UNIVERSITY OF GHANA

NOGUCHI MEMORIAL INSTITUTE FOR MEDICAL RESEARCH, UNIVERSITY OF GHANA

ANNUAL RESEARCH MEETING 2022

THEME

Epidemics, Pandemics and Diseases of Public Health Importance: Bridging the Research-Policy Divide

NOGUCHI MEMORIAL INSTITUTE FOR MEDICAL RESEARCH, UNIVERSITY OF GHANA

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INTEGRI PROCEDAMUS

ANNUAL RESEARCH MEETING 2022

THEME

Epidemics, Pandemics and Diseases of Public Health Importance: Bridging the Research-Policy Divide

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WELCOME MESSAGES

PROF. DOROTHY YEBOAH-MANU

DIRECTOR, NMIMR

Dear Colleagues and Friends

I welcome you to the Annual Research Meeting of the Noguchi Memorial Institute for Medical Research (NMIMR). The NMIMR has three mandates, which are: to conduct research into diseases of public health importance, to provide specialized diagnostics support for global health interventions, and to build the capacity of the next generation of young scientists through postgraduate training and health workforce by organising several workshops for allied health professionals across the sub-region. The Institute has been a lead and active stakeholder in several global health interventions as was exemplified during the height of the COVID-19 pandemic. The Institute takes pride in being the lead centre for COVID-19 testing in Ghana, the first to test for COVID-19 in Ghana and as of now, still the largest single testing facility for COVID-19 in the country. This was possible due to the timely donation of an Advanced Research Laboratory facility by JICA to the institute.

During the early phase of the pandemic, we trained more than 40 laboratories to test for COVID-19 in Ghana and supported the establishment of PCR diagnostic capacity across Africa. I am happy to say that the NMIMR is now one of the Africa CDC Centres of Excellence and a genomic hub responsible for 5 countries in West Africa, including Ghana, Togo, Benin, Liberia and Sierra Leone. Scientists from these countries also visit the Institute for training. The Institute also serves as the GHS/WHO reference laboratory (Collaborating Centre) for several diseases including, Rotavirus, Poliomyelitis and influenza.

Ladies and gentlemen, the theme for this year's meeting: **Epidemics, Pandemics and Diseases of Public Health Importance: Bridging the research-policy divide,** is appropriate based on the role the Institute has played in the last few years. The NMIMR has been at the forefront of tackling epidemics/pandemics and local outbreaks. Notable examples are the West African Ebola virus disease outbreak in 2014, the H1N1 influenza outbreaks in 2009 and 2017, the H5N1 outbreak in 2018. The swift response to the national call led to the rapid detection of the recent Marburg outbreak leading to the institution of appropriate interventions, dampening an otherwise disastrous event. The Institute also confirmed the first case of monkeypox in Ghana in July this year and has been involved in the surveillance of other diseases across the country. Aside from these, the Institute conducts research into many other infectious and non-infectious diseases, many of which you will hear about in this meeting.

The NMIMR, ladies and gentlemen, has been involved in developing and shaping public health policy in the country. It has a long-standing collaboration with the Ministry of Health and the Ghana Health Service and works closely with agencies under these bodies to deliver healthcare. There is constant collaboration between national programmes such as HIV/AIDS, TB and Malaria control programmes just to mention a few. We continue to support the national surveillance for malaria drug efficacy, providing directions for malaria treatment regimens in the country.

This year's meeting brings researchers within and outside Ghana together to share evidence-based data that may clear the path for great collaborations. As a believer in south-south

partnerships, this meeting offers an opportunity for us all to establish new collaborations that may last for several years. I cannot also forget our northern partners, some of whom have been with us for as long as I have been in this Institute. The excellent work done by the researchers and students at the Institute will be on display both at the oral and poster sessions. For this year's meeting, more than 250 abstracts were received, with the majority coming from graduate students we are mentoring. This is a testament to the Institute's mandate as a centre for professional training and the presentations will collectively showcase the contribution of NMIMR to public health in Ghana.

The NMIMR as a leading biomedical research institute in Africa will continue to work hard to support the University of Ghana's vision of **becoming a world-class research-intensive University.**

I welcome you once again to the serene premises of NMIMR and look forward to a successful meeting.

Thank you

PROF. JULIUS FOBIL

PROVOST, COLLEGE OF HEALTH SCIENCES, UNIVERSITY OF GHANA

The Noguchi Memorial Institute for Medical Research (NMIMR) is one of the seven constituents of the College of Health Sciences, University of Ghana, and is a flagship institution for the conduct of impactful research that is relevant to national development. I am delighted to be part of the reintroduction of the NMIMR's Annual Research Meeting (ARM) and this will be the 7th time the meeting is being organised by the Institute. Over the last decade, the world has witnessed several life-threatening infectious diseases including outbreaks of influenza, Marburg virus as well as the monkeypox and COVID-19 pandemics. The 2022 meeting, which like the previous meetings, seeks to establish stronger connections between research outcome and policy formulation, is appropriately themed Epidemics, Pandemics and Diseases of Public Health Importance: Bridging the research-policy divide.

Increasing global travel and trade, rapid urbanization, limited access to health care, environmental degradation, and other trends have contributed to the emergence of new pathogens and re-emergence of previously eradicated ones which are responsible for spreading diseases of epidemic and pandemic proportions. The ravaging global health crisis brought about by the SARS-CoV-2 virus has not only destabilized the global economy but has also heightened the threat to global health security on account of the constantly evolving natural history of the disease, thus necessitating the development of innovative new approaches that have proven effective in controlling the outbreaks and disease management.

The Noguchi Memorial Institute for Medical Research over the past years has been very instrumental in supporting both national and regional responses to such epidemics in West Africa region. As part of its mandate, the NMIMR has been at the forefront of not only combating infectious pathogens through research, diagnosis and human capacity development but also key in strengthening regional capacity for pandemic preparedness through training. The Institute has over the years partnered with national and international bodies such as the Ghana Health Service (GHS), the World Health Organisation (WHO), the West African Health Organisation (WAHO) and the Africa Centres for Disease Control and Prevention (Africa CDC) to conduct regionally relevant research, develop tools for disease monitoring and surveillance as well as establishing the diagnostic capacity for outbreak detection across the African continent. To this end, the NMIMR has trained laboratory personnel across Africa as part of building capacity for surveillance and laboratory support for emerging pathogens of public health importance.

This research meeting which will have seasoned researchers from both NMIMR, the University of Ghana, international experts as well as policy and decision-makers, will be a unique avenue for sharing relevant scientific data and scientific information that directly impact policy and practice. Over the two days of the meeting, it is expected that stakeholders at this meeting will engage one another in useful and deeply engaging interactions that will ultimately result in an increased understanding of the health challenges confronting our society and an improved collective approach to healthcare delivery. Of special significance is the large number of very young and early career researchers who will be showcasing their work at this meeting, as this is a testament to the Institute and College's strategy of ensuring the continuous development of human capacity and the next generation of scientists.

I take the opportunity to welcome you all to the College of Health Sciences of the University of Ghana and look forward to engaging deliberations.

MEET OUR SPEAKERS

DR ANARFI ASAMOA BAAH

PRESIDENTIAL COORDINATOR FOR GHANA'S COVID-19 RESPONSE

Dr Anarfi Asamoa-Baah is currently the Presidential Coordinator for Ghana's COVID-19 response.

He retired from the World Health Organization five years ago, where he worked for twenty years. Ten years as the Deputy Director General and ten years as an Assistant Director General for four different clusters, Governing Bodies, External Relations and CouWntry Support, Health Technology and Pharmaceuticals, Communicable Diseases and Emergencies as well as for HIV/Malaria and Tuberculosis.

Before joining WHO, he had worked at all levels of the health system of Ghana to the very top. He was appointed the Director of Medical Services in 1997. He is remembered for the key role he played in strengthening district health systems, establishing the concept of Budget Management Centres, developing the first 5-year health sector-wide programme of work, in establishing the Ghana Health Service, the National Health Insurance Scheme, the Food and Drug Authority and the University of Ghana School of Public Health.

Dr Asamoa-Baah qualified as a Clinician from the University of Ghana Medical School and has postgraduate qualifications in public health, health planning, health financing and health policy from the UK, Denmark and USA. He has honorary doctorate degrees from the University of Ghana, the University of Health and Allied Sciences and the Liverpool School of Tropical Medicine.

DR ABDOURAHMANE SOW, MD, MSc, MPH, PhD

SENIOR MEDICAL EPIDEMIOLOGIST, PUBLIC HEALTH AND RESEARCH DEPARTMENT, WEST AFRICAN HEALTH ORGANIZATION (WAHO)

Abdourahmane Sow is a Senior Medical Epidemiologist and head of Epidemic and Public health laboratory systems and networks at the West African Health Organization (WAHO). He has more than 15 years of experience both at national and international levels (10 years) in the Management of public health programmes and epidemics response, emerging and reemerging diseases surveillance and control, laboratory diagnostic and infectious diseases modelling. He is coordinating the West Africa Reference Laboratory Network as well as the regional AMR and Biosecurity Networks. Dr Sow is also a member of various technical advisory/steering committees at WHO, Africa CDC and FAO.

He received a PhD in Epidemiology from both the Bordeaux School of Public Health (ISPED) and the University of Dakar. He earned the degree of Medical Doctor in 2008, a Master of Public Health in 2012 and a Masters in Biomedical Sciences in 2005 from the University of Dakar. He also received certifications in *"Crisis and Emergency Situation Management"*, from Galilee International Management Institute (Israel) in 2016 and in "Leadership and Management in Global Health" from the University of Washington in 2021.

Before joining WAHO as head of laboratory services and acting head of the laboratory division of the ECOWAS Regional Centre for surveillance and Diseases Control, Dr Sow was an Assistant Professor in Epidemiology at the Public Health Department, at the University of Dakar and Senior Medical Epidemiologist at the WHO Collaborating Centre on Arboviruses and hemorrhagic fever viruses in Dakar Pasteur Institute from 2009 to 2016.

PROF WILLIAM KWABENA AMPOFO, PhD

CHAIR, AFRICAN VACCINE MANUFACTURING INITIATIVE

Prof William Kwabena Ampofo is an Associate Professor of Virology with the College of Health Sciences, University of Ghana. He is the immediate past Head of, the Virology Department, at Noguchi Memorial Institute for Medical Research (NMIMR). His research interests include molecular and serological investigations of viruses, prevention of viral infections, anti-viral therapy, and viral disease burden. He has participated in several research studies and has over 120 research papers published in the medical sciences. He has worked on basic virology, epidemiology and prevention of viral infections and capacity building of laboratory medicine practitioners. He has conducted various assignments throughout Africa with the WHO, Commonwealth Secretariat Health Division, US Department of Defense, German International Development Agency, US Agency for International Development and Africa CDC. Prof Ampofo has represented Africa on WHO advisory groups for Ebola, Influenza vaccine production, Immunization, and Pandemic influenza preparedness. Recently, he assisted the COVAX Procurement Reference Group, International Taskforce Influenza Vaccine Roadmap, WHO Global Task Team Pandemic Influenza Vaccine Response Operational Plan and the US National Academies Committee on Global Coordination, Partnerships, and Financing Recommendations for Advancing Pandemic and Seasonal Influenza Vaccine Preparedness and Response. He also serves on the Implementation Consultation Group of the International Pathogen Surveillance Network - Global Pandemic Radar. He is a member of the Kano Independent Research Trust, and Chair of, the African Vaccine Manufacturing Initiative. Prof. Ampofo is the Coordinator of, the National Laboratory Network for COVID-19 Testing and Secretary to the Presidential Committee for Vaccine Development and Manufacturing.

PROF SEBASTIEN GAGNEUX, PhD

MEDICAL PARASITOLOGY AND INFECTION BIOLOGY, SWISS TPH

Sébastien Gagneux is a Professor of Infection Biology and Head of Department at the Swiss Tropical and Public Health Institute (Swiss TPH)/the University of Basel. After receiving his PhD from the University of Basel, he worked as a postdoctoral fellow at Stanford University and the Institute for Systems Biology in Seattle, USA. He then started his laboratory at the MRC National Institute for Medical Research in London, UK, before joining Swiss TPH. His research focuses on the ecology and evolution of Mycobacterium tuberculosis with a particular focus on antimicrobial resistance.

DR JOHN ODOOM, PhD

HEAD, DEPARTMENT OF VIROLOGY, NMIMR

Dr John Kofi Odoom is a Senior Research Fellow and Molecular Virologist at the Noguchi Memorial Institute for Medical Research, University of Ghana. Dr Odoom holds his MSc and PhD. in Virology from the London School of Hygiene and Tropical Medicine. Dr Odoom's research focuses on enteroviruses (polio, echoviruses and coxsackieviruses) and wastewater surveillance for enteric viruses. He also coordinates the COVID-19 research and diagnosis in the Department. He is a member of some local and international committees including the National Taskforce on Containment of Poliovirus and the National Verification Committee on Measles Elimination.

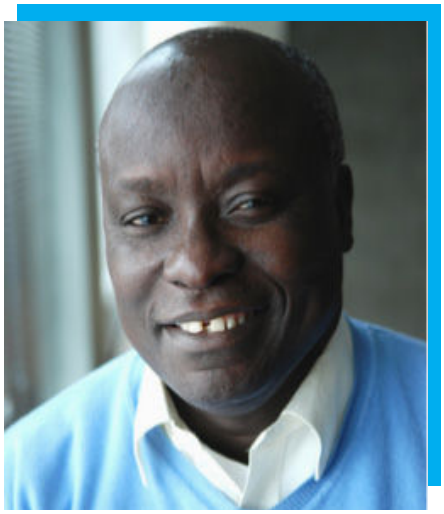
DR ANTHONY ABLORDEY, PhD

HEAD, DEPARTMENT OF BACTERIOLOGY, NMIMR

Dr Ablordey is a Senior Research Fellow at the Bacteriology Department of the Noguchi Memorial Institute for Medical Research, University of Ghana. He holds a PhD in Biochemistry from the University of Gent, Belgium. He is also a Senior Fellow of the European Foundation Initiative for Neglected Tropical diseases and his research mainly focuses on the Molecular epidemiology of infectious diseases.

Dr Ablordey is extensively involved in Buruli ulcer research and has made a significant impact in this field. He was part of an international team of scientists that successfully cultivated *Mycobacterium ulcerans* from the environment for the first time. He is credited with developing molecular typing methods widely used for the confirmation of *M. ulcerans* in clinical/environmental samples as well as for the investigation of Buruli ulcer transmission.

Dr Ablordey in collaboration with the Foundation for Innovative New Diagnostics (FIND) has developed a prototype LAMP-based rapid diagnostic test for Buruli ulcer disease. His portfolio also includes research in diarrhoeal diseases, antimicrobial resistance and food microbiology and he has mentored over fifty graduate students in these disciplines.

