covid 19 Pandemic Between October 2020 to September 2021

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BACKGROUND: The MOH Uganda and WHO recommends that all people living with HIV (PLHIV) who are receiving ART should have their viral load monitored so as to achieve the last 95% of the UNAIDS target for HIV epidemic control by 2030. By end of the quarter October to December 2020, TASO (The AIDS Support Organisation) Mbale had conducted viral load tests for only 64% of the clients eligible. Problem analysis revealed that factors contributing to suboptimal viral load coverage were; missed appointments by clients, representation of clients by their next of kin/care takers on dates earmarked for their viral load bleeding, inadequate viral load tracking for clients under multi month drug refill models, insufficient mobilization of clients for viral load bleeding especially at community drug refills, inadequate reporting and COVID-19 lockdown. A CQI project was started in January 2021 to scale up viral load coverage from 64% to 95% by the end of September 2021.

METHODS: Intervention included; clients education about viral load, line-listed all clients who missed viral load bleeding, file audits to confirm whether viral load monitoring was done, mapped the location for those clients, flagged files of clients who needed bleeding, home visits were conducted to bleed those clients who missed. The team is now at the planning phase of instituting a viral load outreach camp at different sub counties so as to increase service delivery to those who have been affected by COVID-19 lock down.

RESULTS: TASO Mbale recorded gradual improvement in viral load coverage from 64% (December 2020), to 78% (March 2021) and at 86% (June 2021).

CONCLUSIONS: Integration of Quality Improvement approaches to close identified gaps in monitoring clients for Viral Load coverage and Viral Load suppression within HIV clinics is crucial to achieving set targets for viral Load indicators among PLHIV.

5265325 | Leveraging Existing ICT Infrastructure in Supporting Data Management During the COVID-19 Pandemic in Kenya

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BACKGROUND: Effective functioning of public health information systems is dependent on a combination of infrastructure, human resources, tools and quality data, balancing a combination of rapid response while accounting for long term impact. When the first COVID-19 case was reported in Kenya in March 2020, the Association of Public Health Laboratories (APHL), in collaboration with the National Public Health Laboratory (NPHL), implemented a national COVID-19 laboratory data repository within weeks, enabling immediate centralization of COVID-19 test data while allowing for future submission of priority disease test data.

METHOD: APHL and NPHL used existing resources and data standardization best practices to standardize the Case Investigation Form and develop a Sample Manifest to highlight critical COVID-19 testing data elements. To ensure NPHL had adequate infrastructure for increased data flow, APHL and NPHL conducted an audit and noted 3 needs for the repository: 1) uninterrupted up-time, 2) handling multiple and increasing processing requests, and 3) system security given increased user traffic and external user access.

RESULTS: Standardization enabled expansion of COVID-19 testing capacity from 1 to 15 laboratories within 2 months and reporting of quality COVID-19 test data into the repository for further analyses. Upgrade of NPHL's ICT infrastructure ensured system availability, improved response and security allowing for processing of multiple requests without compromising repository performance. The repository receives and reports data from over 80 PCR and over 200 rapid antigen testing facilities and exchanges data with multiple external systems.

CONCLUSION: The decision to use existing ICT infrastructure was key in rapidly ensuring a working solution while assuring reliable system support. This multi-pronged approach put Kenya ahead of many countries in COVID-19 data collection and reporting from both public and private facilities. This infrastructure can continue to be used to support the needs of future public health emergencies or routine surveillance reporting.

5265929 | Maintaining Routine HIV and Tuberculosis Testing Services in the Context of COVID-19: Lessons Learnt and Opportunities for Improvement

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The African Society for Laboratory Medicine (ASLM) through the Laboratory Systems Strengthening Community of Practice (LabCoP), conducted an online survey in June 2020 among 14 member African countries to seek a deeper understanding of the disruptions that COVID-19 posed to HIV/TB laboratory services. The outcome of the survey was intended to provide solutions for maintaining HIV/TB laboratory services in the context of COVID-19.

METHODS: The scope of the survey included HIV/TB service delivery, stock out, equipment capacity and human resources among others areas. There were open response questions that only collected free text and these constitute the qualitative responses. The responses to the survey were shared by the LabCoP country team leads and represented the consensus agreement of the 5-15-member multidisciplinary (clinicians, laboratorians, civil society) country teams designated by the ministries of health. We used descriptive statistics and thematic analysis to interpret responses.

RESULTS: Responses were received from 10 of the 14 countries. Seven of 10 confirmed that the COVID-19 pandemic had resulted in disruption of HIV/TB testing services and that more testing equipment (8 countries) and personnel (4 countries) had been committed to COVID-19 testing at the expense of HIV/TB testing services. Other reasons cited were: stock-outs of testing kits, reagents and laboratory consumables (5 countries), shortage of healthcare workers (4 countries), and insufficient molecular testing capacity (2 countries). Eight of 10 countries reported re-purposing between 25% to 83% of the total HIV and tuberculosis testing equipment capacity in-country. All the 10 countries highlighted the need for guidance on incorporating COVID-19 into routine testing while maintaining HIV and TB services.

CONCLUSIONS: The difficulty in maintaining routine testing of HIV/TB is related to pre-existing laboratory systemic weaknesses. Better knowledge, management and optimisation of national tiered networks to become more resilient in the face of health emergencies is needed.

5266442 | Scaleup of Coronavirus-19 Testing in Uganda – The Uganda Virus Research Institute Experience

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BACKGROUND: Coronavirus-19 (COVID-2019) infections first appeared in China during December 2019 and rapidly spread globally, significantly affecting the livelihood of many people. In March 2020, the World Health Organization (WHO) declared COVID-19 as a pandemic and urged all its member states to prepare and expand their testing capacity as part of the pandemic preparedness. Thus, Uganda confirmed its first COVID-19 case on March 21, 2020. We report on the experience of Uganda Virus Research Institute (UVRI), Entebbe, while implementing the WHO's directive.

METHODS: As the wave of infections in other countries were getting closer to Uganda, UVRI was designated as the National Reference laboratory by the Ministry of Health, given its history as the National Influenza center for many years. The laboratory was immediately equipped with diagnostic reagents from international collaborating partners such as the Africa Centers for Disease Control and Prevention. Refresher training of all staff on molecular diagnostic techniques, including the biosafety requirements for COVID-19 testing, were immediately instituted. Later in June 2020, as the need for increased testing arose, the laboratory opened up and took on more roles of training and accrediting other public and private laboratories from the capital Kampala and the countryside.

RESULTS: As of 31st July 2021, UVRI has trained staff from more than 30 laboratories representing all the regions of Uganda. Consequently, from June 2020 to date, Uganda has been able to test 1,505,054 samples, of which 29.3% (n=440,661) have been tested at UVRI. The scaling up program has expanded and now includes method validations, a proficiency testing program, sample referrals and biobanking. Subsequently, the national turn-around time for COVID-19 result reporting has consistently remained at 24 hours.

CONCLUSION: The UVRI experience shows that COVID-19 testing can be quickly scaled up through training of more laboratories in both government and private sector.

5266527 | Rapid Scale Up of COVD-19 Testing in Kenya: The Positive Impact of SLMTA

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BACKGROUND: The 1st case of Coronavirus disease 2019 (COVID-19) in Kenya was confirmed in 13 March 2020 at National Public Health Laboratory. In March 2021, Kenya scaled up molecular testing for SARS-CoV-2 to more than 30 laboratories at Sub-regional, Regional and National levels. Majority testing sites are public facilities. All these laboratories have undergone the Quality Systems through Strengthening Laboratory Management Towards Accreditation (SLMTA). In this paper we describe the positive impact of SLMTA on the repurposing of laboratories in Kenya for emergency testing including SARS-CoV-2.

METHODS: The laboratories were provided with technical assistance to expand testing to include SARS-CoV-2. Technical assistance was derived from the SLMTA resource base and included: preparation, review of guidance documents and tools for laboratory network optimization, specimen collection and transport, data management, commodity management, quality assurance, Infection Prevention and control, biosafety training and communication management. In addition, the network of GeneXpert equipment distributed across the 47 regions in Kenya was provided similar technical assistance to commence SARS-CoV-2 testing. SLMTA-trained laboratory personnel were also used to train and implement antigen rapid tests (Ag RDT) to complement molecular testing. To enable real-time reporting for surveillance purposes, laboratory staff were mentored on sample management and use of laboratory information systems (LIS). By July 2021, Kenya had more than 40 laboratories testing SARS-COV-2 coordinated by the Ministry of Health and reporting through a National COVID-19 emergency response system.

LESSONS LEARNT: Running on SLMTA-built improved laboratory quality systems using the available resource and expertise base, Kenya was able to rapidly scale up molecular testing for SARS-CoV-2. By expanding scope to include SARS-CoV-2, Kenya was able to rapidly increase access to meet emergency testing needs. Training and mentorship on rapid tests have led to increase in use of these tests at affordable, accessible and easy alternative point of care test.

WORKFORCE DEVELOPMENT AND THE LABORATORY PROFESSION

5203747 | Laboratory System Strengthening – A Partnership Model for Laboratory Leadership and Management Training: Optimizing an In-Person Laboratory Leadership Training Program to a Virtual Format During the COVID-19 Pandemic

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BACKGROUND: Becton Dickinson's (BD) Labs for Life partnership with CDC/PEPFAR helps laboratories improve quality management systems and supports them on their journey to achieve accreditation. The COVID-19 pandemic limited in-person instruction, creating the need for alternate approaches for training. A partnership of BD, the William Davidson Institute (WDI), and Association of Public Health Laboratories (APHL) developed an effective virtual training program (VTP) for laboratory management – a key factor in sustainability of laboratory impacts. The course leveraged APHL's experience in leadership training and WDI's expertise in virtual learning pedagogy.