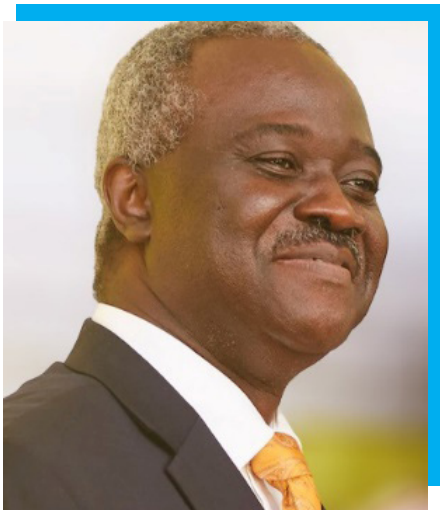


PROF. GEORGE ENYIMAH ARMAH

DIRECTOR, WHO WEST AFRICA REGIONAL ROTAVIRUS REFERENCE LABORATORY, NMIMR

Prof George Armah holds an MSc in Physics from the University of Ghana, Legon, and a PhD in Biophysical Chemistry and Immunology from Osaka University, Japan, and is a foundation and active member of the African Rotavirus Network and Head of the West African WHO Regional Rotavirus Reference Laboratory in Accra, Ghana. He also holds an adjunct position as a senior lecturer in the Clinical Trials programme at the School of Public Health of the University of Ghana. His interest is in enteric viral diarrhoea disease in African children and his research focus has been centred on the burden and aetiology of diarrhoea disease, the epidemiology of rotaviruses and their evolution in the African setting. He is also interested in understanding the observed low efficacy of rotavirus vaccines in developing countries, especially in Africa. He has over the past two decades been involved in programmes aimed at providing answers to these questions. He has been involved in several clinical trials on the immunogenicity, safety and efficacy of rotavirus vaccines in Africa. His work on the multi-country clinical field trial on the safety and efficacy of the RotaTeq vaccine in Africa was critical in the informed decision to recommend the introduction of rotavirus vaccines in Africa and other developing countries. He continues to be involved in efforts to monitor the impact and safety of rotavirus vaccines as they are introduced in African countries.

Prof Armah is a member of the African group of vaccinologists, scientists and public health promoters, who seek to reduce the long wait for new vaccine introductions in the immunization programmes in Africa by advocating for the introduction of available new life-saving vaccines to African children, and also promoting equity in the accessibility of these vaccines. In recognition of these efforts, he was declared a “Vaccine Hero” by the Bill and Melinda Gates Foundation in 2013. He is a foundation member of the International Rotavirus Organisation of Technical Advisers (ROTA) council. He presently chairs the National Immunization Technical Advisory Group of Ghana (NITAG) and sits on several International Scientific Advisory Boards.



PROF JOHN OWUSU GYAPONG

IMMEDIATE PAST VICE CHANCELLOR, UNIVERSITY OF HEALTH AND ALLIED SCIENCES, HO

Prof John Owusu Gyapong is a Public Health Physician and an Epidemiologist. He was Vice Chancellor of the University of Health and Allied Sciences in Ho, from August 2016 to July 2022. Before that, he served the University of Ghana for five years as Pro-Vice-Chancellor for Research, Innovation and Development and Professor of Epidemiology and Disease Control. He is also an Adjunct Professor of International Health at Georgetown University in Washington.

He received his medical training at the Kwame Nkrumah University of Science and Technology in Ghana before going on to the London School of Hygiene and Tropical Medicine for a Master of Science in Public Health in Developing Countries and a PhD in Epidemiology.

He worked for about a decade as a general practice doctor in many parts of Ghana, including Kumasi, Navrongo, and Dormaa Ahenkro, and participated in the Navrongo Health Research Centre's Ghana Vitamin A Supplementation Trials. Whilst in Navrongo, he oversaw the Navrongo War Memorial Hospital's paediatric department and periodically served as the District Director of Health Services. He spent 12 years as the Ghana Health Services' Director of Research and Development, where he was responsible for Implementation Research and Health Systems Research. He led large-scale field intervention studies in NTDs, Malaria, TB and Micronutrient Supplementation. He established the Ghana Neglected Diseases Control Programme in the Ghana Health Service and managed it for eight years.

Prof Gyapong's primary area of study and research is Infectious Diseases Epidemiology, particularly lymphatic filariasis, other under-researched tropical diseases, and malaria. He has been the Chairman or Member of several WHO TDR and NTD Committees. He has been a member of many other global, regional and national research review groups and boards, such as the UK MRC, Ghana FDA and the European and Developing Countries Clinical Trial Partnership (EDCTP). He has over 150 papers in peer-reviewed journals, several book chapters, and an edited book on Neglected Tropical Diseases in sub-Saharan Africa.

DR SAMUEL KWEKU DADZIE

FORMER HEAD, DEPARTMENT OF PARASITOLOGY, NMIMR

Dr Samuel Kweku Dadzie is a Senior Research Fellow and a Medical Entomologist in the Parasitology Department of the Noguchi Memorial Institute for Medical Research (NMIMR) with over 26 years of experience in the field of Medical Entomology. He holds a PhD in Vector Biology from the Liverpool School of Tropical Medicine in the UK and his research interest focuses on vector biology with an emphasis on insecticide resistance and the application of modern methods to address the burden of vector-borne diseases. Dr Dadzie has worked extensively on vectors of many tropical diseases including arboviral diseases in Ghana and has authored over 60 publications in peered-reviewed journals.

Dr Dadzie is a member of several committees in Ghana including the Malaria Vector Control Oversight and Malaria Research Advisory Group of the Ghana National Malaria Control Programme. He is currently the focal person for the African Network of Vector Resistance (ANVR/WHO/AFRO) in Ghana and served internationally including being an ad-hoc member of the WHO/TDR Scientific Working Group for Research in Implementation, Geneva. He is a co-founder and currently the chair of the West African *Aedes* Surveillance Network (WAASuN) which was established to help strengthen the capacity of West African countries to control arboviral diseases. He also spearheaded and is currently the President of the Ghana Chapter of the Pan-African Mosquito Control Association. He is a member of the American Mosquito Control Association, and the American Society of Tropical Medicine and Hygiene and is currently a member and Vice-Chair of the Technical Advisory Group of the World Health Organization Global Arbovirus Initiative. Dr Dadzie is the immediate past Head of the Parasitology Department of NMIMR and contributed to the Department's resource mobilization through increased grantsmanship and collaborations. He also provided leadership in the mentorship and training of young scientists in the Department.

PROF. DZIEDZOM de SOUZA

HEAD, DEPARTMENT OF CLINICAL PATHOLOGY, NMIMR

Dziedzom K. de Souza is an Associate Professor in the Parasitology Department, and the Head of the Clinical Pathology Department of the Noguchi Memorial Institute for Medical Research (NMIMR), University of Ghana. His interests are in lymphatic filariasis (LF), Neglected Tropical Diseases, medical entomology, and molecular biology of disease vectors and parasites. His main research focus involves assessing the transmission of Lymphatic Filariasis using xenomonitoring methods, as well as evaluating new approaches to address the end-game challenges of the Global Programme to Eliminate Lymphatic Filariasis. He has led several studies on LF and has been involved in providing training, diagnostics, monitoring and evaluation support to less developed project countries in Africa including Liberia, Sierra Leone, Ethiopia, Nigeria and Togo. He has also been involved in studies on Buruli ulcer transmission and diagnosis, onchocerciasis, soil-transmitted helminths and leishmaniasis. He is the leader of the NTD research group in the Parasitology Department. He supports the Ghana NTD programme and has served as a consultant for different organisations including WHO, FIND, Sightsavers, and the Taskforce for Global Health.

DR BENJAMIN ABUAKU

HEAD, DEPARTMENT OF NUTRITION, NMIMR

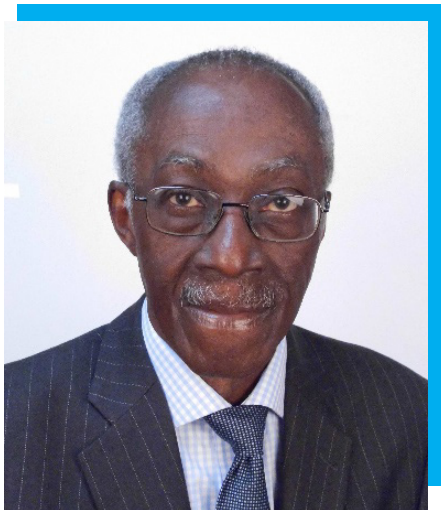
Dr Benjamin Abuaku is an Epidemiologist and Senior Research Fellow in the Department of Epidemiology, and Head of, the Department of Nutrition, Noguchi Memorial Institute for Medical Research. Dr Abuaku has coordinated several malaria epidemiological studies since 1993. One such study on antimalarial therapeutic efficacy, conducted between 1998 and 2004 under his mentor, Prof. Kwadwo Ansah Koram, contributed immensely to the review of Ghana's antimalarial drug policy in 2004 when monotherapy with chloroquine was replaced with Artemisinin-based combination therapy (ACT) in the treatment of uncomplicated malaria. He is currently the focal person for antimalarial therapeutic efficacy testing in Ghana and has been a member of the National Malaria Case Management Technical Working Group (MCM TWG) since 2013. His membership of the MCM TWG and the Technical Experts Committee for the Revision of Antimalarial Medicines Policy (Ghana Health Service) allowed him to contribute towards the publication of the 2014 and 2020 "Guidelines for Case Management of Malaria in Ghana" and the 2020 "Antimalarial Medicines Policy". Dr Abuaku continues to collaborate with the National Malaria Elimination Programme (NMEP) to monitor the impact of malaria interventions on parasite positivity rates in thirty (30) sentinel sites across Ghana.

DR GERALD MBOOWA

IMPLEMENTATION SCIENCE EXPERT FOR BIOINFORMATICS, AFRICA CENTERS FOR DISEASE CONTROL AND PREVENTION

Dr. Gerald Mboowa is a Human Genetics and Genomics research fellow at the Genomics Laboratory, Department of Molecular Biology and Immunology, School of Biomedical Sciences, Makerere University College of Health Sciences. His interests include utilizing Genomics and Bioinformatics approaches to understanding the patterns of host Genetic determinants of resistance and susceptibility to common infectious diseases. He is also interested in Microbial Genomics and Immunology of infectious diseases especially HIV, Tuberculosis, and their co-morbidities. For his PhD research he interrogated NextGen Sequence Genomic data using Bioinformatics tools to investigate and identify the pathogenicity of host functional genetic variants/loci in pediatric HIV/AIDS disease progression in sub-Saharan Africa populations. Gerald has now submitted and successfully defended his PhD at Makerere University.

Gerald has done a postdoctoral research specifically examining HIV viral NGS data to understand its genomic diversity through the HIV Co-infections in Uganda Program funded by the Fogarty International Research Training Grant (Project #2D43TW009771-06) at the Infectious Diseases Institute, Makerere University, Uganda He has worked as a bioinformatics scientist at the African Centre of Excellence in Bioinformatics and Data-Intensive Sciences of Makerere University. He is currently an Implementation Science Expert for Bioinformatics at the Africa Centres for Disease Control and Prevention (Africa CDC) under the Africa CDC Institute of Pathogen Genomics.

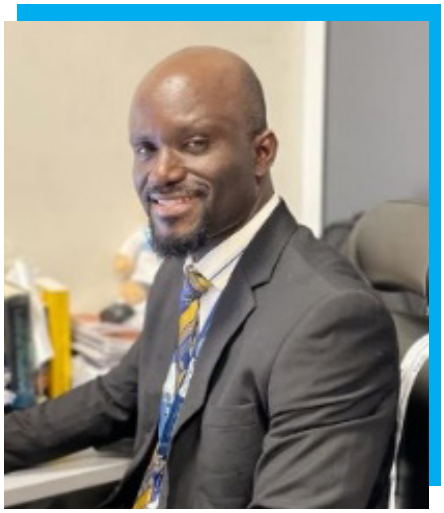


PROF DWOMOA ADU, MD. FRCP, FGCP

CONSULTANT NEPHROLOGIST, KORLE-BU TEACHING HOSPITAL; UNIVERSITY OF GHANA MEDICAL SCHOOL

After a career as a Consultant Nephrologist at the Queen Elizabeth Hospital and Senior Clinical Lecturer at the University of Birmingham, England, Prof. Dwomoa Adu returned to Ghana in 2009 to take up an appointment as Honorary Consultant Nephrologist at the Korle-Bu Teaching Hospital and Senior Research Fellow at the University of Ghana Medical School. He has a long-standing research interest in the immunogenetics and treatment of lupus nephritis and anti-neutrophil cytoplasmic antibody (ANCA)-associated vasculitis. His current research interests have been the prevalence, causes and genetics of chronic kidney disease in Africa. He is Co-PI together with Professor A. Ojo and Professor B.L. Salako of the H3Africa Kidney Disease Research Network grant funded by the NIH to study the genomics of chronic kidney diseases in Africa. He is a past President of the African Association of Nephrology.

MEET OUR DEBATERS



DR ISAAC DARKO OTCHERE

SENIOR RESEARCH FELLOW, DEPARTMENT OF BACTERIOLOGY, NMIMR

Dr Isaac Otchere is a Senior Research Fellow in the Department of Bacteriology of the Noguchi Memorial Institute for Medical Research (NMIMR). After receiving his PhD from the University of Ghana, he has been working on tuberculosis (TB) research focusing on the use of high throughput technologies to study the basis of bacterial pathogenesis and drug resistance whilst searching for new therapeutics and biomarkers for the development of vaccines and diagnostics. He has a broad background in Biochemistry and practical training in biostatistics, bioinformatics, and pathogen genomics. His future aspirations are to use the invaluable applications of bioinformatics and biostatistics to explore mycobacterial pathogenesis and disease control, especially in the search for new biomarkers for vaccines and new therapeutic drugs, and to transfer the skills acquired while working on tuberculosis to other bacterial diseases.

DR PETER KOJO QUASHIE

DEPUTY DIRECTOR (RESEARCH), WACCBIP

Dr Peter Kojo Quashie is a Senior Research Fellow and Deputy Director in-charge-of Research at the West African Centre for Cell Biology of Infectious Pathogens (WACCBIP), where he leads a research group focusing on HIV, SARS-CoV-2 and other viruses of epidemic importance. An alumnus of Mensah Sarbah Hall, with graduate and post-graduate training at McGill University and the University of Toronto respectively, Dr Quashie is a world-renowned virologist with over 45 peer-reviewed publications in high-impact journals such as Science, Nature Communications, Journal of Virology and BMC Medicine. In 2012, he published seminal papers on an HIV wonder drug dolutegravir. Many of his publications have been used in the evaluation of dolutegravir's resistance in the clinic. Some of his roles at WACCBIP include coordinating much of WACCBIP's COVID-19 research portfolio and he is the Principal Investigator of the Ghana site of the Global Immunology and Immune Sequencing for Epidemic Response (GIISER) program, funded by Bill and Melinda Gates (BMGF). Most recently, his group has published the first immunology evidence explaining the low-severity experience of COVID-19 in Ghana. He currently pursues research trying to understand and therapeutically target viruses with pandemic potential.

DR IVY ASANTEWAA ASANTE

SENIOR RESEARCH FELLOW, DEPARTMENT OF VIROLOGY, NMIMR

Dr Ivy Asantewaa Asante is currently in charge of the National Influenza Centre, in Ghana. She holds a master's degree in Microbiology from the University of Ghana Department of Medical Microbiology, UGMS. She had her PhD training at the Heinrich-Pette Institute, Universität, Hamburg, Germany. She has been involved with influenza surveillance in Ghana since 2007. Her research interests include emerging and re-emerging respiratory viruses with an emphasis on the adaptation of avian influenza viruses to mammalian hosts. She won travel grants to the recent Options XI conference held in Belfast and currently holds a grant with the US-CDC. She is a member of the Global Influenza Surveillance and Response System (GISRS) network of the WHO.

DR PAUL OWUSU DONKOR

HEAD OF DEPARTMENT, PHARMACOGNOSY AND HERBAL MEDICINE, SCHOOL OF PHARMACY, UNIVERSITY OF GHANA

Dr Paul Owusu Donkor is a pharmacist, senior lecturer and researcher at the University of Ghana School of Pharmacy. He obtained his B.Pharm (2007) and MPhil in Pharmacognosy (2012), all from the Kwame Nkrumah University of Science and Technology (KNUST) and PhD in Pharmacognosy (2016) from the Tianjin University of TCM, China. His research is focused on the characterization of bioactive compounds from plants and the development of herbal monographs and the standardization and formulation of complementary and alternative medicines into safe and affordable dosage forms. He has also developed a special interest in the quality control of plant-based products using complex chromatographic and spectroscopic methods.

Dr Donkor has served as the Editor-in-Chief of the Pharmaceutical Society of Ghana where he managed all internal and external communications of the Society. He is a finalist in the Independence Day National Debate Contest. He is a board member of the Ghana Cooperative Pharmacists Credit Union Limited and sits on the Advisory Board of the National Electronic Pharmacy Platform.

CONFERENCE PROGRAMME

TIME	ACTIVITY	RESPONSIBLE PERSON/ CHAIRPERSON
Day 1		
OPENING CEREMONY		
8.15 - 08:55	Arrival and Registration	
08:55-9:00	Call to order	Dr Beverly Egyir/Dr Kofi Bonney (MCs)
09:00– 09:05	Welcome Address	Prof Dorothy Yeboah-Manu *Director, NMIMR*
9:05 – 09:08	Introduction of Chairperson	Dr Gloria Ivy Mensah
09:10 - 09:15	Chairperson's Remarks	Prof. Nana Aba Appiah Amfo *Vice-Chancellor, University of Ghana*
9:15 - 9:20	Introduction of Special Guests	MC
9:20 - 9:25	Brief Remarks- JICA	Mr Yasuaki Momita
9:25 - 9:30	Brief Remarks- WHO	WHO Country Office Representative
9:30 - 9:35	Brief Remarks- Africa CDC	Dr Gerald Mboowa
9:35 - 9:40	Brief Remarks - Ministry of Education	Hon. Yaw Osei Adutwum
9:40 - 9:45	Brief Remarks- Ministry of Health	Hon. Kwaku Agyemang-Manu
9:50 - 10:15	Keynote Address 1 Strategies for ensuring uptake of research data for policy formulation - Dr Anarfi Asamoa-Baah, *Presidential Coordinator* for Ghana›s *COVID-19* Response	
10:15 – 10:20	Chairperson's Closing Remarks	Prof. Nana Aba Appiah Amfo
10:20 – 10:25	Announcements	MCs
10:25 – 10:55	Group Photographs Coffee break	All
SCIENTIFIC SESSIONS		
	Plenary session 1 (Pandemic preparedness and emerging Health threats)	
11:00 – 11:45	Plenary speakers *1. West African regional public health research agenda in the context of pandemic preparedness and response* – Dr Abdourahmane Sow 2. *Emerging health threats and the contribution of NMIMR's research to health systems and policy* - Prof William Ampofo	Prof Fred Binka/ Dr Mary Amoakoh-Coleman

11:45 – 11:55	Illumina presentation: **Illumina and Channel Partner ISN Medical Presentation on** *Genomics Research with NGS and Microarray Technologies*		Mr. Rodolphe Vetchenou
11:55 – 12:20	Invited speaker 1 *Pathogen Genomics Initiative (Africa PGI)* – Dr Gerald Mboowa		Dr Bright Adu
12:20 – 13:10	Lunch Break/poster viewing		All
13:10 – 14:25	**Parallel session 1A** *Viral infections of public health importance* *(5 speakers)*	**Parallel session 1B** *Drug discovery* *(5 speakers)*	Dr Stephen Ayisi Addo/Dr George Kyei (1A) Prof Regina Appiah-Opong/Dr Samuel Adjei (1B)
14:25 – 15:40	**Parallel session 2A** *Bacterial infections of public health importance* *(5 speakers)*	**Parallel session 2B** *Malaria and other protozoan Infections* *(5 speakers)*	Dr Yaw Adusi-Poku/ Prof. Eric Sampane-Donkor (2A) Dr Keziah Malm/Dr Benjamin Abuaku (2B)
15:40 – 16:00	Poster viewing		All
	Plenary session 2 (Epidemic and pandemic diseases and interventions)		
16:00 – 16:30	Invited speaker 2 *Evolution and spread of multi-drug resistant Tuberculosis.* **Prof. Sebastien Gagneux** *(virtual presentation)*		Dr Gloria Ivy Mensah/ Dr Adwoa Asante-Poku
16:30 – 17:15	Plenary speakers *1. Virus research and policy at Noguchi* - **Dr John Odoom** *2. The fight against TB and Buruli Ulcer in Ghana; the role of NMIMR* – **Dr Anthony Ablordey** *3. From bench to policy: the Rotavirus vaccine story* – **Prof. George Armah**		Prof Collins Ahorlu/ Dr Evelyn Bonney
End of Day 1			

Day 2			
08:30 – 08:50	Arrival and participant registration		
	Plenary session 3 (Vector-Borne Diseases)		
09:00 – 09:30	Keynote address 2 *NTD research landscape and challenges with elimination.* **Prof John Gyapong**		Prof Daniel Boakye/ Prof Lars Hviid
9:30 – 10:15	Plenary speakers *1. The emerging threat of Aedes-borne arboviral diseases in Africa: the role of research and capacity building in prevention and containment of outbreaks* – **Dr Samuel Dadzie** *2. Neglected Tropical Diseases research and policy at the NMIMR* – **Prof Dziedzom de Souza** *3. Malaria Research and Policy: the contributions of NMIMR* – **Dr Benjamin Abuaku**		Prof. Daniel Boakye/ Prof. Lars Hviid
10:15 – 10:45	Poster presentations (10) - 2 minutes each		Dr Beverly Egyir
10:45 - 11:00	Snack break/poster viewing		
11:00 – 12:15	**Parallel session 3A** *Neglected Tropical diseases research*	**Parallel session 3B** *Climate Change and disease /Health systems research*	Dr Irene Ayi/ Prof John Gyapong (3A) Dr Patricia Akweongo/Dr Daniel Arhinful (3B)
12:15 – 12:45 12:45 – 13:15	**Plenary session 4 (Non-communicable diseases)** **Main speaker:** *Trypanosomiasis, Apolipoprotein L1 variants and Kidney Failure* - **Prof Dwomoa Adu** **Other speakers** *School-based intervention to reduce cardiovascular disease risk factors among students: a cluster randomized controlled trial* – **Mr John Amoah** *Co-prevalence of tuberculosis and diabetes in Greater Accra Region: epidemiology, tuberculosis clinical presentation and treatment outcomes* – **Ms Monica B. Jones** *Network Pharmacology of Chlorogenic Acid with Special Reference to Anti-Cancer Property* – **Mr Nathaniel A. Kotei**		Prof. Michael Wilson/Dr Irene Donkor
13:15 – 14:00	Lunch Break/poster viewing		All

Plenary session 5 (AMED/NMIMR Joint Research Project Symposium)		
14:00 – 14:10	Introductions and overview of AMED/ NMIMR Joint Research Project	Prof. George Armah
14:10 – 14:20	**Viral Haemorrhagic Fevers** *Surveillance for Dengue and Chikungunya viruses in selected health facilities in Ghana, 2018 – 2020* - **Dr Kofi Bonney**	
14:20 – 14:30	**Antimicrobial Resistance** *Molecular epidemiology of Carbapenemase-producing* **Escherichia coli** *sequence type ST410 in Ghana* - **Dr Anthony Ablordey**	
14:30 – 14:40	**Viral Diarrhoea** *Temporal trends and Norovirus genotype distribution in the paediatric population of Ghana* - **Dr Belinda Lartey**	
14:40 – 14:50	**Entomology** *The entomological monitoring of Aedes-borne arboviruses in some selected sites in Ghana* - **Dr Samuel Dadzie**	
14:50 – 15:00	Discussion and questions	
15:00 – 15:10	**JICA Presentation:** *For the future of Noguchi, JICA supports QMS.* **Shigeyoshi Harada,** *Chief Adviser, JICA Noguchi QMS Project*	Dr Charles Quaye
15:15-16:55	**Plenary session 6: The Debate** *Motion: The global race against epidemics and pandemics is a hopeless case.* *Speaking for*: **Dr Isaac Otchere/Dr Peter Quashie** *Speaking against*: **Dr Ivy Asante/Dr Paul Owusu Donkor**	**Judges** Dr Justice Yankson Prof David Ofori-Adjei Prof William Ampofo
16:55 – 17:30	Awards & Recognition, Evaluation, Closing Ceremony	Dr Beverly Egyir/Dr Kofi Bonney (MCs)

ABSTRACTS

PLENARY SESSIONS

1. WEST AFRICAN REGIONAL PUBLIC HEALTH RESEARCH AGENDA IN THE CONTEXT OF PANDEMIC PREPAREDNESS AND RESPONSE

Abdourahmane Sow[1], Issakia Sombie[1]

West African Health Organisation, Public Health & Research Development

The West African sub-region has been ravaged, in the very recent past, with epidemics of diseases of great public health concern that have negatively impacted growth in all sectors with a reversal of gains made by governments in the provision of services for their populations, particularly in the health sector. These epidemics revealed the limitations and deficiencies of the health system, they exposed inadequacies in epidemiological surveillance, outbreak response and public health research capacity. Research and development are the foundation for the development or changing of health policy and planning for national and regional health, through the provision of quality evidence-based data analysis to support trends and direction for intervention. However, we are facing some challenges such as i) Acute limited funding ii) Limited trained human resources and iii) Lack of national research policy and agenda. It is in this context that the West African Health Organization supports evidence-based decision-making that will contribute to improving the quality of health and better preparedness and response strategies in West Africa. The regional objectives are to i) Develop operational public health research technical capacity to enhance emerging and remerging infectious diseases detection and surveillance ii) Develop regional capacity in research in Antimicrobial Resistance iii) Support the establishment of a regional research agenda and database and iv) build capacity the national and regional ethic committees to support clinical research during epidemics.

2. EMERGING HEALTH THREATS AND THE CONTRIBUTION OF NMIMR'S RESEARCH TO HEALTH SYSTEMS AND POLICY.

Prof William Ampofo

Department of Virology, Noguchi Memorial Institute for Medical Research, University of Ghana, Legon, Ghana

The important contribution of research institutions such as the NMIMR in the response towards public health threats and optimal functioning of health systems has been made very clear by the COVID-19 pandemic. For routine health systems operations, determination of excess morbidity and mortality is reliant on systematic surveillance of both communicable and non-communicable diseases. Research that defines case definitions and parameters of active and passive surveillance are fundamental policy determinations that shape health monitoring. New generation research tools now play a critical role in defining emerging pathogens by genomic characterization, human susceptibility, drug resistance /vaccine effectiveness profiling. The contribution by the NMIMR and other research institutions in partnership with national agencies towards improved disease surveillance and response in Ghana will be discussed. Noting the unpredictable emergence of pathogens, continuous strengthening of relevant health research partnerships must be maintained.

3. EVOLUTION AND SPREAD OF MULTI-DRUG RESISTANT TUBERCULOSIS

Prof Sebastien Gagneux

Swiss Tropical and Public Health Institute, University of Basel, Switzerland

Antimicrobial resistance (AMR) is an increasing problem for global health and the economy. One of the most frequent causes of human death due to AMR is multidrug-resistant tuberculosis (MDR-TB). While the patient factors leading to MDR-TB are well understood, the bacterial features promoting AMR in human tuberculosis remain unclear. Based on our recent studies in the country of Georgia and South Africa, I will present recent data on the role of compensatory evolution and other forms of epistatic interactions between bacterial genetic features in the emergence and spread of MDR-TB in these high-burden settings. I will discuss the implications of these findings for our understanding of the AMR pandemic in TB as well as other bacterial pathogens.

4. VIRAL RESEARCH AND POLICY AT NOGUCHI

Dr John Odoom

Department of Virology, Noguchi Memorial Institute for Medical Research, University of Ghana, Legon, Ghana

Virus research started at NMIMR in the early 1980s when HIV was first isolated and characterized in Ghana followed by polio, measles and yellow fever work in the 1990s. Noguchi conducted research to determine the efficacy of the vaccination schedule for polio immunization in Ghana at Ashaiman from 1990-1991. Two other studies were also conducted at Asamankese from 1993-1995; a comparison of the AIK-C measles vaccine in infants at 6 months with the Schwarz vaccine at 9 months and the assessment of antibody responses of yellow fever vaccination (D17) in Ghanaian infants.

Current research has focused on infectious diseases like SARS-CoV-2, Marburg, Monkeypox, Influenza, HIV AIDS polio and wastewater surveillance. In 2020, the first SARS-CoV-2 genomic sequencing to identify imported and circulating variants in the country was carried out at the NMIMR and the Institute continues to play a leading role in the identification of existing and emerging variants in the population.

Research on influenza has focused on sustaining and improving surveillance of human and animal influenza and other respiratory pathogens. Monitoring and characterizing human influenza viruses to determine the disease burden, seasonality and prevalence in Ghana. The platform has been used to monitor SARS-CoV-2 introduction into the country by travellers as well as to enhance strategies to protect and improve health security in Ghana.

The wastewater surveillance research monitors the silent circulation of poliovirus and SARS-CoV-2 from asymptomatic infected individuals that shed the viruses into our sewage/ wastewater systems as an early warning for public health decision-making. Through this research, silent circulation of vaccine-derived poliovirus type 2 has been found which informed policymakers to conduct mass immunization of children under 5 years in 2019 and 2022,

Monkeypox and Marburg virus research characterizes the different strains to determine the origin of the virus and HIV AIDS research focusing on the identification of novel reactivation agents, towards building translational HIV cure research is ongoing.

5. THE FIGHT AGAINST TUBERCULOSIS AND BURULI ULCER IN GHANA: THE ROLE OF THE NOGUCHI MEMORIAL INSTITUTE FOR MEDICAL RESEARCH.

Dr Anthony Ablordey

Department of Bacteriology, Noguchi Memorial Institute for Medical Research, University of Ghana, Legon, Ghana

Tuberculosis (TB) and Buruli ulcer (BU) are important mycobacterial diseases of public health importance. TB is caused by members of the *Mycobacterium tuberculosis* complex which infects a third of the world's population and is responsible for about 1.5 million deaths annually. The global burden of BU, a necrotizing skin disease caused by *Mycobacterium ulcerans* is unknown. BU is reported in 33 countries worldwide with the highest burden in the west African countries of Ghana, Benin and the Ivory Coast. Although BU is associated with low mortality, it often leaves victims with permanent deformities.