METHODS: APHL's Foundations of Laboratory Leadership and Management was revised for WDI's ExtendEd platform, a proven VTP, to deliver the updated curriculum. The course was 8 weeks with each week consisting of 1-3 self-paced video lessons, 1-2 assignments, and a live office-hour session led by local instructors. Delivering the course over a longer time horizon and incorporating synchronous and asynchronous elements were employed to minimize online fatigue. A pre- and post-knowledge test and self-reported behavior assessment evaluated the short-term impact.

RESULTS: Twenty managers from laboratories in East Africa participated. Critical insights gleaned from course implementation included making content visually appealing to learners, adapting implementation to quality of internet, pacing content to allow application of learnings, and creating a participant community. Key benefits include cost-efficiency and scalability. Once initial investment in curriculum development is made, future cohorts can be run at much lower costs than in-person workshops. Sixteen of 20 enrollees completed course requirements and participants increased their knowledge scores by an average of 20%. Self-reports noted improvements in the frequency of managerial tasks such as reviewing lab budgets, holding management meetings, and analyzing quality indicators.

CONCLUSIONS: Hybrid virtual trainings (including synchronous and asynchronous components) are an impactful and sustainable method for providing equitable access to knowledge and training beyond pandemic scenarios.

5226807 | Burkina Faso's Approach on the Assessment of Biological Risks in 16 Molecular Diagnostic Laboratories of COVID-19

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BACKGROUND: The advent of SARS-CoV-2 on March 09, 2020 in Burkina Faso raised the question of the risk of infection and spread of the virus in COVID-19 diagnostic laboratories. Thus, with the technical and financial support of ASLM, a biosecurity / biosafety risk assessment was carried out in 16 molecular diagnostic laboratories for COVID-19.

RESULTS: In total, the ASLM biosecurity / biosafety consultant trained a pool of 16 national biosecurity experts, which made it possible to instill these concepts in the 32 technicians from the 16 laboratories. Following the biological risk assessment in the 16 COVID-19 molecular diagnostic laboratories, several of the risks identified were significant. Indeed, a potential infectious risk was observed first during the sample from the patient, then during the analysis of the samples with the production of aerosol and the dissemination of waste contaminated by SARS-CoV-2 during their disposal. The majority of laboratories did not have sufficient personal protective equipment (PPE) and a lack of biosecurity / biosafety leader was noted. All of the laboratories were working under PSM, however, either there was no SOP for their use, or they were not certified or with an expired certification. of the 16 laboratories assessed, there was no waste management procedure. In order to mitigate the biological risks observed in the laboratories, a corrective action plan was developed in collaboration with the technical team of the Department of Medical Biology Laboratories (MoH).

CONCLUSIONS: Mitigating the likelihood of infection is a daily challenge in laboratories. In fact, reducing the risk of the virus spreading requires sensitization of laboratory personnel on biosecurity measures and the development of biosecurity / biosecurity strategies specific to each laboratory.

5228459 | Impact of Virtual Training for Data Collection and Reporting on Action Taken for HIV Viral Load Results Requiring Attention Using the ELABS Mobile Application in PEPFAR/CDC-Supported Primary Healthcare Facilities in South Africa

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BACKGROUND: To achieve UNAIDS third 95 goal of 95% of people on antiretroviral treatment with suppressed HIV viral loads (VLs), healthcare workers should ensure necessary action is taken on VL **RESULTS:** patients with invalid/rejected specimens return for a repeat blood draw and patients with unsuppressed VL results receive adherence counseling. In South Africa, mHealth device eLABS was implemented in >1,700 primary healthcare facilities to return VL results to the facilities. Training was conducted on data collection and reporting for an Excel dashboard developed to monitor CDC-supported facilities' performance on actioning eLABS VL results for action (RfA).

METHODS: Training consisted of two 1-hour Zoom sessions: (1) demonstrating the data collection tool for recording patients with RfA who were contacted and received necessary action, and (2) group discussions after implementing the tool. Participants included facility staff responsible for checking eLABS, contacting patients with RfA, providing adherence counseling, or performing blood draws. Data from the dashboard before and after training was compared to assess the training's impact on facilities' performance on timely actioning of eLABS RfA.

RESULTS: Between March and June 2021, 19 training sessions were held with 1,285 participants. Percent of patients with invalid/rejected specimens who were contacted and received a repeat blood draw within 2-4 weeks increased from 21% to 77% (KwaZulu-Natal) pre- and post- training. Percent of patients with unsuppressed VL results who were contacted and received adherence counseling increased from 16% to 22% (Gauteng); from 20% to 30% (North West); and from 36% to 51% (KwaZulu-Natal). A Zoom poll showed that 79% of participants used the data collection tool.

CONCLUSIONS: Skills-based virtual training on data collection and reporting on action taken for HIV VL results is an effective and efficient method for improving health facility performance on VL results management. Training and continuous monitoring is essential for further improvement.

5234071 | Key Factors to Improve Biosafety and Biosecurity Programs in 22 African Countries via the African Center for Integrated Laboratory Training Course

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BACKGROUND: The African Centre for Integrated Laboratory Training (ACILT) offered the "Strengthening Laboratory Biosafety and Biosecurity" (SLBB) course to improve laboratory biosafety programs in low-and-middle income countries. This review evaluated transference of newly gained knowledge and skills to participant's work environment.

METHODS: ACILT offered 14 SLBB courses between 2009-2014 in Johannesburg, SA with a total of 402 participants from 22 countries worldwide. In 2015, participants received an e-questionnaire to determine training effectiveness on biosafety practices at the participant's laboratory. Beside demographic data, the e-questionnaire retrospectively assessed biosafety practices six months before and after the SLBB with 22 questions divided into four categories: 1) Safety Policies, 2) Management's Engagement, 3) Safety Programs and 4) Assessments of Safety Practices. A Kirkpatrick model assessed transference of newly gained knowledge and skills to participant's laboratory and obstructive factors to implementation.

RESULTS: Approximately 20% (81/402) of the participants completed the e-questionnaire. For all safety practices questions, the overall percentage of positive responses increased from 50% to 84%. Participant's responses indicated that all four categories had improvements after the SLBB course, with the greatest increases in Safety Policies (67% to 94%) and Safety Programs (43% to 91%). Having a safety committee, resources, and a facility safety policy were important drivers for implementing and maintaining laboratory safety practices. In addition, accredited laboratories and countries with national safety regulations or policies had a higher percentage of improvements in safety practices in place. The most reported challenge was with funding, followed by lack of management compliance. Study limitations were low response rate (20%) and potential for recall bias.

CONCLUSION: ACILT's SLBB course positively impacted laboratory biosafety practices and identified important drivers, both at facility and nationally to shape the response to biosafety needs in future. To assist laboratory accreditation efforts countries continue to sponsor laboratory safety equipment maintenance programs.

5236667 | Improving Knowledge of Quality Management Systems: The First MOOC on "Quality Management on Medical Laboratories"

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BACKGROUND: To improve performance of medical laboratories, the ISO15189 standard was developed. By implementing a Quality Management System (QMS) based on those requirements, laboratories can ensure reliable results for patient care. To address a high demand of QMS training, the first Massive Open Online Course (MOOC) of Mérieux Foundation, in partnership with Afnor and Institut Pasteur, was launched in 2019 through the Quality Initiative project. Digital tools are expending, and with the current pandemic of COVID-19, there were a need to reinvent training methods especially in the context of developing countries.

METHODS: The training objectives are: i) Understand why quality management is imperative for a laboratory; ii) Gain insights into the mechanisms of the ISO 15189 standard; iii) Use methods and tools to set up a QMS. This 8-week course program is organized in 5 sections based on the process approach. It is available in French and English. Two paths are proposed: "Knowledge" which is free of charges, and "Skills" that allows participants to earn a certificate for a moderate financial participation.

RESULTS: More than 7,500 subscribers followed the 2 sessions overall. Almost 60% were from 25 African countries. As the outcome of the two sessions: 981 subscribers got the certificate of knowledge, and 134 validated the skills certificate, with respectively 52% and 60% of African learners. The MOOCs allowed the community to share and discuss. More than 900 messages were generated on the forum, and several YouTube Lives were casted and counted all together 3,739 views.

CONCLUSIONS: This format improves access to training contents for laboratory professionals in developing countries. It opens a new path for learning. MOOCs are a good opportunity for organization to offer a complete training program and enhance knowledge sharing on QMS, but also to work toward blended learning, which responds to today challenges.

5237202 | A Comprehensive Training Program Improves Laboratory Staff Knowledge on Clinical Antimicrobial Resistance (AMR) in Vietnam

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BACKGROUND: Building laboratory staff capacity to perform quality antimicrobial resistance (AMR) testing is essential for patient treatment. Findings of an assessment supported by the Fleming Fund (FF) Vietnam Country Grant in 2019 demonstrated that staff in only nine of 19 AMR clinical laboratories nationwide participated in routine in-service AMR-related testing training programs. The FF-funded FHI 360-led consortium implemented a comprehensive in-service training program to improve AMR testing quality in targeted clinical laboratories in Vietnam.

METHODS: The training program consisted of in-person and virtual modes of delivery, with 2-5 days of lectures and hands-on exercises focusing on AMR testing topics. Participants included laboratory managers and staff from target laboratories within Vietnam's AMR surveillance network (eight in the North, six in the Center, and five in the South). Trainers were microbiologists from the FF project consortium and from six national hospitals. To quantify training effectiveness, participants took pre- and post-tests that assessed knowledge improvement and a survey evaluating course satisfaction.