The World Health Organization (WHO) recommend early case detection and antibiotic treatment for the control of TB and BU. However, there are several challenges to this strategy. The Noguchi Memorial Institute for Medical Research (NMIMR) in collaboration with the National TB and BU Programmes and other partners continue to make significant contributions to the fight against these diseases by conducting studies to improve existing laboratory diagnosis as well as develop new rapid diagnostic tests to facilitate early case detection. The NMIMR is part of the WHO-sponsored network of laboratories for PCR-based diagnosis of BU.

The Institute has contributed to improving understanding of TB and BU epidemiology through the development and implementation of various molecular biology techniques that have allowed among others, the determination of the molecular diversity of the different circulating strains of these pathogens in Ghana, defining the molecular basis of drug resistance within the *Mycobacterium tuberculosis* complex and generating hypothesis about the mode of transmission of BU disease.

The NMIMR has also undertaken studies to identify factors affecting early case detection and treatment-seeking behaviour. These findings have enabled the implementation of appropriate social interventions in affected communities to improve early case detection and treatment.

Details of the challenges militating against the control of TB and BU as well as contributions made by the NMIMR in reducing the burden of these diseases in Ghana are discussed.

6. FROM BENCH TO POLICY: THE ROTAVIRUS VACCINE STORY

Prof. George Enyimah Armah

Department of Electron Microscopy & Histopathology, Noguchi Memorial Institute for Medical Research, University of Ghana, Legon, Ghana

Diarrhoeal disease is a major cause of morbidity and is responsible for a third of all under-five deaths globally. More than half of these diarrhoea deaths in children can be attributed to rotaviruses. Vaccines have long been identified as the only cause of intervention to help ameliorate this high burden. Historically, it has taken between 10 and 15 years for vaccines to reach the developing world after a global and regional recommendation and introduction introduced in the developed world. The influencing factors amongst others include providing evidence-based information on the epidemiology and burden of the disease, the available interventions and using this evidence-based data to influence and drive public health and political priorities. The Noguchi experience and lessons learned

from the research to generate the evidence, using the evidence to inform stakeholders and to drive the public health and political priority for rotavirus vaccine introduction in Ghana and other African countries are discussed. The impact of these efforts, after a decade of vaccine introduction, is also shared and discussed.

7. NTD RESEARCH LANDSCAPE AND CHALLENGES WITH ELIMINATION

Prof John Owusu Gyapong

Centre for Neglected Tropical Disease, Institute of Health Research, University of Health & Allied Sciences, Ho

Neglected Tropical Diseases are a broad spectrum of diseases that result in chronic, disabling, and disfiguring conditions which have not received enough attention in the past. They are usually diseases of neglected populations who are vulnerable to multiple infections and are strongly associated with poverty in tropical and subtropical environments, especially among the rural poor and some disadvantaged urban populations. They affect child development, pregnancy outcome, and productivity. About 1.5 billion people are infected with NTDs worldwide, with Africa accounting for nearly 40%.

With an estimated 51% of the population in sub-Saharan Africa (SSA) living on less than US$1.25 per day, SSA represents the world's largest concentration of poverty and NTDs. More than 500 million people in SSA are affected by four of the most common NTDs including lymphatic filariasis (LF), onchocerciasis, soil-transmitted helminth (STH) infections and schistosomiasis. This is worsened by the very conducive environmental factors such as temperature and humidity necessary for the development of the disease pathogens and the vectors that transmit them, coupled with poverty, unsafe water, poor sanitation, and inadequate housing which perpetuate the transmission cycle.

The level of knowledge generated through research for many of these diseases is currently just adequate for programme development but a lot more research is required for elimination. To achieve elimination the disease should be easily diagnosed or recognised, there should not be a non-human reservoir, it must be geographically restricted, and there should be effective interventions such as vaccines or drugs and other transmission-disrupting alternatives.

This presentation reviews the progress made so far for NTDs locally, regionally, and globally and looks at how the WHO roadmap for the control of NTDS is contributing to the elimination of NTDs. In addition, there will be a discussion of the policy options to ensure more effective implementation. Finally, it will discuss the potential role of academic and research institutions in the global fight against NTDs.

8. THE EMERGING THREAT OF AEDES-BORNE ARBOVIRAL DISEASES IN AFRICA: THE ROLE OF RESEARCH AND CAPACITY BUILDING IN PREVENTION AND CONTAINMENT OF OUTBREAKS

Dr Samuel Kweku Dadzie

Department of Parasitology, Noguchi Memorial Institute for Medical Research, University of Ghana, Legon, Ghana

Africa has recently been the focus of attention for some emerging and reemerging *Aedes*-borne arboviral diseases that pose a serious public health concern and economic burden to many of these countries. Outbreaks of some of these arboviruses such as Dengue,

Chikungunya and Zika have occurred in some countries in Africa and recently in West Africa. Various research findings and hypotheses have postulated several reasons why there has been a sudden increase in Dengue, Chikungunya and Zika cases in African countries, especially in West Africa. This plenary speech will give an update on Dengue, Chikungunya and Zika in Africa and provide insight into research findings as well as discuss the capacity-building efforts within the West Africa sub-region within the context of recent outbreaks and prevention of arboviral diseases.

9. NEGLECTED TROPICAL DISEASES RESEARCH AND POLICY AT THE NMIMR

Prof Dziedzom de Souza

Department of Clinical Pathology, Noguchi Memorial Institute for Medical Research, University of Ghana, Legon, Ghana

Ghana is endemic for 14 neglected tropical diseases (NTDs). Through collaboration with the NTD programme of the Ghana Health Service and other local and international stakeholders, the Noguchi Memorial Institute for Medical Research is actively involved in studies on ten of these NTDs including Lymphatic Filariasis, Onchocerciasis, Schistosomiasis, Soil Transmitted Helminthiases, Cutaneous Leishmaniasis, Buruli ulcer, Trachoma, Yaws, Human African Trypanosomiasis, and Snakebite envenoming. These studies aim to understand the challenges linked to these diseases and improve diagnosis, control, surveillance, and care for affected patients. In this presentation, the activities of these diseases, their contribution to the control and policy implications will briefly be discussed. Two of these diseases, Buruli ulcer and lymphatic filariasis will be used as case studies. For Buruli ulcer, recent clinical validation studies of a dried-reagent-based loop-mediated isothermal amplification (DRB LAMP) assay at point-of-care facilities indicates the ability to decentralize testing to point-of-care facilities, thus reducing the current turnaround time for diagnosis at reference centres using the polymerase chain reaction (PCR) and initiating early treatment. On Lymphatic filariasis (LF) our recent studies indicate the need for novel strategies to address the current endgame challenges. Ghana is one of the first countries to initiate mass drug administration (MDA) in 2001 as part of the global programme to eliminate lymphatic filariasis. Despite 16 to 18 years of MDA some districts are yet to stop treatment. Among the challenges observed in these districts are the non-participation in MDA and inadequate treatment coverage. Novel strategies to address non-participation in MDA in one district have revealed a significant level of infection among individuals who seldom or never take part in MDA, with implications for treatment coverage and transmission. The example from LF has implications for the overall monitoring and evaluation strategy of other preventive chemotherapy NTDs, and the attainment of the NTD elimination targets not only in Ghana but other endemic countries in Africa.

10. MALARIA RESEARCH AND POLICY: THE CONTRIBUTION OF NOGUCHI MEMORIAL INSTITUTE FOR MEDICAL RESEARCH

Dr Benjamin Abuaku

Department of Epidemiology, Noguchi Memorial Institute for Medical Research, University of Ghana, Legon, Ghana

The Noguchi Memorial Institute for Medical Research (NMIMR) was set up in 1979 to conduct research into diseases of public health importance, train postgraduate students in biomedical sciences, and support the public health programmes of the Ministry of Health and the Ghana Health Service. The Institute has, over the years, contributed to malaria policy

directions of the Ministry of Health (MOH) and the World Health Organization (WHO) in the areas of epidemiology, diagnosis, treatment, and prevention. Scientists in the Institute provided insights into malaria endemicity in Ghana, showing that malaria morbidity was mainly a problem of young children, with *Plasmodium falciparum* accounting for over 90% of all malaria infections. This necessitated the introduction of interventions targeted at children < 5 years. The Institute has been at the forefront of providing information on malaria vector behaviour, ecology, and transmission as well as insecticide resistance. Regarding diagnosis, malaria rapid diagnostic tests (mRDTs) have played a major role in malaria diagnosis in Ghana since 2010, when the country started implementing the WHO's recommendation on parasitological confirmation of all suspected malaria cases. The Institute has been supporting the National Malaria Elimination Programme (NMEP) to monitor the levels of histidine-rich protein gene deletions that cause negative HRP2 mRDT results. Prompt and effective treatment of uncomplicated malaria remains one of the key interventions in Ghana because it has the advantage of preventing progression to severe illness and death. The Institute has been supporting the NMEP to monitor the therapeutic efficacy of first-line and second-line antimalarials for uncomplicated malaria in Ghana. The efficacy data feeds into WHO's global data. A molecular surveillance system has also been established to monitor the prevalence of putative markers of drug resistance to inform the NMEP. Malaria prevention studies in the Institute have focused on the identification of vaccine candidates and mass testing and treatment (MTT), among others. Impact studies have also informed policy in the country. A case in point is the evidence of non-superiority of two rounds of Indoor Residual Spraying (IRS) over one-round IRS in reducing malaria prevalence in northern Ghana using pyrethroids. Annual IRS using an organophosphate at the time was enough to significantly reduce malaria prevalence. The Institute continues, with keen interest, its contribution to malaria policy decisions in Ghana and globally.

Keywords: Malaria, Research, Policy, Noguchi

11. TRYPANOSOMIASIS, APOLIPOPROTEIN L1 VARIANTS AND KIDNEY FAILURE

Prof. Dwomoa Adu

Korle-Bu Teaching Hospital & University of Ghana Medical School

Africans and people of African descent have an increased risk of developing chronic kidney disease (CKD) as compared with Europeans. This is in part because Africans have inherited variants in the gene for Apolipoprotein L1 (APOL1). The APOL1 G1 and G2 variants developed some 10,000 years and because they provided protection against fatal sleeping sickness (Trypanosomiasis) rose to a high level in Africans and people of African descent. These very same APOL1 variants are associated with an increased risk of HIV-associated nephropathy, hypertension-attributed end-stage kidney disease, focal segmental glomerulosclerosis, HIV-associated nephropathy and other non-diabetic renal diseases.

Methods: Ethics approval was obtained locally at each clinical site. We recruited patients aged 1-74 years with CKD as well as healthy controls. *APOL1* kidney risk variants G1 (rs73885319, p.S342G and rs60910145, p.I384M) and G2 (rs71785313, p.N388_Y389del) were genotyped by custom TaqMan assays (Applied Biosystems, Foster City, CA. Association with CKD was determined using logistic regression controlling for clinical site, age and sex.

Results: We recruited 8475 subjects comprising 5628 cases of CKD and 2847 healthy controls in Ghana and Nigeria. The mean age was 46.2±16.1 years and 52.8% were female. Overall, 44.6% of participants had hypertension, 21.4% diabetes mellitus and 14.2% HIV. In the healthy controls, 27.3% had 2 APOL1 risk variants (G1G1, G2G2, G1G2) whilst in patients with CKD, this was 32.51. Adjusted odds of CKD among high-risk carriers was 1.29 (95%CI: 1.14-1.45) compared with low-risk carriers with similar results by haplotypes (G1/G1, G1/G2, G2/G2).

Conclusion: Among West Africans from Ghana and Nigeria, 28% carry high-risk *APOL1* variants for kidney disease and are at 29% higher odds of CKD than those that are low-risk carriers. Early identification of CKD and adequate treatment should reduce the risk of disease progression. Novel small-molecule inhibitors of APOL1 are being developed and may reduce the risk of CKD progression.

NC001: School-based intervention to reduce cardiovascular disease risk factors among students: a cluster randomized controlled trial

Amoah, John[1]* Asante, Kwaku P[1]

Affiliations: [1]*Kintampo Health Research Centre, Ghana Health Service, Box 200, Kintampo, Bono East*

Abstract:

Globally, cardiovascular disease (CVD) was responsible for 17.5 million deaths, accounting for 46.2% of non-communicable disease deaths. The study aimed to develop, implement and evaluate the effects of an intervention to reduce CVD risk factors among students. A cluster randomized controlled trial was conducted over six-month with pre and post-intervention evaluations. A Generalized linear mixed model (GLMM) was used to assess the effects of the intervention. The GLMM showed the intervention was significant in attaining 0.77($p<0.001$), 0.72($p<0.001$), 0.47($p<0.001$), and 0.56($p<0.001$) higher physical activity, fruits, vegetables, and protein scores respectively for the intervention group over the control. The intervention was also significant in reducing -0.23($p<0.001$), -0.90($p<0.001$), -0.38($p<0.001$), -0.63($p<0.001$), -1.63($p<0.001$), -0.61($p<0.001$) and -1.53($p=0.005$) fats and oils, carbonated drinks, sweet snacks, salted fish, weight, BMI, and diastolic BP. The odds of quitting alcohol use in the intervention group were 1.06 times more than in the control. There was no significant effect of the intervention on reducing smoking and systolic BP. The intervention was successful in reducing CVD risk factors among students in the intervention group but did not affect smoking and systolic BP. A study is recommended to be adopted in secondary schools to prevent CVDs.

Keywords: cardiovascular disease, risk factors, intervention, students

NC 002: Co-prevalence of tuberculosis and diabetes in Greater Accra Region: epidemiology, tuberculosis clinical presentation and treatment outcomes

Monica B. Jones [1], Francis Anto [1], Michael Lauzardo [2], Blanca I. Restrepo [3], Awewura Kwara [2], Margaret Lartey [4], Kwadwo A. Koram [5]

Affiliations: [1]*Department of Epidemiology and Disease Control, School of Public Health, College of Health Sciences, University of Ghana*; [2]*Department of Medicine, Division of Infectious Diseases and Global Medicines, Emerging Pathogens Institute, University of Florida, USA*; [3]*School of Public Health, University of Texas Health Science Center at Houston, Brownsville Campus, USA*; [4]*University of Ghana Medical School, College of Health Sciences, University of Ghana*; [5]*Noguchi Memorial Institute for Medical Research, College of Health Sciences, University of Ghana*

Abstract:

Evidence suggests that diabetes mellitus may worsen tuberculosis (TB) disease and treatment outcomes. However, little is known about the magnitude of TB-diabetes comorbidity (TBDM) in Ghana. Here, we characterised the epidemiology of TBDM and assessed the relationship

of diabetes with TB disease severity and treatment outcomes in the Greater Accra Region. A prospective cohort study was conducted among 204 adult pulmonary TB patients receiving 6 months of TB treatment at 14 selected health facilities in Accra. Participants were screened at TB treatment initiation (M0) and categorised as having TBDM if they self-reported it, or had glycated haemoglobin ≥6.5% or fasting plasma glucose ≥7.0mmol/L. Diabetes screening was repeated at 3-month intervals (M3 and M6). Data were obtained through interviews, physical and laboratory examinations, and medical records review until TB treatment outcomes were evaluated. The prevalence of diabetes was 22.1%, 17.1%, and 14.8% at M0, M3 and M6 respectively. Older age (>59years), a higher BMI (≥25kg/m2) and a family history of diabetes were independently associated with M0 diabetes. TBDM patients had fewer pulmonary cavities (p=0.014) and infiltrate (p=0.040) on chest radiographs than patients without diabetes (TBNDM). Overall, there were no differences in the severity of TB disease, sputum smear positivity at two months, TB treatment failure, death during TB treatment and loss of follow-up between the two groups. Our findings support recommendations that TB patients should undergo routine diabetes screening. However, further research is needed to identify factors that may influence TB-diabetes-related outcomes in this setting.

Keywords: tuberculosis, diabetes, comorbidity, clinical presentation, treatment outcomes

NC 003: Network Pharmacology of Chlorogenic Acid with Special Reference to Anti-Cancer Property

Nathaniel Amasah Kotei [1], Nicholas Awuku Offei [1,2], and Anastasia Rosebud Aikins[1,2]

Affiliations: [1]*Department of Biochemistry, Cell and Molecular Biology, University of Ghana, Legon, Accra, Ghana*; [2]*West African Centre for Cell Biology of Infectious Pathogens (WACCBIP), University of Ghana, Legon, Accra, Ghana*

Abstract:

Cancer is a complex disease with a high prevalence and mortality rate, resulting from changes in several pathways. The use of chlorogenic acid (CGA) in the treatment of cancer has received substantial reporting and demonstration in cell lines, and clinical and preclinical tests because of its exceptional and potent anti-cancerous impact. Yet the scientific rationale and metabolic mechanism of CGA on cancer remain obscure. An *in-silico* study of network pharmacology was used in this study to identify potential multi-binding targets of CGA. The network pharmacology of CGA was studied using data acquired from various databases and the Cytoscape software. The networks detail the interaction of CGA with protein targets, their pathways, and their connection to diseases, particularly cancer. Furthermore, an *in vitro* study was conducted to examine the proliferative and morphological changes induced by CGA in DU145 human prostate cancer cells to validate the *in-silico* work. The network analysis determined 7 different targets concerning cancer in humans. Core genes in this network are AKR1B1, AKR1B10, HSP90AB1, METAP2, TRPC4, ELANE, and PRKCA. The types of cancers which were identified by CGA targets include breast, prostate, pancreatic lung, gastric, liver, and colorectal cancers. AKR1B1 and AKR1B10 were shown to be involved in cancer metabolic pathways. Also, CGA binds PRKCA and HSP90AB1, causing the PI3K/Akt signalling cascade to be downregulated, resulting in apoptosis. The *in vitro* research revealed that cell viability was reduced upon treatment with CGA via MTT assay. CGA-treated DU145 cells exhibited morphological features of apoptosis. This research identified the complex components and pharmacological action of CGA, as well as some prospective cancer treatment targets. The *in vitro* results showed that CGA induces apoptosis in DU145 cells

Keywords: Chlorogenic acid, network pharmacology, bioactive

ABSTRACTS

PARALLEL SESSIONS

PARALLEL SESSION 1A: VIRAL INFECTIONS OF PUBLIC HEALTH IMPORTANCE

VR 001: Re-emergence of circulating vaccine-derived poliovirus (cVDPV2) in Ghana: a public health emergency

Gberbi Emmanuel[1*] Anane, Abraham[1] Duker Oduma, Ewurabena[1] Attiku Okyerebea, Keren[1] Anang Asantewaa, Sisi Yaa[1] Antwi Nuamah, Comfort[1] Darko, Patience[1] Mensah Yayra, Jude[1] Nayan, Josephine[1] Odame, Deborah[1] Boakye Dufie, Jessica[1] Agbotse Deladem, Gayheart[1] Boa-Amponsem Nyantakyiwa, Edith[1] Ansong Bimpong, Sharon[1] Obodai Evangeline[1] Odoom Kofi, John[1]

Affiliations: [1]*Noguchi Memorial Institute for Medical Research, University of Ghana*

Abstract:

Low vaccination coverage over long periods in any part of the world coupled with poor sanitation results in the emergence of vaccine-derived poliovirus. Here we describe the re-emergence of circulating vaccine-derived poliovirus type 2 (cVDPV2), and factors contributing to the spread of the virus in Ghana. Wastewater samples collected on April 14, 2022, from two sites in the Northern region and received in the polio laboratory were processed for virus isolation using RD and L20B cell lines. The isolated virus was amplified with RT-PCR using degenerate primers and the VP1 region was sequenced. Sequenced data obtained were classified and an outbreak investigation was followed. A total of 632 acute flaccid paralysis cases from patients and 132 wastewater samples were processed between January and August 2022. Two AFP cases, three healthy children and ten wastewater samples were identified as VDPV2 and classified as cVDPV2. Isolates from wastewater shared 99.8% nucleotide identity and were linked to a 2021 cVDPV2 sequence from Nigeria of the emergence group (NIE-ZAS-1). Reported cVDPV2 from wastewater was from Northern, Ashanti, Bono East and Greater Accra regions while cVDPV2 from patients was seen in North-East and Savanna regions. Circulating vaccine-derived poliovirus is endemic in Ghana and has become a threat to the polio eradication initiative with a driving force of low quality and delayed polio outbreak response. Quality vaccination campaigns using the new tool – type 2 novel OPV (nOPV2) will help circumvent the challenge and provide herd immunity to the country.

Keywords: Poliovirus, Wastewater, cVDPV2, AFP, RT-PCR

VR 002: Genetic characteristics and phylogenetic analysis of avian influenza viruses detected during animal surveillance activities in Ghana in 2021

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Abstract:

Sporadic outbreaks of the highly pathogenic avian influenza A H5N1 have been recorded among poultry in Ghana since 2005 with an ongoing outbreak which started in 2021 yet to subside. These sporadic outbreaks in animals are a concern for human health. In 2021, the National Influenza Centre (NIC) in collaboration with the Ghana Armed Forces (GAF) and the Veterinary Services Directorate (VSD) carried out a countrywide animal surveillance exercise for avian influenza. We present findings from this activity. Tracheal and cloacal swabs from healthy, sick, and dead poultry were collected from live markets, poultry farms, and backyard poultry holdings. We also collected water and feed from farms as well as bird faeces from Ramsar sites. The presence of influenza viruses was determined using specific molecular assays. Specimens found positive for Influenza A viruses were sequenced by Oxford nanopore technology methods. We tested 2541 tracheal and cloacal samples,145 environmental samples (feed, water, faeces) as well as 39 feather samples. We detected 88 avian influenza subtype H5N1 strains and 1 subtype H7 strain. However, the environmental and feather samples tested negative for the influenza virus. Genetic analysis of H5N1 samples confirmed they possessed the characteristic REKRRKR/GLF in the haemagglutinin (HA) at the cleavage site. Mammalian adaptive motifs were also identified in HA. BLAST analyses combined with phylogenetic analysis showed close to 98% similarity to 2015 avian influenza H5N1 viruses from Nigeria, suggesting the probability of importation. These findings highlight the importance of continuous genomic surveillance for these zoonotic pathogens in Ghana.

Keywords: Avian influenza, Ghana, surveillance

VR 003: Timely detection of an outbreak of Influenza during the midst of COVID-19 in Ghana

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Abstract:

The Ghana Health Service (GHS) through the National Influenza Centre (NIC) at the Noguchi Memorial Institute for Medical Research (NMIMR) monitors influenza activity via various sentinel surveillance sites. Here, we describe the detection of an outbreak of influenza A (H3N2) in Ghana and present recent surveillance data from January to August 2022. Respiratory samples from both sentinel and non-sentinel sites across the country are daily analysed for influenza and SARS-CoV-2 using the US CDC multiplex assay in real-time PCRs at the NIC. Data is shared weekly with the GHS, submitting institutions, and partners. A

rapid increase in cases of influenza A H3N2 was observed from epi-week 19 (120 cases) and peaked at epi-week 20 (251 cases). Individuals between the ages of 10 to 20 years recorded the highest number of cases (30%, 451/1489). This age group comprises high school students in boarding facilities in the Eastern and Greater Accra Regions of Ghana. Eventually, cases were recorded in all sixteen regions in the country with the Eastern and Greater Accra regions being the most severely affected, with no recorded fatalities. From January 05 to August 24, 2022, a total of 5921 samples were processed with 17.8% (1054/5921) positive for influenza A out of which 1053 were H3N2 and 0.4% (25/5921) positive for influenza B. Our surveillance system provided timely data on the AH3N2 outbreak which guided important public health responses. Investments in strengthening the national respiratory pathogen surveillance platform provided value for money for monitoring respiratory pathogens.

Keywords: influenza, surveillance, outbreak, COVID-19, respiratory pathogens

VR 004: Genomic surveillance of SARS-CoV-2 in Ghana: leveraging an integrated national influenza and SARS-CoV-2 platform

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Abstract:

We leveraged an existing influenza Surveillance Network to integrate SARS-CoV-2 surveillance and to provide insights into SARS-CoV-2 transmission and genomics in Ghana and across West Africa. We sequenced SARS-CoV-2 positive samples from this integrated system, along with a subset of returning travellers from September 2020 to November 2021 using Oxford Nanopore Technology and the ARTIC tiled amplicon method. We observed the co-circulation of influenza and SARS-CoV-2 during our study period. Overall SARS-CoV-2 caused 14.1% of influenza-like illness cases and influenza 8.6%. We detected four waves of SARS-CoV-2 infections in Ghana, each driven by a different variant. The. B.1 and B.1.1. were the most prevalent lineages in wave one, while the B.1.1.7/Alpha variant was responsible for the second wave. The third wave was driven by Delta and Delta+ variants. This study was the first to detect the Omicron variants among travellers which subsequently spread to cause the 4th wave of infections in Ghana. Our data suggest that B.1.1.318 (which contains the E484K mutation shown to impact antibody recognition) has a high cumulative prevalence rate in several neighbouring West African countries, suggesting potential regional circulation. Our study demonstrates the value of repurposing existing influenza surveillance platforms for SARS-CoV-2. We highlight the continued circulation of Influenza during 2020 and 2021 and that it remained a major cause of severe acute respiratory illness, especially

in younger individuals. We were able to detect importations of SARS-CoV-2 variants into Ghana including those which did and did not lead to onward community transmission.

Keywords: SARS-CoV-2, Ghana, variants, influenza

VR 005: Modeling SARS-CoV-2 antibody seroprevalence and its determinants in Ghana: a nationwide cross-sectional survey

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Abstract:

Ghana announced its first case of COVID-19 on March 12, 2020, after which a nationwide age-stratified cross-sectional study was conducted from February to December 2021 to assess the understand the extent of COVID-19 transmission. Study sites were selected based on disease burden stratification according to real-time disease reports gathered. Naso/oropharyngeal swabs and venous blood were collected from 5898 participants. Swabs were tested using quantitative reverse-transcription Polymerase Chain Reaction (qRT-PCR), and serum was tested using the WANTAI ELISA total IgG/IgM assay. The overall seroprevalence was 67.9%, with the highest rate in Greater Accra (76.0%). Seroprevalence was lowest in young children, and highest in teens and young adults. (5-9 years, 52.2%; 10-14, 63.9%; 15-19, 72.6%; 30-39, 72.5%). A total of 5389 participants were unvaccinated, and 65% were seropositive in this group. Of the 4,003 seropositive individuals, 69.2% were asymptomatic and 26.4% did not adhere to infection prevention guidelines. Of the 2219 samples tested using qRT-PCR, 6.9% were positive for the E gene only, 58.7% were positive for the N gene only, and 9.6% were positive for both. Confirmatory testing with qRT-PCR showed an overall infection rate of 7.6%. (29.7% E gene only, 1.2% N gene only, and 42% E+N genes). Results indicate that more than half of the population has been exposed to the SARS-CoV-2 virus since it was first reported, putting Ghana in the medium to high COVID-19 burden category. The infection rate was low compared to seroprevalence during the sampling period.

Keywords: seroprevalence, COVID-19, qRT-PCR, asymptomatic

PARALLEL SESSION 1B: DRUG DISCOVERY

DD 001: Antibacterial activity of eight (8) medicinal plants on multi-drug resistant bacteria isolates from lymphatic filariasis patients

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Abstract:

Lymphatic filariasis (LF) is associated with the poor living in the tropics of the world. LF patients tend to develop acute dermatolymphangioadenitis (ADLA), which puts them at risk of developing bacterial infections. Secondary bacterial infections associated with antimicrobial resistance results in increased morbidity. This has necessitated an urgent search for potential antimicrobial agents. In vitro antimicrobial activity of *Alchornea cordifolia* (AC), *Combretum glutinosum* (CG), *Holarrhena floribunda* (HF), *Rauwolfia vomitoria* (RV), *Syzygium aromaticum* (SA), *Terminalia macroptera* (TM), *Vismia guianensis* (VG) and *Voacanga africana* (VA) against multi-drug resistant bacteria; methicillin-resistant *Staphylococcus aureus*, *Escherichia coli and Pseudomonas aeruginosa* isolate were performed using standards for agar well diffusion and microdilution with concentrations ranging between 0.5-64.0 mg/mL. The extracts inhibited the pathogens with zones of inhibition ranging between 6.00+00 – 28.33+0.33 mm. AC, HF, SA and RV exhibited lower MIC (below 1.0 mg/mL) against some of the isolates but were not bactericidal as compared to CG, TM and VG. Fourier-transform infrared and Gas chromatography results showed the presence of chemical groups and compounds like carboxylic acid, alkene, 1,2,3-benzenetriol and stigmasterol. These compounds might act in synergy to exhibit the antibacterial activity of the plants. Among the plants used, methicillin-resistant *Staphylococcus aureus* and *P. aeruginosa* were best inhibited by CG. This study corroborates the antibacterial activity of the medicinal plants tested and their potential in fighting secondary bacterial infections. The extracts of plant parts of TM and CG exhibited the highest antibacterial activity.

Keywords: Lymphatic filariasis, Antimicrobial-resistance, Antibacterial activity, Acute-dermatolymphangioadenitis

DD 002: Inhibition of HIV replication in vitro by three local herbal extracts

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Abstract:

Infection with the human immunodeficiency virus (HIV) continues to threaten global public health. Although antiretroviral therapy (ART) has reduced morbidity and mortality, it does not provide a cure. The main obstacle to an HIV cure is the persistence of the provirus in resting CD4+ T cells. HIV cure strategies being investigated include using novel compounds, medicinal plants, or herbal extracts that can reactivate latent HIV, inhibit virus replication and/or block and lock the latent virus. We investigated the ability of African herbal extracts to inhibit HIV replication or reactivate the virus from latency. We used U87 cell lines stably transfected with CD4 and CXCR4 (U87CD4CXCR4) for screening the extracts. First, the cytotoxicity level of different concentrations of the extracts was determined using the 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT) assay. The cells were then infected with the full-length HIV NL4-3-luciferase in the presence of the extracts using dimethylsulphoxide (DMSO) and Zidovudine as negative and positive controls respectively. The extracts were tested in triplicates and HIV replication was determined by the average relative luciferase activity (RLA). The extracts were not toxic to the cells at 30ug/ml. At the same concentration, three extracts (JJNC006SB, JJNC057SB, and JJNC064SB) showed average RLA reduction of 6, 7, and 3-fold respectively compared to DMSO. Repeated assays yielded consistent results. These preliminary results indicate the inhibitory activity of the three extracts against HIV replication. Further work will determine the mechanism of action of these extracts and assess their potential use for HIV remission

Keywords: Inhibition, Replication, HIV cure, Persistence, Provirus

DD 003: Immunomodulatory effect of Moringa oleifera and Phyllantus niruri extracts on anti-HBV cytokine production by human peripheral blood mononuclear cells

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Abstract:

Chronic hepatitis B (HBV) infection is one of the leading causes of cirrhosis and liver cancer. The currently approved drugs for the treatment of chronic HBV which include pegylated interferons and nucleoside analogues are believed to have limited efficacies and some adverse side effects. Therefore, there has been a need for the development of safer and more effective antivirals for the treatment of chronic HBV. Since ancient times, medicinal plants have been used in the treatment of numerous diseases and these plants are believed to produce complex and structurally diverse compounds, some of which have antiviral properties. This study aimed to evaluate the immunostimulatory properties of *Moringa oleifera* and *Phyllantus niruri* leaf extracts in vitro on human peripheral blood mononuclear cells (PBMCs) from chronic HBV carriers and HBV-negative controls. Phytochemical analysis showed that both aqueous and ethanol leaf extracts of the two plants predominantly contained tannins, sterols, alkaloids, flavonoids, saponins, terpenoids and polyphenols.