RESULTS: A total of 10 trainings with 239 participants were conducted from June 2020 through July 2021 on various AMR testing topics, including laboratory techniques (AMR diagnosis and sexually transmitted disease [STD] pathogen), sample management, equipment maintenance, and biosafety. All trainings were conducted in-person except for virtual biosafety trainings-of-trainers (ToT). Overall, average pre-test score for trainings was 66% and average post-test scores was 91%, indicating an average improvement of 25% ($p<0.001$). The biosafety ToT demonstrated the greatest knowledge increase (32%; $p<0.001$) while the STD diagnosis training showed the lowest increase (15%; $p<0.001$). Participants indicated high satisfaction with training's content (94-100%), duration (81-100%), methodology (95-100%), and overall (94-100%).

CONCLUSIONS: The training program improved participants' knowledge on clinical AMR and was satisfactory. The low average pre-test score (66%) underscores a need to implement effective ongoing in-service training programs on AMR.

SCIENCE AND TECHNOLOGY TO SUPPORT COST-EFFECTIVE AND INTEGRATED LABORATORY NETWORKS

5196353 | Diagnostic Network Optimization and Integration of TB and EID Testing on GeneXpert Can Substantially Increase Access to EID and Improve Same-Day Diagnosis: A Zambian Case Example

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BACKGROUND: Since March 2021, the WHO strongly recommends point-of-care (POC) early infant diagnosis (EID) for HIV-exposed infants and children <18months to increase same-day HIV diagnosis. Diagnostic network optimization (DNO) can model the impact of leveraging existing infrastructure to increase the proportion of POC EID. We used DNO to model the impact of integrating EID, priority HIV viral load, and TB testing on GeneXpert platforms to increase same-day EID.

METHODS: Using OptiDx software, we first established the baseline diagnostic network based on 2020 testing demand, referral linkages, testing sites, platforms, and costs for the HIV and TB programmes respectively in Zambia. Next, we integrated priority HIV testing, including EID, on GeneXpert platforms, historically only utilized by the TB programme. Using programmatic data from January-March 2021, we calculated facility-laboratory and intra-laboratory turnaround-time (TAT) for EID samples at baseline. We then calculated the annualized device cost, variable cost/test, and sample transport cost for each scenario.

RESULTS: 102,423 EID tests were conducted in 2020, 99% of which were on centralized platforms. Currently, 9% of EID samples are tested onsite with an average TAT of 27 days. With integration, the proportion tested onsite increases 3-fold to 45% and the distance travelled/sample decreases from 80km to 12km with an overall 2-week decrease in TAT. Further, 15% of EID tests are likely to be processed within the same-day from a baseline of zero. The cost per same-day result is $143.17. The total cost of the combined HIV and TB programmes following integration and optimization is reduced by 3%, with a cost saving of $622,167.

CONCLUSIONS: The WHO recommends POC EID testing to increase same-day diagnosis. A potential way of easily increasing the proportion of EID conducted onsite to allow for same-day diagnosis, while decreasing overall costs, is through the use of DNO and leveraging GeneXpert platforms for EID testing.

5236987 | Characterization of AsanteT HIV-1 Rapid Recency® Assay for Detecting Recent HIV-1 Infections

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BACKGROUND: Asante™ HIV-1 Rapid Recency® Assay can diagnose HIV infection (verification line) and detect recent HIV-1 infection (long-term line, LTL) in the same device. We sought to determine the mean duration of recent infection (MDRI) and false recent rate (FRR) using specimens previously collected from HIV-1 positive and treatment naïve individuals.

METHODS: A total of 784 longitudinal plasma specimens from 135 HIV-1 seroconverting individuals from Trinidad, Thailand, United States, and Netherlands (subtype B and AE) were used for MDRI determination, while 1,341 cross-sectional plasma specimens from individuals from United States, Thailand, and Ghana infected for >1 year (with or without AIDS) were tested for FRR. Reader or visual results were recorded. Duration of recent infection of each individual was determined using reader result of LTL by linearly interpolating cutoff value between visits. FRR was determined as proportion of long-term infection that were misclassified as recent infection using visual results.

RESULTS: The Asante demonstrated an overall increase in LTL intensity over time since seroconversion. The overall MDRI of Asante was 185 days (95% CI, 156-210) with different subtypes showing similar MDRIs with overlapping confidence intervals [subtype B=169 (137-201) and AE=199 (159-238)]. The proportion of individuals tested recent on Asante decreased over time after seroconversion: 50% by 5 months, 12% by 12 months, and 0% by 18 months. FRR among individuals infected >1 year, with and without AIDS was 5-8% and 2-3%, respectively.

CONCLUSIONS: Our study provides direct evidence of the Asante MDRI and FRR, which are important properties of assay for detection of recent HIV infection. Individuals testing recent on Asante assay are likely (~90%) to be infected within the last 12 months as proposed in the kit insert. Asante can be used at POC for recent infection surveillance to detect recent HIV-1 infections in real-time for targeted prevention and epidemic control.

PATHOGEN GENOMICS TO CONTROL DISEASES

5223119 | Evaluation of the Microbial Contamination of Suya and Spice Sold in Gboko Metropolis, Benue State, Nigeria

Monday Akor
Stetis Limited, Nigeria

Suya is a popular spicy roasted meat delicacy in Nigeria. Ready-to-eat Suya and Spice samples were collected from eight popular suya spots in four selected locations within Gboko Metropolis, Benue State, Nigeria. Microbial analyses of sixteen (16) samples of suya and spices revealed contamination with potential pathogens such as Staphylococcus aureus, Escherichia coli, Salmonella, Pseudomonas, Streptococcus, Klesiella, Bacillus species and Moulds (Aspergillus, Rhizopus, Fusarium, Alternaria and Mucor species) and Yeast (Candida species) from the processing, display for sale and holding at ambient temperature (280C). Results from the analyses revealed that the highest aerobic plate count for suya was 2.4 x 105 cfu/ml, while that of spice was 0.4 x 105cfu/ml. The highest fungal count in suya was 0.3 x 105 cfu/ml and that of spice was 1.0 x 105 cfu/ml. the result also revealed that suya samples recorded more bacterial load than fungi, whereas, spice samples recorded more fungal load than bacteria. Occurrence of such organisms (isolates) which are pathogenic to humans in the samples constitute a food safety issue which demands urgent education of suya producers on the health hazards, critical control points and the importance of personal hygiene and clean environment. Thus from the result obtained from this study, the products are unfit for human consumption.

5227894 | Molecular Epidemiology of Genital Chlamydia Trachomatis Infection Among Women of Reproductive Age Living with HIV/AIDS in Ilorin

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BACKGROUND: C*hlamydia trachomatis* is the most prevalent bacterial pathogen which causes sexually transmitted infection (STI) worldwide. With the emergence of HIV/AIDS, STIs have also re-emerged as a grave public health problem, especially in developing countries. This study aims at investigating the genovars of genital *C. trachomatis* infection among women of reproductive age living with HIV/AIDS in Ilorin.

METHODOLOGY:A total of 402 endocervical samples were collected from HIV infected women attending the anti-retroviral clinic in University of Ilorin Teaching Hospital. Demographic information as well as clinical data was also collected. Genomic DNA was extracted from the endocervical samples using DNA extraction minikit from Favorgen Biotech Corp. A conventional PCR technique targeting the cryptic plasmid was used to detect *C. trachomatis.* Multiplex PCR was used to identify the genovars of *C. trachomatis*.

RESULTS: Out of the 402 participants, the prevalence of *C. trachomatis* was 18% (72/402). The infection was most frequently detected in women in the age group 31-40 years 24 (33%), followed by age group 41-45 years 23 (32%), and 46-49 years 22 (30%). There is a significant association between the marital status of the HIV infected subjects with *C. trachomatis* infection (p=0.001) with higher prevalence of infection among married women (87.5%) compared to single (2.7%), widowed (5.6%), separated (2.8%) and divorced (1.4%) women. Genovars D-K was detected in 31 (43.0%) cases, L1-L3 in 17 (23.6%) while 24 (33.3%) could not be genotyped by the method used. Risk factors for acquisition of *C. trachomatis* infection included history of previous STI, 53 (73.6%), p= 0.000, non-use of barrier contraceptives 27(37.8%) p= 0.009 and previous treatment for STD, 45 (62.5) p= 0.000.

CONCLUSION: This study has increased our knowledge on the epidemiological distribution of *C.trachomatis* genovars. Genovars D-K, LGV were identified which is important for appropriate management including that of complications, contact tracing and prevention.

5237022 | Association Between Diarrhoea Severity and Circulating Rotavirus Genotypes in Enugu Nigeria

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BACKGROUND: Rotavirus is the most important aetiology of severe diarrhoea in children under 5 years in developing countries like Nigeria. We conducted a hospital-based surveillance to examine the possible relationship between the severity of diarrhoea and the various rotavirus G-types circulating in Enugu Nigeria.

METHODS: Three thousand four hundred and ninety-seven (3497) diarrhoea stool samples were collected from U5 children with diarrhoea admitted to the paediatric wards of University of Nigeria Teaching Hospital Ituku Ozalla, Enugu Nigeria between 2014 and 2019. Group A rotavirus antigen was determined using ProspecT® ELISA Antigen kit (Oxoid, UK). A subset of rotavirus positive samples was subjected to RT-PCR genotyping to determine the VP7 (G-type) and VP4 (P-type). Single G- genotypes were reported in 815 stool samples and were compared to determine severity using modified Vesikari scale (VS).

RESULTS: Genotype was performed on 985 samples. Among those with G12 rotavirus diarrhoea, very severe diarrhea (VSD) (VS ≥ 16) was seen in 3 (1.3%) children, severe diarrhea (SD) (VS 11-15) in 126 (52.7%) children, moderate diarrhoea in 102 (42.7%) children and mild diarrhoea in 8 (3.3%) children. Among the children with G1 diarrhoea, 1 (0.4%) child had VSD, 121 (54%) children had SD, moderate diarrhoea was seen in 95 (42.4%) children and mild diarrhoea reported from 7 (3.1%) children. G3, 3 (1.8%) children had VSD, 87 (53%) children had SD, moderate diarrhoea was seen among 67 (40.9%) children and mild diarrhoea was seen in 7 (4.3%) children. G4 genotypes caused more "VSD" (VS ≥ 16), we did not identify an association between these genotypes and overall diarrhoea disease severity (p=0.973).

CONCLUSION: Most children showed moderate to severe acute gastroenteritis. The result did not indicate any association between genotypes and diarrhoea severity. Rotavirus vaccines would be effective against all rotavirus genotypes if introduced into Nigeria's EPI schedule.

5237168 | Pathogen Discovery Attempts Using Next Generation Sequencing Detects a Sphingobacteria Infection in a Fatal VHF Suspect Case, Uganda, 2021

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BACKGROUND: Traditional diagnostic methods such as culture, serology, or polymerase chain reaction have limited utility in investigations where there is no prior knowledge on the identity of potential infectious agents. The Ugandan VHF lab developed a pathogen discovery algorithm whereby PCR-negative Viral Hemorrhagic Fever (VHF) suspected samples are subjected to Next Generation Sequencing (NGS) which in contrast is capable of comprehensively identifying all potential pathogens in clinical samples. On 8th February 2021, the VHF lab received such a sample from Bundibugyo hospital and we report on our attempts to determine the etiology.

METHODS: Submitted whole blood and swab specimens were inactivated and RNA extracted with the 5X Magmax™ 96 Viral Isolation kit. The RNA was treated with RNase-free DNase and prepared for unbiased NGS using the NEBNext Ultra II Directional RNA library preparation kit. The libraries were sequenced using an Illumina iSeq100. We used Geneious to analyze the sequence data.

RESULTS: Blasting contigs to the NCBI database identified the majority of reads as belonging to Sphingobacterium or closely related species. The reads were mapped to a Sphingobacterium reference genome . A complete coverage of the 16S gene and a 16S rRNA blast identified the bacterium as *Sphingobacterium caeni*. Plylogenetically, *S. caeni* is on the same clade as S. *multivorum*, which has previously caused human infections.

CONCLUSION: We were able to give a provisional diagnosis for this particular case although the mere discovery of the candidate pathogen is only the first step in determining whether or not it is associated with disease. A follow-up study to establish causality is needed to establish a link between the candidate infectious agent and disease. The current availability of NGS provides an unprecedented opportunity to 'cast a wide net' and survey the full breadth of as-yet undiscovered pathogens in nature that pose significant threats to human health.

5237916 | Pattern of Nasal Carriage and Urinary Tract Infection Due to Staphylococcus Aureus and Genetic Lineages Among People Living with HIV/AIDS in Nigeria, 10-Year Systematic Review of Cross-Sectional Studies

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BACKGROUND: The nasal microbiota, S*taphylococcus aureus (S. aureus)* could pose significant risk of life-threatening infections when translocated from its predilection sites in people living with HIV/AIDS (PLWHA). This study determined the pooled prevalence and antimicrobial resistance pattern of nasal and urinary *S. aureus*, MRSA, *spa* types and PVL producing isolates from PLWHA in Nigeria from January 2012 to January 2021 by systematic review and meta-analysis.

METHODS: A comprehensive *bibliometric* search was conducted on 'PubMed', Scopus', and 'Google Scholar' for published articles using the key words 'nasal *S. aureus* carriage', 'Urinary *S. aureus*', 'nasal MRSA', 'staphylococci-HIV coinfection', 'urinary MRSA' and 'all states of Nigeria'. Eligible studies and number of subjects (n) were analysed according to the PRISMA criteria.

RESULTS: of the 49 examined studies, only 6 (n=1181) and 6 (n= 872) on nasal and urine samples, respectively, were eligible. The pooled nasal carriage of *S. aureus* and MRSA were 29.1% (range: 21.0-37.8%, p=0.065; I2 =85.8) and 8.9% (range: 4.3-16.1%, p=0.781; I2 =75.5,), respectively with no significant heterogeneity. However, the pooled urinary *S. aureus* and MRSA infection were 7.5% (range: 6.0-42.5%, p=0.033; I2 =12.9) and 13.4% (range: 0.6- 40.0%, p<0.0001; I2 =22.7) with significant heterogeneity. The pooled prevalence of *LukSF-PV*-positive *S. aureus* from nasal samples was 35.5% (range: 2.8- 62.3%). Molecular typing from 3 studies showed t064 and t084 as the predominant *spa* types. The *S. aureus* isolates from both sample types from 7 studies had highest (>75%) resistance to amoxicillin-clavulanate, sulfamethoxazole-trimethoprim, erythromycin, and tetracycline. Multi-drug resistance was not significantly higher among *S. aureus* isolates from urine than nasal samples (60% versus 33.3% of eligible studies) (*p*= 0.472).

CONCLUSION: Moderate and high pooled prevalence of MRSA and *LukSF-PV*-positive *S. aureus* was obtained from PLWHA, respectively. The reported t084 and t064 are quintessential *spa* types in Africa and often associated with community-acquired (CA)-MRSA.

5238904 | Magnitude of Phenotypic and MTBDRplus Line Probe Assay First-Line Anti-Tuberculosis Drug Resistance Among Tuberculosis Patients; Northwest Ethiopia

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BACKGROUND: Mycobacterium tuberculosis (Mtb) drug resistance is a key challenge in ending TB.

OBJECTIVE: The study aimed to determine anti-TB drug resistance and compare the discordance between phenotypic and genotypic drug-susceptibility testing (DST).

METHODS: Prospective enrollment and sputum collection from patients suspected of active pulmonary TB from May 2018 to December 2019 at the University of Gondar Hospital. Phenotypic DST study for streptomycin, isoniazid, rifampin, and ethambutol was done by MGIT 360 SIRE Kit. Genotypic resistance for isoniazid and rifampin was performed by MTBDRplus v2 line probe assay (LPA) and compared to phenotypic drug resistance.

RESULTS: A total of 376 patients, median age 32 years, and 53.7% male were enrolled. Mtb was isolated from 126 patients. 106/126 (84%) patients were newly diagnosed with TB and 20 patients with prior TB treatment. Seventy (66.0%) were susceptible to all anti-TB drugs tested. Twenty-five (19.8%) of the isolates were resistant to isoniazid, 12 (9.5%) to rifampicin and six (5%) were multidrug resistant. Among previously treated TB patients, 4 (20.0%) and 5 (25.0%) were mono-resistant and poly-resistant, respectively. The sensitivity and specificity of LPA resistance for isoniazid were 94.4% and 100%, and for rifampin was 75.0% and 100%, respectively.

CONCLUSION: The frequency of mono- and poly-drug resistance among both newly diagnosed and previously treated TB patients was high to the rest of the nation.

5265475 | Comparison of HPV Prevalence in South African Adolescents Randomized to Receive Injectable, Oral, or Vaginal Hormonal Contraceptives

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BACKGROUND: Human papillomavirus (HPV) is one of the most prevalent sexually transmitted infections (STI) in South Africa, particularly in adolescents. Factors contributing to this increased HPV risk in adolescents are not yet fully understood. While some observational studies have suggested that hormonal contraceptives (HC) influence HPV risk, others found no effect. In a randomized cross-over study, the impact of commonly used HCs (including the injectable norethisterone enanthate [NET-EN]), combined oral contraceptive pills [COCP]) were compared with the combined contraceptive vaginal ring [CCVR]; NuvaRing) with respect to HPV prevalence in adolescents from Cape Town, South Africa.

METHODS: Eighty-nine healthy HIV-uninfected adolescent females (15-19 years), naïve to Cervarix HPV vaccine (part of national roll-out), were randomized (1:1:1) to receive NET-EN, CCVR NuvaRing, or COCP for 16 weeks. HPV genotyping was performed from cervical swabs using the HPV Direct Flow CHIP assay.

RESULTS: HPV prevalence was high, with 91% of young women (81/89) having at least one HPV type detected. Overall HPV prevalence did not differ significantly by HC arm: 96.7% (29/30) using CCVR were HPV+, 96.4% (27/28) of those using COCP, and 80.6% (25/31) of those randomized to NET-EN were HPV+. Furthermore, the majority of adolescents were infected with high-risk (HR) HPV types, with HPV-51 and HPV-52 being the most common (each 17.3%). Adolescents on CCVR had significantly higher numbers of HR-HPV types than those randomized to using either COCP (n=67; n = 46, respectively; p=0.04) or NET-EN (n = 42; p=0.03).

CONCLUSION: The overall and HR-HPV prevalence was high in this cohort, with non-vaccine types HPV-51 and -52 being the most common. While HC arm did not appear to impact overall HPV prevalence, the prevalence of HR-HPV types was significantly higher in young women randomized to the CCVR arm compared to either COCPs or Net-EN.

OWNERSHIP, PARTNERSHIP AND INNOVATION

RESEARCH FOR BETTER LABORATORY SYSTEMS AND NETWORKS

5182432 | Usability of Xpert HIV-1 Qualitative Assay Using Dried Blood Spots for Early Infant Diagnosis In Field Settings In Kenya

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BACKGROUND: The Xpert HIV-1 Qualitative assay has been in use in Kenya since 2016 for infant HIV diagnosis. The assay has recently been improved by reducing the total number of steps to results from ten to seven when using DBS. The purpose of our study was to determine usability of the Xpert HIV-1 Qualitative assay using DBS for Early Infant Diagnosis following this improvement.

METHODS: This was a usability study undertaken in two health facilities in Kenya from November 2020 to February 2021. Lab technicians already familiar with the assay were retrained for this study. Research materials were provided. HIV exposed infants were recruited with the consent of their parents. Patient data was recorded; DBS samples were collected and tested for HIV on the improved assay. Usability questionnaire were filled in by each lab technician performing the assay. Data on test errors were collected from machine logs. Data collected were analysed using STATA for windows.