Using the MTT assay, we showed that aqueous extracts were not cytotoxic and increased cell metabolic activity whiles the ethanol extracts decreased cell metabolic activity. The extracts were found to induce the release of TNF-α, IL-1β, IL-10, IL-6, IFN-γ and CCL5/RANTES from PBMCs. *M. oleifera* and *P. niruri* leaf extracts were found to be safe and also stimulate the release of HBV replicating-limiting cytokines and therefore could aid in the treatment of chronic HBV.

Keywords: cytokines, *Moringa oleifera*, *Phyllantus niruri*, immunostimulatory

DD 004: Molecular docking and molecular dynamics simulation studies identifies potential neuropilin 1 inhibitors against the spike protein of SARS-CoV-2

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Abstract:

The SARS-CoV-2 genome encodes notable proteins including spike, envelope, membrane and nucleocapsid. The SARS-CoV-2 spike protein is activated by proteases before it binds to angiotensin-converting enzyme 2 (ACE2). Neuropilin 1 (NRP 1) binds to the spike protein as a virus entry receptor for SARS-CoV-2. This study aims at identifying putative inhibitors of the spike-NRP1 interaction with the potential to ameliorate viral infectivity and disease severity. A library of 1933 prefiltered compounds was virtually screened against NRP 1 and the compounds were characterized to determine novel insights into the binding mechanisms. The spike protein interacts with Tyr297, Trp301, Thr316, Asp320, Ser346, Thr349, and Tyr353 for the virion to gain entry into the cell of the host. A total of 84 compounds interacted with at least one of the critical residues via hydrogen bonding. The antiviral activity and mechanisms of action were elucidated using an Open Bayesian machine learning system. The top complexes of the top hits were subjected to 200 ns molecular dynamics simulations and Molecular Mechanics-Poisson Boltzmann Surface Area (MM-PBSA) to study the conformational dynamics, stability of the complexes and the energy contribution per residue of the protein. Further biocomputing and in vitro approaches are being explored to understand how the compounds inhibit NRP 1-spike protein viral entry mechanisms.

Keywords: Neuropilin 1, spike protein molecular docking

DD 005: Evaluation of anti-inflammatory, antimicrobial and antioxidant activities as markers for the wound healing potential of Monodora myristica

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Abstract:

Wound healing is an essential process that when delayed, puts a lot of economic and financial strain on the patient. This study investigated the anti-inflammatory, antimicrobial and antioxidant activities of the methanol, ethyl acetate and petroleum ether extract of the

leaves and stem bark of *Monodora myristica* as markers for the wound healing potential of the plant. Preliminary phytochemical screening was done to identify the secondary metabolites present in the leaves and stem bark of *M. myristica*. Anti-inflammatory activity using the carrageenan-induced foot oedema model, antimicrobial activity using agar well diffusion and micro broth dilution, and antioxidant assays were performed. The extracts produced varying degrees of anti-inflammatory effects with the petroleum ether extract of the bark showing significant dose-dependent reduction ($p<0.0001$) in oedema with the highest percentage inhibition of 82.11 ± 10.08% at 300 mg/kg body weight. The methanolic extract of the stem bark demonstrated the highest free radical scavenging activity (FRSA) with a percentage inhibition of 90.34% at 0.016 µg/ml. Both plant parts exhibited activity against *Staphylococcus aureus* and *Escherichia coli* with MIC of 32 mg/ml and 128 mg/ml, respectively. The leaves and stem bark of *M. myristica* showed significant anti-inflammatory, antioxidant and antimicrobial activities. These indicators provide scientific validation for the folkloric use of *M. myristica* as a wound-healing plant.

Keywords: Wound healing; *Monodora myristica*; anti-inflammatory; antimicrobial

PARALLEL SESSION 2A: BACTERIAL INFECTIONS OF PUBLIC HEALTH IMPORTANCE

BA 001: Identification of blaCTX-M gene among Extended Spectrum Beta-Lactamase positive Klebsiella pneumoniae and Escherichia coli isolated from surgical site infections in Accra, Ghana

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Abstract:

Extended Spectrum Beta-Lactamase (ESBL) enzyme is associated with multi-drug resistance in Gram-negatives such as *Escherichia coli* and *Klebsiella pneumoniae*. The enzyme is encoded by several genes, for example, blaCTX-M, blaTEM, and blaSHV. This study investigated the prevalence of the ESBL phenotypes and genes among *E. coli* and *K. pneumoniae* recovered from surgical site infections. Isolates were characterized by Matrix Assisted Laser Desorption Ionization Time of Flight Mass Spectrometry (MALDIToFMS), antimicrobial susceptibility testing (AST) and multiplex Polymerase Chain Reaction (PCR) amplification of ESBL genes (blaSHV, blaTEM and blaCTX-M). A total of 452 patients were enrolled in this study. The *E. coli* and *K. pneumoniae* isolates recovered were resistant to trimethoprim/sulfamethoxazole (8%), tetracycline (85%), cefuroxime (68%), cefotaxime (67%), ciprofloxacin (62%), but susceptible to amikacin (85%) and meropenem (94%). ESBL phenotypes and genes were detected in *K. pneumoniae* (78%) and *E. coli* (59%); these were resistant to cefuroxime (98%), cefotaxime (97%), tetracycline (92%) and trimethoprim/sulfamethoxazole (92%) but susceptible to meropenem (96%) and amikacin (94%). blaCTX-M gene was detected in 95% *K. pneumoniae* and 66% *E. coli*. In 92% of the *K. pneumoniae* isolates, the blaSHV gene was detected and in 77% the blaTEM gene. The majority of ESBL-positive isolates were found harbouring blaCTX-M and blaSHV genes. Detection of the blaCTX-M and blaSHV genes could be beneficial in guiding antimicrobial therapy.

Keywords: ESBL, AST, Bls, MALDIToF-MS

BA 002: Antibiotic resistance profiles of bacteria species recovered from water samples for human use

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Abstract:

There is a dearth of data on antibiotic-resistant (ABR) bacteria in Ghana's drinking water. In this pilot study, we investigated the microbial quality of drinking water and the presence of different ABR bacterial species. 25 different water samples were assessed for their microbial quality using membrane filtration and serial dilutions. Isolates were investigated with MALDI-TOF-MS and Microscan/Disk diffusion antibiotic susceptibility testing. Results showed high heterotrophic counts (1.96 × 10^1 to 2.66 × 10^5 CFU/ml) in fifteen samples (60%) and the presence of coliforms (1.88 × 10^3 and 8.80 × 10^2) in two samples (8%) exceeding the WHO limit of <500 CFU/ml and zero coliforms per ml of water, respectively. Isolates (n=23) recovered include Bacillus species (n=9; 39%), Coagulase-Negative *Staphylococcus species* (CoNS) (n=5; 22%), *Pseudomonas species* (n=4; 17%), *Klebsiella pneumoniae* (n=2; 9%), *Enterobacter kobei* (n=1; 4%), *Acinetobacter baumanii* (n=1; 4%) and *Providencia rettgeri* (n=1; 4%). Enterobacterales were resistant to amoxiclav (n=2, 50%), cefotaxime (n=2, 50%) and azithromycin (n=1, 25%). *Acinetobacter baumanii* was resistant to cefotaxime, tetracycline, and trimethoprim/sulfamethoxazole. The CoNS (n=4; 80%) were resistant to clindamycin (n=4; 80%), cefoxitin (n=2; 40%), oxacillin (n=2; 40%), and amoxiclav (n=2; 40%). Multi-drug resistance (MDR) was detected among six (26%) isolates. The detection of significant levels of heterotrophic and coliform bacteria in samples examined renders them unsafe for use; continuous surveillance will help monitor pathogens for safe drinking water.

Keywords: Water; microbial quality; coliforms; antibiotic-resistant bacteria

BA003: What's in the salad? Extended Spectrum βeta- lactamase producing Escherichia coli in lettuce irrigated with various water sources in Ghana

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Abstract:

Raw vegetables including lettuce can be contaminated via irrigating sources, which could serve as a conduit for the transmission of antibiotic-resistant bacteria such as Extended Spectrum Beta-Lactamase-producing *E. coli* (ESBL-Ec). Irrigating water sources used mostly include untreated wastewater flowing into open drains and streams, which often are contaminated with human and animal wastes due to poor sanitation infrastructure. Thus, consuming lettuce contaminated with ESBL-Ec could cause severe health issues. In lettuce irrigated farms in Ghana, we aimed to determine the presence of *E. coli*, its antimicrobial susceptibility, ESBL-Ec counts and resistant genes on irrigated lettuce. It was a cross-sectional study conducted in January-May 2022, involving five major vegetable farms in Ghana. *E. coli* was found in all 25 composite lettuce samples analysed. Counts expressed in CFU/g ranged from 186 to 3,000 with the highest counts found in lettuce irrigated from open drains (1,670) and tap water using hose pipes (3,000). Among all isolates, resistance ranged between 49% to 70% for the Watch group of antibiotics, 59% for the Reserved group and 82% were multidrug resistants. Of 125 isolates, 60 (48%) were ESBL-Ec of which 5 (8%) had the blaTEM-resistant gene. Lettuce was found to be contaminated with ESBL-Ec with high levels of antibiotic resistance capable of causing difficult-to-treat urinary tract infections and acute gastroenteritis. We call on the Ghana Ministry of Food and Agriculture, Food and Drugs Authority, and other relevant stakeholders to support farmers to implement measures for improving vegetable safety.

Keywords: Ghana; *Escherichia coli*; Lettuce;nESBL;

BA 004: Genomic characterization of bacteria isolated from febrile patients in Ghana

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Abstract:

Invasive bacteria like typhoidal, non-typhoidal *Salmonella spp.* and nosocomial bacteria like *Bacillus spp.* have been implicated in severe sepsis. In this study, we used whole genome sequencing (WGS) to better understand the genomic epidemiology and antimicrobial resistance (AMR) patterns of these pathogens isolated from the blood of febrile patients in Ghana. Five bacteria were isolated from blood cultures of acutely febrile patients from selected health centres. Whole genome sequencing (WGS) was performed on the Illumina Miseq Platform. Assembled genomes were used to query PubMLST.org, the Comprehensive Antimicrobial Resistance Database (CARD) for genomic epidemiology and AMR gene information. The four *Salmonella spp.* were identified as *S. typhi* (3/4) and *S. typhimurium* (1/4). The *S. typhi* and *S. typhimurium* were determined to have sequence types (STs) ST-2 and ST-313, respectively. All Salmonella bacteria coded different virulence genes such as beaR, Mdtk and CRP. These isolates also contained multidrug resistance genes like AAC(6)-Laa (4/4), tet(B) and tetR (1/4), dfrA15 (2/4), TEM-1 (2/4), and gyrA(D87Y) (1/4), which confer resistance to aminoglycosides, tetracyclines, chloramphenicol, ß-lactams, and fluoroquinolones, respectively. The *B. cereus* strain carried a resistant gene for fosfomycin, fosB. The ST for *B. cereus* could not be determined, indicating a probable novel ST. Despite

the limited sample size of bacterial isolates recovered, this study demonstrates evidence of emerging multidrug resistance in *S. Typhi* to the current first-line antibiotics used in Ghana. This study highlights the need for prospective genomic surveillance of bacteria isolated to further improve local antibiograms.

Keywords: Whole Genome Sequencing, AMR genes

BA 005: Genomic surveillance and antimicrobial resistance of commonly isolated bacteria species in Ghana: insights from studies and related activities.

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Abstract:

Antimicrobial resistance (AMR), a silent pandemic and public health menace, continues to rise worldwide. Information obtained on AMR pathogens via antimicrobial susceptibility testing (AST) is important to inform treatment decisions and public health policies. AST data is vital but is limited when it comes to the provision of information on circulating clones and genes associated with resistance and virulence mechanisms. Whole genome sequencing (WGS) on the other hand, provides massive information and high resolution for the detection of resistance and virulence genes, and tracking of AMR clones locally, regionally and globally. WGS and AST data together with epidemiological data, therefore, enhance AMR surveillance. In total, >500 commonly isolated bacteria species originating from human clinical sources sequenced, revealed global clones carrying multiple resistance and virulence genes. This presentation will provide insights into AMR and genomic characteristics of *Klebsiella pneumoniae*, *Escherichia coli* and *Staphylococcus aureus* isolates and related AMR activities.

Keywords: Antimicrobial-resistance, Whole-genome-sequencing

PARALLEL SESSION 2B: MALARIA/OTHER PROTOZOAN INFECTIONS

MA 001: Inflammatory Cytokines as Potential Biomarkers for Early Diagnosis of Severe Malaria in Children in Ghana.

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Abstract:

Severe malaria (SM) is a fatal multi-system disease which accounted for an estimated 627,000 deaths globally in 2020. About 96% of these deaths were recorded in Sub-Saharan Africa out of which Ghana reported 1.9%. Less than 30% of children presenting with SM are diagnosed and treated promptly, resulting in increased mortality and neurologic impairments in survivors. Studies have identified cytokine profiles that differentiate the various clinical manifestations of malaria (severe and uncomplicated). However, the diagnostic capability of these cytokines in terms of cut-off values has not yet been determined. We measured and compared the plasma levels of 25 inflammatory cytokines (both pro- and anti-inflammatory) using the Human Cytokine Magnetic 25-Plex Panel in plasma samples obtained from children with SM, uncomplicated malaria (UM) and other febrile conditions. The receiver operating characteristic (ROC) curve analysis was done to determine the diagnostic value of these cytokines. Children with SM had higher levels of pro-inflammatory cytokines compared to the UM and Febrile control groups. However, levels of the anti-inflammatory cytokines did not differ significantly among the SM and UM groups. Interleukin (IL)-1beta and IL-17A showed good diagnostic abilities after the ROC curve analysis was carried out. The data suggest that levels of pro-inflammatory cytokines correlate with malaria disease severity. IL-1beta and IL-17A showed good diagnostic potentials and can be considered for incorporation into the development of rapid diagnostic test kits (RDTs) for early SM diagnosis.

Keywords: Severe malaria, Biomarker, Inflammatory Cytokines

MA 002: Effect of mass testing, treatment and tracking on malaria prevalence among children in the Pakro subdistrict of Ghana

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Abstract:

Global efforts to scale-up malaria control interventions are gaining steam. Despite several ongoing intervention strategies, malaria elimination seems far from being realistic in sub-

Saharan Africa. This is partly because asymptomatic parasite carriage, not targeted by most interventions fuel transmission, Mass testing, treatment, and tracking (MTTT) could be an alternative strategy to target asymptomatic individuals. We report the impact of implementing MTTT over 2 years on asymptomatic malaria parasitaemia. 4000 participants were targeted in seven communities in the Pakro sub-district using community registers. Trained community-based health volunteers conducted house-to-house testing using RDTs every 4 months, treating positive cases with Artemisinin-based Combination Therapy. MTTT Coverage was 78.6% in July 2020 and 85.4% in July 2021. Of those tested, asymptomatic infection with malaria parasites reduced from 29.3% (922/3145) in July 2020 to 18.7% (638/3414) in July 2021 ($p = 0.001$). Prevalence of asymptomatic parasitaemia among children under 15 years declined from 43.4% (533/1229) in July 2020 to 29.1% (377/1294) in July 2021 ($p < 0.001$) while in the above 15 groups 20.3% (389/1916) in July 2020 to 12.3% (261/2120) in July 2021 ($p < 0.001$). Implementing MTTT significantly reduced asymptomatic parasitaemia by 30.8% from July 2020 to July 2021 after adjusting for age, ITN use and axillary temperature (OR = 0.56, CI = 0.52, 0.66 $p < 0.001$). We conclude that implementing MTTT could reduce the prevalence of asymptomatic malaria parasitaemia in children under 15.

Keywords: Malaria, mass testing, treatment, and tracking

MA 003: Serum heam-hemopexin ratio alteration is associated with adverse malaria clinical outcomes in female ICR mice

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Abstract:

Malaria-induced erythrocyte lysis releases toxic heam which mediates pathogenic processes associated with disease severity. Endogenous plasma protein 'hemopexin', is well characterized for its protective role in mitigating heam toxicity. The heam-hemopexin relationship has largely been explored in studies involving time point quantification of heam or hemopexin following their injections into the host, dose modulations as well as targeted gene deletions in animal models. We, therefore, extended these findings by analysing the heam-hemopexin ratio longitudinally for malaria illness in mice. Murine malaria clinical markers were quantified in female ICR mice inoculated with Plasmodium berghei NK65 over 18 day post-infection period alongside controls. At two days intervals, serum levels of heam and hemopexin were measured. Malaria was characterized by loss of body weight and temperature, lethargy, piloerection, anaemia, icterus, dehydration, reduced activity, dyspnoea, abdominal pain, spleen, and liver damage. Longitudinal analysis of the serum heam-hemopexin ratio showed a significant change in axis as the infection progressed ($p <0.0001$). The ratio was low and steady (0.08-0.70 µM/ngmL-1) for the first 12 days post-infection and sequentially increased (3.5 ± 0.22 to 26 ± 2.1 µM/ngmL-1) until 18 days post-infection. Temperature ($r = -0.6186$; $p = 0.003$), body weight ($r = -0.4721$; $p = 0.0097$) and SHIRPA score ($r = -0.6628$; $p <0.0001$) negatively correlated with heam-hemopexin ratio

while markers of spleen and liver damage positively correlated with the ratio along the days of infection. These data highlight that normalizing the heam-hemopexin ratio throughout malaria disease may contribute to reducing adverse outcomes.

Keywords: Heam, hemopexin, malaria, ICR mice

MA 004: Countrywide monitoring of insecticide susceptibility status of Anopheles gambiae s.l. (Diptera: Culicidae): implications for malaria vector control in Ghana

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Abstract:

The use of insecticides for public health remains the main strategy for controlling disease vectors such as malaria in Ghana. The distribution and use of Insecticide Treated Nets (ITNs) as well as Indoor Residual Spraying (IRS) have been scaled up as the main malaria vector control tools in the country. The development of insecticide resistance in malaria vectors *Anopheles gambiae s.l.* remains the main challenge to the success of vector control interventions. This study generated insecticide resistance data across 30 sentinel sites in Ghana from 2015-2020. High resistance to pyrethroids and DDT was detected in all the sites with reduced susceptibility to carbamates and organophosphorus observed in all the sites over the period. *An. gambiae s.s* and *An. coluzzii* were the most dominant species of the complex living in sympatry mostly in the southern sentinel sites with variation in the frequency of L1014F and G119S mutations. The implications of the findings for malaria vector control will be discussed.

Keywords: Mosquitoes, Anopheles gambiae, Insecticide Resistance, Malaria

MA 005: Therapeutic efficacy of artemisinin-based combination therapy for uncomplicated malaria in 10 sentinel sites across Ghana

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Abstract:

Since the introduction of artemisinin-based combination therapy (ACT) in Ghana in 2005, there has been a surveillance system by the National Malaria Control Programme (NMCP) and the Noguchi Memorial Institute for Medical Research (NMIMR) to monitor the therapeutic efficacy of ACTs for the treatment of uncomplicated malaria in the country. A total of seven (8) rounds of surveillance have been conducted since 2005 using the WHO protocol for surveillance of anti-malaria drug efficacy. Data obtained over the years have guided anti-malaria medicines policy in the country. Therapeutic efficacies of currently used ACTs (artesunate-amodiaquine, artemether-lumefantrine, and dihydroartemisinin-piperaquine) have remained over 90%, supporting their continuous use in the treatment of uncomplicated malaria in the country.

Keywords: Efficacy, Artemisinin-based, Therapy, Uncomplicated Malaria, Ghana

PARALLEL SESSION 3A: NEGLECTED TROPICAL DISEASES RESEARCH

NT 001: Whole genome comparisons suggest random distribution of Mycobacterium ulcerans genotypes in a Buruli ulcer endemic region of Ghana.

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Abstract:

Efforts to control the spread of Buruli ulcer – an emerging ulcerative skin infection caused by *Mycobacterium ulcerans* - have been hampered by our poor understanding of reservoirs and transmission. To help address this issue, we compared whole genomes from 18 *clinical M. ulcerans* isolates from a 30 km2 region within the Asante Akim North District, Ashanti region, Ghana. Contrary to our expectations of finding minor DNA sequence variations among isolates representing a single *M. ulcerans* circulating genotype, we found two distinct genotypes. One genotype was closely related to isolates from neighbouring regions of Amansie West and Densu, consistent with the predicted local endemic clone, but the second genotype most closely matched *M. ulcerans* from Nigeria, suggesting another introduction of *M. ulcerans* to Ghana, perhaps from that country. Interestingly, there was no discernible spatial clustering of genotypes at the local village scale. Interviews revealed no obvious epidemiological links among BU patients who had been infected with identical *M. ulcerans* genotypes but lived in geographically separate villages. We conclude that *M. ulcerans* is spread widely across the region, with multiple genotypes present in any one area. These data give us new perspectives on the behaviour of possible reservoirs and subsequent transmission mechanisms of *M. ulcerans*. These observations also show for the first time that *M. ulcerans* can be mobilized, introduced to a new area and then spread within a population. Potential reservoirs of *M. ulcerans* thus might include humans, or perhaps *M. ulcerans*-infected animals such as livestock that move regularly between countries.

Keywords: *Mycobacterium ulcerans*, whole genome, genotypes

NT 002: Preclinical immuno-recognition and neutralization assessment of antivenom against ten African snake venoms

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Abstract:

Snakebite envenomation is a major health concern in developing countries causing significant mortality and morbidity. Over 1.2 million cases annually are caused by medically important snake species belonging to the two families Viperidae (*Echis spp.* and *Bitis spp.*) and Elapidae (*Naja spp.* and *Dendroaspis spp.*). Several antivenoms are being produced

and distributed to western sub-Saharan Africa for the treatment of envenomation with the absence of preclinical efficacy studies. The present study evaluated the preclinical efficacy of venoms from *Echis leucogaster*, *Echis ocellatus*, *Bitis arietans*, *Bitis gabonica*, *Naja haje*, *Naja melanoleuca*, *Naja nigricollis*, *Dendroaspis jamesoni*, *Dendroaspis polylepis* and *Dendroaspis viridis* against a polyvalent Snake Venom Antiserum - African IHS (lyophilised), manufactured by VINS Bioproducts Limited (Telangana, India). Our in-vitro results showed that the SVA- AIHS contains antibodies that are capable of recognizing and the binding majority of protein components representative of all eight major protein families of venoms of the snake species tested by double immunodiffusion assay and confirmed by western blot. The venom antiserum exhibited high neutralization efficacy against all the viperid and elapid snake species venoms in *in-vivo* studies and confirmed the manufacturer's recommended neutralization capacity. This is clear evidence that the VINS polyvalent SVA-AIHS batch tested has a strong neutralizing capacity and will be useful in treating envenoming by most African viperid and some elapid snake species.

Keywords: Envenomation, Antivenom, Neutralization, Western blot

NT 003: Development and characterization of Anti-Naja ashei threefinger toxins (3FTxs)-specific monoclonal antibodies and evaluation of their in vitro inhibition activity

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Abstract:

Antivenom immunotherapy is the mainstay of treatment for snakebite envenoming. Most parts of the world affected by snakebite envenoming depend on broad-spectrum poly-specific antivenoms that are known to contain a low content of case-specific efficacious immunoglobulins. Thus, advances in toxin-specific antibody production hold much promise in future therapeutic strategies of snakebite envenoming. We report anti-three-finger toxin (3FTxs) monoclonal antibodies (mAbs) developed in mice against *Naja ashei* venom. All three test mAbs (P4G6a, P6D9a, and P6D9b) were found to be Immunoglobulin G (IgG) antibodies, isotyped as IgG1. Sodium dodecyl-sulfate polyacrylamide gel electrophoresis (SDS-PAGE) analysis of the test mAbs showed two major bands at approximately 55 and 29 kDa, suggestive of immunoglobulin heavy and light chain composition, respectively. The immunoaffinity-purified test mAbs demonstrated higher binding efficacy to the target antigen compared to the negative control. Similarly, a cocktail of the test mAbs was found to induce a significantly higher inhibition ($p < 0.0001$) compared to two leading commercial brands of antivenoms on the Kenyan market, implying a higher specificity for the target antigen. Both the test mAbs and 3FTxs polyclonal antibodies induced comparable inhibition ($p = 0.90$). The inhibition induced by the 3FTxs polyclonal antibodies was significantly different from the two antivenoms ($p < 0.0001$). Our results demonstrate the prospects of developing toxin-specific monoclonal-based antivenoms for snakebite immunotherapy.

Keywords: *N. ashei*; 3Ftx toxins, mAbs, ELISA

NT 004: Potential of xenomonitoring as a tool for monitoring and evaluation of community-wide schistosomiasis mass drug administration in Ghana

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Abstract:

The role of freshwater snails as intermediate hosts in the transmission of schistosomiasis cannot be overemphasized, as such monitoring of the prevalence and distribution of schistosomes cercarial is important for indirect estimation of schistosomiasis in human or animal populations. We investigate the impact of mass drug administration on the prevalence of schistosomes in freshwater snail intermediate hosts. Freshwater snails were collected from human contact sites of 3 endemic communities along the Weija Lake in southern Ghana at different time points before and after (1, 2, 6, 12 and 18 months) community-wide praziquantel treatment. Snails were exposed to light to induce the shedding of cercariae. The prevalence of schistosomes cercariae infecting *Bulinus truncatus* and *Biomphalaria pfeifferi* was compared to that of non-schistosomes cercariae infecting the same snail species at each time point. In all, 4223 snails were collected, with the sum of *B. truncatus* and *B. pfeifferi* collected being 827, 221, 330, 458, 74, and 291 at baseline, 1, 2, 6, 12, and 18 months post-MDA, respectively. The prevalence of schistosomes cercariae was 4.11%, 3.17%, 0.60%, 5.24%, 0.00%, and 1.37%, respectively, post-MDA. On the other hand, the prevalence of non-schistosome cercariae within the same time points was 5.08%, 4.52%, 8.79%, 1.97%, 33.37%, and 9.62%, respectively. The prevalence of schistosome cercariae relatively declined, whereas that of non-schistosome cercariae increased post-MDA. Xenomonitoring can be used as a tool for the indirect evaluation of MDA campaigns in schistosomiasis-endemic communities.

Keywords: Malacology, schistosomiasis, monitoring, evaluation, prevalence

NT 005: Integrated skin diseases research detects Leishmania, Mycobacterium ulcerans, Haemophilus ducreyi, and Treponemal Pallidum Sub species pertenue in Oti Region, Ghana

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Abstract:

In 2018, we confirmed cutaneous leishmaniasis (CL) in 32% of skin ulcers screened for Leishmania infection in the Oti Region of Ghana. Cutaneous leishmaniasis (CL) is an important neglected tropical disease of the skin (skin NTD) characterized by skin lesions which may result in ulcers, scars, disability and stigma. A follow-up cross-sectional study was conducted in December 2021 in the Oti region to further investigate other possible causes of the undetermined skin ulcers. A total of 101 skin ulcer samples were obtained from 101 persons in 5 communities located in the Nkwanta South and North Districts of the region using both 3mm punch biopsy and swabs. The biopsy samples were tested for Leishmania **infection** whereas the swab samples were systematically tested for *Leishmania*, *Mycobacterium ulcerans*, *Haemophilus ducreyi*, and *Treponema Pallidum* Sub species *pertenue* using polymerase chain reaction (PCR) molecular methods. Of the 101 samples tested, 83 (82.2%) were positive for Leishmania infection, 68 (67.3%) for *Treponema pallidum* sub. Sp. Pertenue, 74 (73.3%) for *Haemophilus ducreyi* while one sample tested positive for *Mycobacterium ulcerans*. Multiple occurrences of individual skin ulcer-causing agents were also observed in the same ulcers. Detection of multiple skin ulcer-causing agents in this study calls for the development of a comprehensive guideline both for diagnosing and treating skin ulcers in the Oti Region of Ghana.

Keywords: Leishmania, *Mycobacterium ulcerans, Haemophilus ducreyi*

PARALLEL SESSION 3B: CLIMATE CHANGE AND DISEASE /HEALTH SYSTEMS: EQUALITY, EQUITY AND ACCESS

HS 001: Determinants of COVID-19 vaccine hesitancy among adults in sub-Saharan Africa

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Abstract:

There is very limited data on the extent and determinants of COVID-19 vaccine hesitancy among adults living in sub-Saharan Africa since the global roll-out of vaccines began in

2021. This multi-country survey sought to investigate COVID-19 vaccine hesitancy. We conducted surveys among adults residing in nine urban and rural areas in Burkina Faso, Ethiopia, Ghana, Nigeria, and Tanzania in late 2021. Log binomial regression models were used to identify prevalence and factors associated with vaccine hesitancy and beliefs around COVID-19 misinformation. We completed a total of 2,833 interviews. The prevalence of vaccine hesitancy varied by country (Ethiopia 29%, Burkina Faso 33%, Nigeria 34%, Ghana 42%, Tanzania 65%). People who did not think the vaccine was safe or effective, or who were unsure about it, were more likely to be vaccine-hesitant. Those who reported they did not have a trusted source of information about the vaccine (aPR: 1.25, 95% CI: 1.18,1.31) and those who thought the vaccine would not be made available to them within the year were more likely to be vaccine-hesitant. Women were more likely to be vaccine-hesitant (aPR: 1.31, 95% CI: 1.19,1.43) and believe COVID-19 falsehoods (aPR: 1.05, 95% CI: 1.02,1.08). Educational campaigns targeted at misinformation and tailored to suit each country are recommended to build trust in COVID-19 vaccines and reduce hesitancy.