RESULTS: A total of 327 test cartridges were provided for this study and 273(83%) were successfully tested on Xpert HIV-1 Qualitative assay. All the four (100%) trained technicians said the assay had a simple work flow, was easy to use, reported the results as easy to interpret and found the assay throughput sufficient for their work load. Fifty-four (54) errors (error rate of 17 %) were experienced in the study. Eleven (11, 20%) errors were user related while 43 (80%) were hardware related. Ten of the eleven (91%) user errors occurred in the first month of the study.

CONCLUSIONS AND RECOMMENDATIONS: The improved Xpert HIV-1 Qualitative assay has a simple workflow, is easy to use and the tests results easy to interpret. Hardware errors can be reduced by improving the platform design. User errors can be managed through training and decrease with experience.

5228521 | Development of a Comprehensive HIV-DR Genotyping Assay with Integrase Coverage

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BACKGROUND: The life-long medication of anti-retroviral drugs that target the replication cycle of HIV-1 requires regular monitoring of viral load in people living with HIV (PLWH). Escape from viral suppression is triggered by the emergence of mutations in the viral genome causing drug resistance requiring genotyping of the mutated virus population by DNA sequencing. Over the past 30 years, an impressive repertoire of HIV drugs has become available targeting mostly the PRRT gene. The most recent class is integrase strand transfer inhibitors (INSTI, e.g., dolutegravir).

METHODS: We have previously developed and commercialized a research genotyping assay that targets drug resistance mutations in the PRRT gene of HIV-1 subtypes A, B, C, D, AE, AG, CRF01_AE, CRF 02_AG.

RESULTS: Here we present an extension of this PRRT genotyping assay to include also the integrase (INT) gene. This development aimed to provide a comprehensive genotyping solution in a standardized workflow for both target genes. The primer mix for RT PCR was extended with primers for the integrase gene. Both targets can be initially amplified with a minimal amount of input RNA. In a second (nested) PCR step, the PRRT gene and the INT gene are amplified separately. The PRRT amplicon is bi-directionally sequenced with six preformulated sequencing reactions and the integrase gene with four sequencing reactions. The total of ten sequencing reactions are separated by capillary electrophoresis (CE) on an automated Applied Biosystems Genetic Analyzer. The resulting DNA sequences are assembled using ExaType Sanger software (Hyrax Bioscience) and aligned with a reference sequence to determine any mutations and the potential effect on ART drug resistance.

CONCLUSION: A comprehensive and affordable HIV-DR genotyping assay with integrase coverage was developed for resource limited settings.

For Research Use Only. Not for use in diagnostic procedures.

5236553 | Progress Report of an Ongoing Intervention to Improve Long Turn-Around Time for HIV Viral Load and Early Infant Diagnosis in Nigeria

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BACKGROUND: This study aims to identify barriers and design interventions to improve the efficiency of the HIV VL and Early Infant Diagnosis (EID) diagnostic cascade in Nigeria, through Continuous Quality Improvement (CQI) activities. The specific goals are for every VL and EID specimen to have an end-to-end turn-around-time (TAT) ≤ 10 days, and at least 95% results entered into patients' charts/electronic medical records within 48 hours of receipt, in addition to meeting other quality indicator targets.

METHODS: Baseline data was collected for EID and VL specimens between Jan 2020-Jan 2021 from 30 purposively selected PEPFAR supported facilities/clinics served by 3 PCR laboratories. Data were collected on 11 timestamps, specimen rejection status and temperature of transported samples upon arrival at the laboratory. of the 15,226 VL and 511 EID specimens only 4870 VL and 306 EID had complete data for every objective. To maximize the number of specimens analyzed, we included specimens with clean and complete data for the objective being assessed, as indicated in the denominators below.

RESULTS: of the specimens with complete data 47% (2939/6191) VL and 39% (141/361) EID specimens met target TAT of 10 days; 0% (0/5525) VL and 100% (354/354) EID specimens were received at the recommended temperature range; 53% (7061/13418) of VL results and 92% (432/471) of EID results had a timestamp recorded for results entered into patient's chart and 0% of VL (0/1347) and EID (0/471) specimens were rejected in the laboratories. of note, 89% (4901/5525) of VL specimens arrived at the lab within the manufacturer's temperature specifications.

CONCLUSIONS: This baseline analysis indicates gaps in VL and EID testing TAT, transport temperature for VL plasma specimens and documentation of VL results in the patients' charts. The next stage of the project will identify root causes, develop interventions to address gaps and monitor for compliance.

5250766 | Total Clinical Chemistry Laboratory Errors and Evaluation of the Analytical Quality Control Using Sigma Metric for Routine Clinical Chemistry Tests

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BACKGROUND: Currently, the use of clinical laboratory tests is growing at a promising rate and about 80% of the clinical decisions made are based on the laboratory test results. Therefore, it is a major task to achieve quality service. This study was conducted to assess the magnitude of errors in the total testing process of Clinical Chemistry Laboratory and to evaluate analytical quality control using sigma metrics.

METHODS: A cross-sectional study was conducted at Dessie Comprehensive Specialized Hospital Clinical Chemistry Laboratory, Northeast Ethiopia, from 10 February 2020 to 10 June 2020. All Clinical Chemistry Laboratory test requests with their respective samples, external quality control and all daily internal quality control data during the study period were included in the study. Data were collected using a prepared checklist and analyzed using SPSS version 21.

RESULTS: A total of 4719 blood samples with their test requests were included in the study. Out of 145,383 quality indicators, an error rate of 22,301 (15.3%) was identified in the total testing process. of the total errors, 76.3% were pre-analytical, 2.1% were analytical and 21.6% were post-analytical errors ($p<0.0001$). of the total 14 analytes in the sigma metric evaluation, except ALP, all routine clinical chemistry tests were below the standard (<3). In multivariate logistic regression, the location of patients in the inpatient department was significantly associated with the specimen rejection ((AOR=1.837, 95% CI (1.288–2.618), $p=0.001$).

CONCLUSION: The study found a higher frequency of errors in the total testing process in the Clinical Chemistry Laboratory and almost all test parameters had an unsatisfactory sigma metric value.

5265354 | Outils de Communication des Résultats de Biologie Médicale Utilisés dans les Services de Biologie Médicale: Cas du Centre des Urgences de Yaoundé

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CONTEXTE : Environ 70% des décisions médicales dépendent des résultats des examens cliniques. Analyser les outils de communication utilisés au laboratoire permettrait d'apprécier la pertinence et les améliorer. Le but de cette étude est de présenter les différents outils utilisés dans la communication des résultats aux clients du laboratoire du Centre des Urgences de Yaoundé (CURY), d'apprécier le format des résultats le plus utilisé et d'évaluer la compréhension des résultats.

MÉTHODE : Une étude transversale descriptive a été menée au CURY de Février à Juillet 2020. Une enquête réalisée auprès de tous les soignants, aussi les soignés rendus consécutivement au laboratoire pour le retrait des résultats. Les données étaient collectées par des outils testés : questionnaires élaborés à partir des informations issues de la revue de la littérature et grilles de lecture élaborées à partir de la check-list de l'OMS. Les considérations éthiques étaient respectées. Les données ont été collectées avec le logiciel Cs Pro 7.3 et analysées avec SPSS version 21. Le X2, OR avec intervalle de confiance étaient utilisés avec seuil de significativité inférieur à 0,05.

RÉSULTATS : 235 soignants, 100 soignés et 932 CR ont été recrutés. Tous les résultats étaient transmis aux clients sous forme analogique. On retrouvait d'autres outils (4.7%) chez les soignants. Les CR analysés étaient conformes (77.78%) à la norme ISO 15189. La signification des résultats d'analyses était comprise en totalité par 43.4%, 50,6% en partie et pas du tout par 6% des soignants. La compréhension des résultats était liée au grade et la spécialité ($P<0.05$).

CONCLUSION : L'outil le plus utilisé pour la communication des résultats aux clients du laboratoire du CURY était conforme à la norme ISO 15189. La compréhension des résultats était liée au grade et la spécialité. Il serait indiqué de déterminer la place des autres outils dans notre contexte.

PARTNERSHIP, POLICY AND REGULATION TO IMPROVE ACCESS AND EQUITY OF DIAGNOSTIC TOOLS

5223952 | Prevalence and Predictors of Renal Dysfunction Among People Living with HIV on Antiretroviral Therapy in the Southern Highland of Tanzania: A Hospital-Based Cross-Sectional Study

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BACKGROUND: Infection with Human Immunodeficiency Virus (HIV) and antiretroviral therapy (ART) poses a significant risk of developing renal dysfunction in people living with HIV (PLHIV). Renal dysfunction contributes to the morbidity and mortality of PLHIV. There is limited information on renal dysfunction among PLHIV in the Southern Highland, the highest HIV prevalent area in Tanzania.We conducted a study to estimate the magnitude and predictors of renal dysfunction among PLHIV on ART.

MATERIALS AND METHODS: A cross-sectional study was conducted at Njombe Town Council Hospital from December 2019 to April 2020, recruiting 396 participants. Serum was obtained to measure creatinine level then calculated Glomerular filtration rate (GFR) using CKD-EPI and the Bedside Schwartz equations. The participants' informations were collected using a structured questionnaire. Data analysis was performed using STATA version 15; a modified Poisson regression model was used to estimate prevalence ratios (PR). The level of significance was specified at 0.05

RESULTS: The overall prevalence of renal dysfunction defined as GFR less than 90 mL/min/1.73 m2 was 20.7%, which increased by 4% as the age increased. The prevalence of renal dysfunction was higher in PLHIV on ART for more than six months to 24 months compared to their counterparts. Likewise, obese individuals had a 2.5 times higher prevalence of renal dysfunction than normal individuals

CONCLUSION: There is a relatively high prevalence of renal dysfunction among PLHIV on ART, predicted by age, duration on ART, and nutrition status. The findings suggest a need for routine screening and monitoring renal function status at CTC service delivery for early detection of kidney impairment for proper treatment.

5225123 | Championing Biosafety, Biosecurity and Bio-Risk Management Using Cost Effective and Sustainable Models Following Multi-Sectoral and Multidisciplinary Approach in South Sudan

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Biosafety and Biosecurity Association of South Sudan (or BBASS) calls for government, civil societies, academic and other institutions to pay more attention to the cultivation of biosafety and bio-security management especially after the occurrence of emergent public health events. The GHSA is aiming at mitigating risks that could arise from emerging and re-emerging infectious agents. This can be achieved by equipping health care workers in bio-risk management. Increasing visibility and needs to poster for safety of professionals and their roles in biosafety and biosecurity, an opportunity to highlight multisectoral, multidisciplinary approach to create awareness at workplace, especially the occupational health and at community level about the nature of biosafety and biosecurity good practices in the Republic of South Sudan. BBASS in collaboration with government line-ministries, international and national organizations, and the implementing partners for health has started a roadmap to develop South Sudan sustainable models that build and/or support and strengthen national capacity to prevent, detect and respond to public health emergencies of International Concern in areas of biosafety and biosecurity. BBASS, with the help of IFBA, Africa CDC, IHR 2005, BWC & USCR 1540 & GHSA will take following actions: (i) Develop biosafety and biosecurity legal framework for South Sudan, (ii) Establish national secretariats to coordinate & monitor the implementation of biosafety and biosecurity activities, (iii) Establish a regulatory and certification framework for institutions handling high risk pathogens, (iv) Strengthen National Public Health Institutions/Laboratories and capacities, (v) Develop a strategic roadmap to strengthen good practice in relation to biosafety and biosecurity for South Sudan with timeframes, implementing matrix and monitoring.

5227906 | Developing a New Accurate HIV Testing Algorithm in Chad: Results from a Verification Study of New HIV Testing Algorithm in Chad

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BACKGROUND: Current WHO guidelines encourage countries to use a standard serology-based HIV testing strategy that requires three consecutive reactive results to provide a positive diagnosis. These guidelines advise countries to conduct rapid verification studies that will prevent cross-reactivity between assays and allow for selection flexibility to mitigate shortages. We report on a rapid verification study conducted in Chad from June 1 to June 25 2021.

METHODS: This prospective cross-sectional study was conducted using venous whole-blood specimens from 171 consenting individuals at two HIV testing sites in N'Djamena, Chad.

All specimens were collected by trained staff and characterized using two assays (GenScreen Ultra HIV Ag-Ab and First Response HIV 1-2-0 Card Test). 100 HIV-negative specimens were then randomly selected and tested in duplicate on two lots of six candidate assays pre-selected by the Ministry of Health: Determine HIV-1/2, Genie Fast HIV 1/2, Bioline HIV 1/2 3.0, Insti HIV-1/HIV-2 Antibody Test, HIV 1/2 STAT PAK, and Uni-Gold HIV.

RESULTS: No cross-reactivity or inter-reader variability was detected for any candidate assays. Only one assay, Determine HIV-1/2, showed false-reactive results on both lots (4/400; 1%).

National authorities used this information, as well as each assays performance characteristics (sensitivity, specificity, subtype detection), operational characteristics (storage conditions and shelf life upon manufacture), costs, and user feedback, to refine the assay selection and order within the algorithm.

Authorities have proposed for Assay 1 (Determine HIV-1/2 plus Genie Fast HIV 1/2 as second option) and), for Assay 2 and 3 (Bioline HIV 1/2 3.0, HIV 1/2 STAT PAK plus Uni-Gold HIV as additional option).

CONCLUSIONS: Rapid verification studies are feasible and can help identify multiple assays which can be used to provide high quality and flexibility of testing algorithms. Resource-limited settings should consider adapting similar protocols to optimize testing services and to minimize negative effects of possible stock-outs.

5237060 | Integrated Approaches to Support the Roll Out of SARS-CoV-2 Rapid Antigen Testing in DRC: The IASAT Project

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BACKGROUND: The Democratic Republic of Congo (DRC) established a multi-sectoral response to address COVID-19. A national strategic plan of response emphasized scaling-up testing capacity for COVID-19. With the Ministry of Health (MOH), African Society for Laboratory Medicine and Africa Centres for Disease Control and Prevention, the Elizabeth Glaser Pediatric AIDS Foundation (EGPAF) supported the implementation of an integrated approach to facilitate the roll-out of SARS-CoV-2 rapid antigen testing (the IASAT Project) across the health system in DRC.

METHODS: From March15-April30 2021, EGPAF, alongside the MOH and partners (the Health Laboratories Directorate, National Institute for Biomedical Research, Epidemiological Surveillance Directorate, U.S. Centers for Disease Control and Prevention, President's Emergency Plan for AIDS Relief, World Health Organization, Global Health Systems Solutions, Clinton Health Access Initiative, and three coronavirus treatment centers), supported adoption of locally-contextualized, normative guidance; scale-up of training of trainers; and step-down trainings for health providers on rapid antigen testing in 12 health zones across Kinshasa and Tshuapa provinces.

RESULTS: Standardized training materials covering use, quality implementation, monitoring, and management of rapid antigen tests for SARS-CoV-2 diagnosis were developed. National-level training certified 21 national trainers, who conducted two provincial trainings, certifying 27 trainers to provide COVID-19 diagnostic services. Zonally, provincial trainers certified 79 providers, including doctors, biologists, laboratory technicians, and nurses who implement COVID-19 diagnostic services at their respective facilities. COVID-19 testing supplies and services were made more readily available across health zones.

CONCLUSIONS: The IASAT Project supported the DRC MOH to produce adapted, normative documents on rapid antigen testing for SARS-CoV-2. IASAT benefitted from active engagement and partnership between stakeholders in leveraging expertise, scope, and authority. The project increased capacity for COVID-19 testing among healthcare workers at facilities and supported a systems-level approach in creating a national, provincial, and local set of trainers who continue to support the COVID-19 response.

HARNESSING THE POWER OF COMMUNITY

5266374 | Global Fund and APHL Partnership to Develop a Repository of Global Laboratory Tools

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BACKGROUND: The Global Goods project was initiated by the Global Fund to enable country leaders to select appropriate laboratory tools/systems/solutions based upon their needs rather than silo programmatic focus or implementing partner driven. Global goods are tools adaptable to different countries and contexts to help address key laboratory system challenges and support varied aspects of laboratories including laboratory information management systems, sample transport networks, biosafety, biosecurity, laboratory network assessment and mapping, and External Quality Assurance (EQA) systems.

METHODS: APHL will gather information on current and planned tools and systems in use in public sector laboratories; develop a standardized questionnaire; utilize existing relationships with government partners, international development partners, and country governments to identify providers/implementers of laboratory tools and utilize these to conduct targeted interviews; develop a stakeholder registry with a worldwide listing of groups/individuals that can contribute towards the establishment of a laboratory global tools repository. Parameters to collect and analyze the information will be agreed upon and may include: 1) Implementing partner, 2) Functionality supported, 3) development timeframe, 4) Coverage, 5) Strengths, 6) Challenges, 7) Transition to country government, 8) support options, 9) interoperability, 10) Government role, 11) best practices, 12) Costs/sustainability. APHL will develop an online catalog of tools identified for users to access.

RESULTS: The following are expected results

- Development of a web based repository or catalog of global laboratory tools
- Maturity framework based on parameters and score provided to each laboratory tool
- Establishment of a Community of Practice to champion the use of repository within country and promote global use
- Guidance on integrated laboratory information systems

CONCLUSION: Global Fund and APHL expect the repository of laboratory tools to be in place by April 2022 and the Community of Practice to be functioning by July 2022. For more information please email Patrick.Royle@theglobalfund.org and Reshma.Kakkar@aphl.org

THE ONE HEALTH APPROACH TO SHAPE NEW LABORATORY SYSTEMS

5237679 | Appui de IDDS Pour la Révision, la Validation et la Mise en Ouvre des Documents de Biosécurité et Biosûreté au Mali

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CONTEXTE : Le Mali a entamé depuis 2015 un processus de renforcement de capacités de ses institutions en sécurité et sûreté biologique afin de répondre aux obligations du Règlement Sanitaire Internationale (RSI 2005). C'est ainsi qu'un guide national de biosécurité pour les établissements de santé a été élaboré en 2019.

Le Projet pour la détection et la surveillance des maladies infectieuses est un projet quinquennal visant l'amélioration de la détection des maladies prioritaires pour la santé publique, la détection de la résistance aux anti-microbiens, la gestion de la qualité, la biosécurité et la biosûreté dans les laboratoires.

MÉTHODES : Un consultant a été recruté et chargé de

- o Réviser les documents de «Politique Institutionnelle» et «manuel de procédures d'intervention d'urgence en biosécurité et biosûreté»
- o Développer un formulaire d'évaluation des laboratoires en matière de biosécurité/biosûreté ;
- o Evaluer avec les documents révisés les laboratoires de l'INSP à Bamako et de l'établissement public hospitalier Nianankoro Fomba de Ségou
- o Fournir les plans d'améliorations des deux laboratoires
- o Accompagner les laboratoires dans les premières étapes de l'application des plans d'amélioration.

RÉSULTATS : Les documents de politique et du manuel de procédure d'intervention d'urgence en biosécurité et biosécurité au laboratoire révisés ont été validés lors d'un atelier national selon l'approche « une seule santé ». Ensuite une évaluation en termes de biosécurité et biosûreté a été conduite dans deux laboratoires (Ségou et INSP). A partir des résultats de l'évaluation, un plan d'amélioration a été élaboré puis un soutien a été fourni pour la mise en œuvre des plans d'amélioration dans les deux laboratoires.

CONCLUSION : Cette évaluation a permis de dégager les insuffisances des deux laboratoires. L'amélioration de ces insuffisances permettra de répondre aux obligations du RSI et augmenter le score du Mali à l'évaluation Conjointe externe.

5266126 | Developing National Guideline for Specimen Management and Referral System in Liberia: Application of One Health Approach for Strengthening Laboratory Systems

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BACKGROUND: The Global Laboratory Leadership Programme (GLLP) identifies quality management systems as one of the core competencies in the Leadership Competency Framework. A GLLP workshop was conducted in Liberia between December 7-11, 2020, for human, animal, and environmental sector stakeholders to develop an integrated One Health guidelines for a national specimen management and referral network.

METHODS: A One Health participatory approach was adopted. In addition to GLLP multisectoral laboratory technical group members, other human, animal, and environmental laboratory professionals, disease program managers, epidemiologists, courier services personnel, policymakers, and implementing partners were invited. Representatives were divided into three groups to conduct a landscape analysis of the existing mechanisms in their respective sectors, highlighting the gaps and challenges. This was followed by collective brainstorming sessions to address the existing challenges and identifying opportunities for potential collaborations across sectors.

RESULTS: The workshop fostered concerted efforts and constructive exchanges across different sectors resulting in an integrated national guideline that streamlined existing mechanisms and strengthened the national laboratory quality management system. These guidelines provide guidance for the proper collection and handling of human, animal, and environmental samples and defined the roles and responsibilities of all entities involved in the national One Health specimen referral networks.

CONCLUSIONS: The National guideline for One Health specimen management and referral system serves as a guiding document for the delivery of quality and coordinated laboratory services with an efficient sample transportation system in the country across all sectors. The One Health approach embodied in GLLP brought together the key players from human, animal and environmental sectors facilitating coordination and ensuring national ownership and commitment.

OTHER

5239033 | OTOI-NARIMA Model for Forecast Seasonality of COVID-19 Waves: Case of Kenya

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BACKGROUND: Kenya has experienced three COVID-19 waves which caught authorities mandated to do surveillance and estimate the burden of disease by surprise. Mathematical modelling of the spread of disease informs surveillance, planning, budgeting, and response to save lives and livelihoods. Accurate forecasts of likely magnitude, start and end dates and duration are critical.

METHOD: Daily infections data between March 13, 2020, and April 3, 2021, is used. The data is tested for stationarity and cointegration using ADF test and Johansen Cointegration test respectively. A moving average of the daily cases and normalized series are superimposed and estimated. Then the combined series are used to construct Otoi-NARIMA model. The resulting model's residual is tested for auto-correlation using ACF and PAFC tests. Also, validity of the model is tested using Ljung-Box test. The model is used to forecast daily cases from April 4, 2021 to May 18, 2021. Likely dates for end of third wave and potential beginning of fourth wave are picked from visualization and output of Otoi-NARIMA model. The results are compared with results of standard ARIMA model.

RESULTS: The series are **I(1)** stationary and have cointegration rank. Implication is that the series and superimposed normalized version would not drift apart overtime. ACF and PACF revealed that both models show no autocorrelation. The Ljung-Box test showed that Otoi-NARIMA is superior, distinctly shows the seasonality of waves, and gives better restricted forecasts. There is likelihood of Kenya's third wave declining briefly between April 29 and May 9, 2021 and peaking on June 26, 2021. Lastly, based on assumption that Kenya will not have fully vaccinated 51 in 100 people the fourth wave is likely to take place after July 10, 2021.

CONCLUSION: Recommended for most accurate forecasts. The Model has been used to fight Delta infections in LREB -Kenya successfully.

5239213 | Phenotypic Determination of Phage Susceptibility Among Multidrug-Resistant Bacteria Isolated from Clinical Samples of Patients of Tertiary Care Center, Nepal

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BACKGROUND: Emergence of multidrug-resistant (MDR) bacteria have become a global threat that has led to increased interest in therapeutic alternatives. Bacteriophages (BPs) have been studied as a therapeutic agent to treat the bacterial infections for around 100 years. The lytic BPs can lyse bacteria without attacking on mammalian cells. Thus, it is thought that BPs are significantly safer and better tolerated, and utilize the novel mechanisms of action to achieve antibacterial activity.

METHODS: A laboratory-based descriptive cross-sectional study was conducted. BPs were isolated from environmental sources by the Double layer agar assay. Concentrations of phage were determined in Plaque forming unit per milliliter by Plaque assay and susceptibility test was done by observing their lytic effect on pre-identified MDR bacteria.

RESULTS: A total of 73 BPs were obtained from 11 different sources, out of which 52 (71.2%) showed clear lysis. BPs recovered against specific MDR isolates were ϕEC-21.3%, ϕPS-17.3%, ϕKP-19.2%, ϕCF-19.2%, ϕPR-11.5% and ϕSA 11.5%. Majority of the isolated phages had lytic effect on their respective specific MDR bacteria with varying degree, mostly high efficacy (+++) showing high specificity. However, ϕCF showed minimum lytic effect even on *Citrobacter freundii*, indicating narrow spectrum. Phages specific for *Proteus* spp. i.e., ϕPR42 andϕPR44 had wider spectrum of lytic effect on majority of the MDR isolates. Overall, phages specific for Gram Negative Bacilli (GNB) and Gram-positive cocci (GPC) showed lytic effect predominantly on GNB and GPC respectively.

CONCLUSIONS: Phage therapy can be a promising alternative to antibacterial therapy for treatment of patients with severe MDR bacterial infections.

5264731 | Variations des Vitamines Antioxydantes A, e et LDLoxydées Selon le Niveau Tensionnel Chez les Patients Hypertendus

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Le stress oxydant et le syndrome métabolique sont étroitement impliqués dans la physiopathologie de l'hypertension artérielle.

OBJECTIFS DE L'ÉTUDE : Déterminer le statut en vitamines A et E et LDL oxydées chez les patients hypertendus, selon le statut métabolique (sMet) et le niveau tensionnel.

MATÉRIELS ET MÉTHODES : Il s'agit d'une étude prospective, réalisée chez 245 patients hypertendus (54.33 ± 8.40 ans). Ont été déterminés à jeun : le bilan métabolique, les paramètres du stress oxydant (LDL oxydées, SOD, GPx, total antioxydant et vitamines antioxydantes A et E). L'insulinorésistance a été estimée par l'indice de HOMA. Pour le sMet la définition du NCEP-ATPIII a été utilisée.

RÉSULTATS : La prévalence du syndrome métabolique, selon la définition du NCEP-ATPIII dans notre série est de 47.35% ; 36,32% des patients sont obèses et l'indice de HOMA révèle 46.53% d'insulinorésistance. On observe une carence en vitamines A et E respectivement chez 8.06% et 9.31%, La considération de la présence ou pas du sMet, révèle une différence statistique significative entre les patients pour la vitamine E (p=0.002) et l'index alpha tocophérol (p<10-6), tandis que pour la vitamine A (p=0.06) elle est non significative. Dans le groupe HTA avec sMet, on retrouve une corrélation significative pour la SOD avec le TT (p=0.04), l'IMC (p=0.01) et les LDL oxydées (p=0.06). Pour la vitamine A, avec les TG (p=0.02), l'acide urique (p=0.001) et la PAS (p=0.02). Pour la vitamine E avec le HOMA (p=0.04), la CRPus (p=0.03) et l'index alpha tocophérol (p<0.0001).

CONCLUSION : Les résultats de notre étude ont révélé une prévalence importante de l'obésité et du syndrome métabolique chez les patients hypertendus. Les vitamines A et E jouent un rôle majeur dans les défenses anti oxydantes, les concentrations sont plus faibles chez les patients HTA avec sMet et HTA stade 1 et 2, d'où l'intérêt d'une nutrition équilibrée.

5265039 | Rhipicephalus Microplus (Acari: Ixodidae) in Uganda: New Findings Reveal Widespread Establishment

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BACKGROUND: The cattle tick, *Rhipicephalus microplus*, was first introduced in Africa more than 100 years ago. However, recent evidence shows a rapid expansion of its range across the continent. This tick not only transmit a fatal form of bovine babesiosis and several rickettsial diseases resulting into high economic losses among farmers, but its ecological impact is also worrying as it has been found to displace and potentially crossbreed with other tick species leading to unpredictable effect. In Uganda, the presence of this tick was first reported in the north-eastern parts of the country during 2017. We report on findings from an extensive, nationally representative tick survey, that was conducted during the same year.

METHODS: We performed a cross-sectional study, in which ticks were handpicked from cattle, goats and sheep that were obtained from selected districts of Uganda, especially those that either border with neighbouring countries or lie within the 'Cattle Corridor'. Thereafter, all collected ticks were transported to Uganda Virus Research Institute, Entebbe, where they were identified morphologically.

RESULTS: A total of 1,012 ticks, comprising of 17 tick species were collected from 30 districts. Specimens belonging to *R. microplus* were identified from the districts of Apac (n=2), Agago (n=3), Lamwo (n=3), Arua (n=8), Moyo (n=2), Serere (n=3), Mayuge (n=4) and Ntungamo (n=1). Its closely related autochthonous species, *R. decoloratus*, was found in only 5 of these districts (Apac, Agago, Lamwo, Arua and Ntungamo) at a significantly lower frequency (p = <0.001).

CONCLUSIONS: This study confirms that the invasive *R. microplus* is more widespread in Uganda than previously known. As observed in many countries, it may already be affecting the distribution of other environmental tick species such as *R. decoloratus*. Additionally, its impact on the human and livestock health within the country remains unknown. Further investigations are therefore warranted.

5265079 | The Use of a European Union Reference Material, EURM-019 for Monitoring Performance of Eight In-Country Standard of CareSARS-CoV-2 Assays and Quality Monitoring in South African Laboratories

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BACKGROUND: Reference materials are advantageous because they validate are used as a comparison across assays and platforms. EURM-019 is a stabilised in-vitro synthetic ssRNA containing SARS-CoV-2 E, N, S and *RdRp* gene targets and was initially evaluated to determine its use across eight in-country standard-of-care assays followed by assessment of Xpert Xpress SARS-CoV-2 performance in public sector laboratories.

METHODS: Currently in public sector, multiple assays and platforms are used for diagnostic testing of SARS-CoV-2: Allpex 2019-nCoV assay(29%), TaqMan TaqPath SARS-CoV2 Multiplex assay(20%), Xpert Xpress SARS-CoV-2 assay(18%), cobas SARS-CoV-2 assay(16%), Abbott Molecular SARS-CoV-2 assay(7%), Alinity-m SARS-CoV-2 assay(3%) and other(11%). To confirm stability and compatibility, EURM-019 was evaluated using the Xpert Xpress SARS-CoV-2, BioGX SARS-CoV-2 HMP, TaqMan TaqPath SARS-CoV2 Multiplex, cobas SARS-CoV-2, Abbott Molecular SARS-CoV-2, Viasure SARS-CoV-2, Biofire Respiratory Panel 2.1 and Allpex 2019-nCoV assays. Following evaluation, as Xpert Xpress SARS-CoV-2 contributes significantly to SARS-CoV-2 testing repertoire, EURM-019 was applied to assess performance across ten Xpert testing laboratories using panels of 3 samples.

RESULTS: On evaluating, SARS-CoV-2 was detected using the Xpert Xpress SARS-CoV-2, BioGX SARS-CoV-2 HMP Multiplex and Allplex 2019-nCoV assays only, indicating that the gene sequences detected by the remaining assays may not be present in EURM-019 or assay incompatibility, possibly due to inhibition. Of ten enrolled laboratories performing Xpert Xpress SARS-CoV-2 testing, 100% detected SARS-CoV-2 with indicating the assay is being performed correctly with consistent detection of the *E*- and *N2*-gene targets.

CONCLUSION: EURM-019 is not suitable for use across all assays. The Xpert Xpress SARS-CoV-2 assay was able to accurately and consistently detect SARS-CoV-2. Since majority of current mutations within occur in the S-gene, there are no implications for detection by Xpert Xpress SARS-CoV-2 assay unless new variants harbouring *E* and N-gene mutations are introduced. Ongoing surveillance and quality monitoring is required in context of newly introduced variants.

5265503 | Fine Needle Aspiration Cytology Findings of Breast Lesions in Female Patients Presenting with Palpable Breast Lumps at Makerere University College of Health Sciences, Kampala-Uganda

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BACKGROUND: Palpable breast lumps are a common manifestation encountered by physicians during clinical practice. The use of fine-needle aspiration cytology (FNAC) method has proven to be quick, simple and cost-effective in the evaluation of these lumps for benign, atypical and malignant changes. This study aims to determine the type of breast lesions diagnosed by FNAC and to determine the age-wise distribution for such lesions.

METHODOLOGY: A prospective study consisting of 291 females presenting with palpable breast lesions was carried out at Makerere College of Health Sciences (MakCHS) pathology laboratory from January 2019 to May 2019. FNAC results were grouped into tier five reporting categories as C1, C2, C3, C4 & C5 in accordance to the International Academy of Cytology (IAC).

RESULTS: Out of the 291 cases examined, 14 (4.8%) were insufficient (C1), 192 (66%) were benign (C2), 9 (3.0%) were atypical (C3), 15 (5.2%) were suspicious of malignancy (C4) & 61 (21%) were malignant (C5). In the benign category, lesions of fibroadenoma were the most commonly diagnosed constituting 110/192 (57.3%) whereas under the malignant category lesions of invasive ductal carcinoma were the most commonly diagnosed constituting 27/61(44.3%). The peak age group for benign lesions was 21-30 years whereas the peak age group for malignant lesions was 41-50 years.

CONCLUSION: Fine-needle aspiration cytology (FNAC) was found to be an effective diagnostic tool in the categorization of palpable breast lumps into benign, malignant, atypical, suspicious and inadequate categories.

5265770 | Stability of Ion Selective Electrode for Chloride Measurement on Roche Cobas® 6000 C501 System

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BACKGROUND: The manufacturer (Roche) of the ion selective electrode (ISE) for sodium, potassium and chloride claims the onboard stability is 2 months or 9000 total number of tests. However, frequent negative trends and unexplained hypochloraemia was observed in patient results and stability of the chloride electrode was thus questioned. The laboratory changes the ISE every 4 weeks, as serum electrolytes are requested as a profile test amounting to 34000 tests per month. This study aimed to determine if monthly replacement of the chloride ISE is adequate for its stability.

METHODS: The Roche cobas® 6000 c501 system has two ISE's in use (Line A and B). The stability of each for serum chloride was tested over one month. Four healthy volunteers were selected and 30 serum aliquots were prepared separately for each, one for each day of the month. Tests were performed in duplicate on both lines as part of routine runs and the results were analysed for trends. The stability was calculated as bias% between assigned mean and cumulative mean, and compared to the reference change value (RCV) for chloride of 6,97%.

RESULTS: The total number of chloride tests performed in this study was 480. The total number of chloride tests performed for the month on the ISE was 14310. The volunteers' results demonstrated negative trends on both lines with the bias% on line A and B respectively -6,5% and -5,3%, although these were below the RCV for serum chloride (6,97%). The internal quality control (IQC) trends of the same month also demonstrated a negative trend, but with a bias% of -0.47 and -0,77% against target values respectively.

CONCLUSION: The findings suggest that although the chloride ISE showed deterioration over a one-month period, this is unlikely to affect medical decisions. Patient samples showed more apparent negative trends compared IQC material.

5266191 | Étude de la Séroprévalence des Marqueurs du Virus de L'hépatite B Chez les Patients Reçus au Laboratoire de Virologie du CHU Aristide le Dantec en 2019

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BACKGROUND : L'infection par le virus de l'hépatite B (VHB) constitue un véritable problème de santé publique dans le monde mais aussi pour le Sénégal avec 85% de la population générale qui ont au moins un marqueur du VHB. L'objectif de ce travail était d'étudier la séroprévalence des marqueurs biologiques du VHB en interprétant les résultats des demandes émanant des cliniciens et adressés au laboratoire de Bactériologie-Virologie du Centre Hospitalier Universitaire Aristide le Dantec.

MÉTHODE : La population d'étude comportait 1645 patients avec 37% d'hommes et 63% de femmes reçus entre le 1er janvier et le 31 décembre 2019. Parmi ces patients, 50% étaient dans l'intervalle d'âge de [20-40] ans. L'automate d'immuno-analyse Architect Plus Ci 9000 avait permis la recherche de tous les marqueurs demandés.

RÉSULTATS : Les résultats avaient montré que parmi les patients, 31 % étaient porteurs de l'antigène (Ag) HBs et 9% de l'antigène HBe et que respectivement 57% et 78% avaient les anticorps anti-HBs et Anti-HBc. La co-infection entre l'infection au VHB et virus de l'hépatite C (VHC) était de 0,84%. Cependant une fréquence de 14,2% de l'Ag HBs avait été retrouvée chez les femmes enceintes mais qu'aucune d'entre elle n'aveint le marqueur du virus sauvage (AgHBe).

CONCLUSION : Ces résultats montrent combien le nombre de personnes en contact avec le virus au Sénégal est élevé mais également la nécessité d'un meilleur suivi des femmes enceintes infectées par le VHB afin de rompre la transmission mère-enfant.

5266545 | Valeur Pronostique du Fibrinogène dans la Cirrhose du Foie Décompensée

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INTRODUCTION : Les limites du score Child Pugh et MELD, dans la stratification de la maladie et la prédiction de la rechute et du décès ont été signalées à maintes reprises dans la littérature. Dans cette optique, le Fibrinogène apparait comme un élément de choix, un test facilement réalisable, non invasif et peu couteux.

MATÉRIEL ET MÉTHODES : Il s'agit d'une cohorte pronostique, portant sur l'étude de la relation entre la diminution du Fibrinogène et la survenue de décès dans la cirrhose du foie. La population d'étude était composée de patients cirrhotiques décompensés. Le dosage du fibrinogène a été fait par méthode de clauss sur STA Compact max. Les patients ont été suivis moins tous les 6 mois avec comme critère de jugement: la survenue de décès.

RÉSULTATS : 94 patients avec une cirrhose décompensés ont été inclus dans cette étude. L'âge moyen était de 60 ans [IC : 57 – 63 ans], le sexe ration H/F était de 1,00. 46.8% des étiologies étaient virales. 7.4% des patients avaient un Child Pugh A, 63.8% Child Pugh B et 28.7% Child Pugh C. A l'admission, l'ascite était la complication la plus fréquente, constatée chez 80% des cas. La durée moyenne de suivi était de 16 mois, à l'issu de laquelle nous avons enregistré un taux de mortalité de 36.2%.

Selon la courbe de ROC une valeur seuil de 1.8 gr/L pour le Fibrinogène, prédisait la mortalité avec une sensibilité de 61.8% et une spécificité de 72.7%. Le risque de décès était significativement plus élevé chez les patients ayant un taux de Fibrinogène inférieur à 1.8 gr/L avaient un H.R = 4.31 [IC : 1.73 – 10.72].

CONCLUSION : Le Fibrinogène semble être un bon marqueur pronostique pour la cirrhose du foie décompensée et il serait judicieux de l'inclure dans les actuels scores pronostiques validés.