Keywords: COVID-19, vaccines, hesitancy, adults, telephone survey

HS 002: Effects of Behaviour Change Communication Intervention on Utilization of Preventive Child Care Services among Selected Health Facilities in Greater Accra Region.

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Abstract:

One important means of improving the health status of children is the provision of promotive, preventive and curative health services delivered via child welfare clinics (CWCs). In Ghana, CWC attendance has been indirectly proportional to the age of children especially after one year, hampering the effort of the government to reduce child mortality and morbidity. This study employed a quasi-experimental design. Eight districts were randomly selected out of the 29 health administrative districts within the Greater Accra Region, and within each district, one health facility was selected for the study. Thus, each of the study arms (intervention and control arms) has four health facilities comprising a hospital, polyclinic, health centre and CHPS zone. Both qualitative and quantitative data were collected and analyzed. One thousand two hundred and two (1,202) nursing mothers/ caregivers with children between the ages of 6-9 months and 16 public health workers were recruited for the study. Text messages were followed by audio robocalls sent to 601 nursing mothers in the intervention arm. All the participants in the two arms were followed for nine months. For the qualitative part of the study, ten nursing mothers in each of the facilities were randomly selected for a focus group discussion (FGD) whilst two public health nurses were selected for key informant interview (KII). Again, the public health nurses in the intervention arm were trained on how to reduce some of the perceived barriers to Child Welfare Clinic attendance. It is expected that increase in CWC attendance, uptake of Measles and Rubella 2, Meningitis A and Vitamin A supplementation are anticipated. Intermediate outcomes like awareness, attitudes of caregivers and their intention to change behaviours towards CWC service uptake using appropriate communication channels were determined accordingly. Ultimately, the impact of SMS messaging followed by the audio robocall on CWC attendance and vaccination coverage beyond 6 months of birth

Keywords: Attendance, utilization, indicator, uptake, nursing mothers

HS 003: Diet and hormonal imbalance in adolescent girls: An awareness exploratory study

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Abstract:

Hormones are important regulators of a wide range of bodily processes including the female reproductive function. Adolescent girls are more sensitive to hormonal changes with an estimated prevalence of 30%. Hormones have a major impact on the mental, physical and emotional health of adolescents. Poor diet, the environment and early menarche are partly responsible for hormonal imbalance; however, the effect of knowledge, perceptions, attitudes and beliefs on the contribution of diet to a hormonal imbalance among adolescent girls is limited. This study seeks to explore adolescent girls' knowledge and perceptions about hormones and their link to diets and hormonal imbalance. An estimated 120 in-school adolescent girls aged 10 – 19 years old will be recruited to participate in the study. They will be recruited from two urban and two rural communities in Greater Accra and Northern regions using a multi-stage sampling approach. Using a convenient sampling approach, consented/parental consent/assented participants will be recruited from upper primary, junior high and senior secondary schools in the selected communities. Focus group discussions, 24-hour dietary recall, anthropometry and a clinical assay of participants' hormones and haemoglobin levels will be employed to collect the relevant data. Qualitative data will be analyzed thematically using both inductive and deductive approaches while appropriate descriptive analysis will be applied to the quantitative data. The expected output of the study includes participants' knowledge and perceptions of the importance of hormones and their relationship to diet. Also, their dietary, anthropometric, haemoglobin and hormonal (estrogen, androgen and progesterone) statuses will be assessed.

Keywords: Adolescents, girls, hormonal imbalance, diet

HS 004: Raising awareness on antimicrobial resistance: A case study of top-down and bottom-up engagements with livestock farmers' in Dormaa Districts, Ghana

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Abstract:

Ensuring the safety, health, and overall well-being of animals raised for food is both an ethical obligation and a critical component of providing safe food products. The use of antibiotics for maintaining animal health has come under scrutiny in recent years due to the rise in antibiotic resistance globally. This has contributed to the increase in disease outbreaks and antimicrobial resistance (AMR) in bacterial pathogens, which is a major global health concern for both human and animal health, with potential risks of antimicrobial-resistant bacteria being transmitted from animals into the environment and food chain. Part of the strategy to address this has been top-down public education campaigns aimed

at instructing livestock farmers on antimicrobial use (AMU) and antimicrobial resistance (AMR). The overarching objective of this study was to gain a better understanding of the public engagement activities that best elicit information on the factors that motivate rural livestock farmers towards antimicrobial use (AMU) and their level of awareness about antimicrobial resistance (AMR). We adopted a case study approach in interrogating four distinct community engagement activities (FDGs, KIIs, public engagement workshops, and media discussion shows) involving livestock farmers and animal health officials in Dormaa districts in Ghana on antimicrobial use and antimicrobial resistance. The main outcome of the study was that when farmers are empowered through dialogical public engagements through both top-down and bottom-up approaches they can disseminate information on antimicrobial use and resistance and contribute to peer learning through their networks and the media.

Keywords: antibiotic resistance, animal health, livestock

HS 005: Community views on the aetiology of Leprosy, Buruli ulcer and yaws diseases in the Atwima Mponua District, Ashanti Region, Ghana

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Abstract:

Skin NTDs including Buruli ulcer, yaws and leprosy are major causes of morbidity in sub-Sahara Africa. Although treatable, they are associated with morbidity, disability, and stigma when diagnosed late. Negative assumptions about causality can lead to the social exclusion of individuals and close relations. The objective of the study was to highlight how affected people understand and experience Skin NTDs along their illness pathways. Focus group discussions, in-depth interviews and ethnography were conducted with affected people, their caretakers, traditional healers and community members. Using MAXQDA v2020, a 3-level thematic coding system was used to analyse responses. Findings showed that respondents have appreciable knowledge of the conditions in terms of signs and symptoms, with some misconceptions about the causes, which ultimately determine the first point of call for treatment. Local (Twi) names such as 'kwata' and 'dei' were mentioned for leprosy and yaws respectively, however, no local name for BU was mentioned. Those who were aware of the condition only called it Buruli or BU. Causes were mainly linked to environmental, human, and spiritual factors and these informed which care pathway they chose. Divergent views exist on the causes and modes of transmission of skin NTDs among the study population which influence their care-seeking. Hence, the need to intensify education and awareness on the causes and modes of transmission of skin NTDs in the district.

Keywords: Leprosy, Buruli ulcer, yaws, stigma

ABSTRACTS
POSTER PRESENTATIONS

VIRAL INFECTIONS OF PUBLIC HEALTH IMPORTANCE

VR 001: Serological and genomic surveillance of SARS-CoV-2 infection among health-care workers, students and volunteers at a tertiary hospital in Ghana

Mac-Arthur Clara Owusuwah[1]* Kafintu-Kwashie Anna Aba[2] Asare Yaa Yeboaa[3] Obodai Evangeline[4] Trebi Israel Nicholas[5]

Affiliations: *[1]Department of Medical Laboratory Sciences, School of Biomedical and Allied Health Sciences, University of Ghana; [2]Department of Medical Microbiology, University of Ghana Medical School; [3]Department of Biochemistry and Biotechnology, Kwame Nkrumah University of Science and Technology; [4]Department of Virology, Noguchi Memorial Institute for Medical Research; [5]Department of Medical Laboratory Sciences, School of Biomedical and Allied Health Sciences, University of Ghana.*

Abstract:

The COVID-19 pandemic, caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), continues to be a public health problem globally. An understanding of the factors influencing SARS-CoV-2 seroconversion and host immunity, and the efficacy of protective antibodies in both vaccinated and exposed individuals will help inform control measures. This study assessed the serostatus of both vaccinated and unvaccinated individuals and further confirmed SARS-CoV-2 infection status through reverse transcriptase polymerase chain reaction (RT-PCR) of viral RNA from oropharyngeal swab samples from IgM reactive individuals. Of a total of two hundred and seven (207) samples collected from August to September 2021, 70 were vaccinated and 137 were not vaccinated. Importantly, 13 (18.6%) of the vaccinated group were IgM reactive, while 19 (27.1%) of the vaccinated group were unreactive for IgG. Conversely, 75 (54.7%) of the 137 unvaccinated individuals were IgG reactive, suggesting natural immunity that comes from exposure to the virus. RT-PCR assay confirmed 8 out of 46 (17.4%) IgM reactive individuals to have active SARS-CoV-2 infection. Low virus titer and possibly lower sensitivity of oropharyngeal swabs for RNA detection might have affected the PCR results. Our study findings indicate that some vaccinated individuals were not yet protected against the virus while some unvaccinated individuals appeared to have protective antibodies. Host and viral factors might underlie the differential immunity patterns observed among the participants in this study. Accumulation of these data will enhance our understanding of the outcome of SARS-CoV-2 infection in various populations to aid appropriate control approaches.

Keywords: COVID-19 pandemic, immunity, swab, vaccinated, exposure

VR 004: Who should be the first in line to receive the COVID-19 vaccine? Public preferences for prioritization in Ghana: a discrete choice experiment

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Abstract:

The COVID-19 pandemic has urged scientists and other medical health experts to help control the virus by providing vaccines. Due to the limited number of vaccines that can be produced immediately, health experts, countries, and world leaders are discussing who should be prioritized regarding vaccination. This is a critical issue of which Ghana is no exception. This work used data from a cross-sectional study involving a random sample of 200 subjects conducted in the Greater Accra region between April and May 2021 through interviewer questionnaire administration and the discrete choice experiment design to critically examine who should be the first in line to receive the COVID-19 vaccine. The research findings indicated that priority should be given to the occupational status of its personnel, followed by those at risk of catching and transmitting the COVID-19 virus, income level, age category, risk of COVID-19-related death, societal/influential status, dependent category. Frontline workers, key workers, those at greater risk of contracting and transmitting the virus, and those who earn a low and average amount of income should be prioritized during COVID-19 vaccination. We noticed that people with social influence in the country were given less priority regarding COVID-19 vaccination. These results provide insight into policy discussions on optimizing COVID-19 vaccination in Ghana.

Keywords: Discrete choice design, COVID-19, vaccine, preference

VR 005: Expression and purification of the SARS-CoV-2 nucleocapsid antigen for ELISA-based COVID-19 serology studies

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Abstract:

The SARS-CoV-2 nucleocapsid protein has been an essential component of a good number of COVID-19 diagnostic and surveillance tools. In this study, we sought to express and purify tag-free recombinant SARS-CoV-2 nucleocapsid in the scalable and relatively low-cost E. coli expression system. To achieve this, the SARS-CoV-2 nucleocapsid gene was cloned into the pHYRSF53 plasmid backbone, which has a hexahistidine tag. The His-tagged Nucleocapsid protein was purified using affinity purification. The His tag was then cleaved by purified ULP protease and tag-free nucleocapsid protein was obtained as the eluate after passing the cleavage reaction again through a Nickel IMAC column. After the successful expression of the protein in BL21 cells and subsequent purification using Ni-NTA affinity chromatography, the protein was treated with a ubiquitin-like protease to remove the hexahistidine tag. We validated the functionality of the expressed protein in terms of antibody recognition by Western blot using a monoclonal antibody and serum from a SARS-CoV-2 exposed individual. We also showed that this protein can be used and optimized for low-cost, large-scale seroprevalence studies using indirect ELISA. This study contributes to the tools for COVID-19 seroprevalence studies.

Keywords: Expression, nucleocapsid, serology, affinity chromatography

VR 006: Prevalence and risk factors associated with HIV comorbidities among children and adolescents in the Eastern Region, Ghana

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Abstract:

Children and adolescents living with HIV are primarily at a greater risk of HIV comorbidities because of their susceptibility to infections. The study determined the prevalence and risk factors associated with HIV comorbidities among children and adolescent patients at the Eastern Regional Hospital, Koforidua. This was a hospital-based retrospective cross-sectional study, which used clinical record review to obtain retrospective data for 1,437 children and adolescents from January 2018 to January 2021. Logistic regression was used to determine the socio-demographic and clinical factors associated with the presence of HIV comorbidities as well as the treatment outcomes. Odds ratios, p-values, and confidence intervals were reported. The prevalence of HIV co-morbidities among the study population was 33.0%. The most frequent comorbidity reported was bronchopneumonia. Children aged 5–9 years old were 30% (cOR = 0.70; 95% CI: 0.52–0.93; p = 0.017) less likely to have a comorbidity than children under 5 years old. After adjusting for all other factors, at 95% CI, children aged 5–9 and 15–19 years old are 36% (aOR = 0.64, 95% CI; 0.40–0.89; p = 0.008) and 25% (aOR = 0.75, 95% CI; 0.56–0.99; p = 0.047) less likely to have comorbidity. Children and adolescent patients experience a high risk of respiratory comorbidities. There is a need to provide a system that will effectively monitor the comorbidities and health conditions of children and adolescents living with HIV, whether on admission or not, to inform appropriate management.

Keywords: HIV comorbidities, children and adolescents,

VR 008: Detection of sICAM-1 level in HIV and hypertensive patients

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Abstract:

Soluble intercellular adhesion molecule (sICAM) -1 is a biomarker associated with HIV and hypertension. There is a geographical overlap between hypertension and HIV in low and middle-income settings, however, it is not clear how the patterns during each disease can differentiate between the diseases. This study aimed to assess patterns of sICAM-1 level in hypertensive populations and persons living with HIV. This was a cross-sectional study where the plasma was obtained from patients (hypertension only (Hy), HIV only (Hv) and patients with both hypertension (HyHv) and HIV) presenting at the Fevers unit of the Korle-Bu Teaching Hospital and outpatient of the Korle-bu Polyclinic was analysed for sICAM-1 level using ELISA. sICAM-1 levels were higher in patients in the hypertension-only group

compared to those in the Hv, and HyHv. sICAM-1 level were negatively correlated with ages in Hy patients and HyHv patients, whereas no relation was observed between ICAM-1 level and ages of Hv patients. Also, a ROC curve analysis to determine the sICAM-1 potential in differentiating between the three groups, provided an AUC value of 0.851 with a sensitivity and specificity value of 86.7 and 83.0 respectively. Further studies in a larger population may indicate an obvious pattern in this complex relationship.

Keywords: biomarker, sICAM-1, hypertension, HIV

VR 053: Development, optimization and utility of a SARS-CoV-2 antibody ELISA using in-house expressed nucleocapsid antigen

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Abstract:

Seroprevalence studies are necessary for assessing exposure to an infection in a population. Understanding the seropositivity of Severe Acute Respiratory Syndrome Coronavirus-2 (SARS-CoV-2) will serve as an important epidemiological tool for regulatory measures based on the degree of spread or incidence in different populations. Rapid test kits have been used in seroprevalence studies worldwide; however, owing to cost implications, we have developed a cost-effective, specific, and sensitive method to detect antibodies in low- and middle-income countries. In this study, we developed an indirect Enzyme-Linked Immunosorbent Assay (ELISA) to quantify immunoglobulin G (IgG) which specifically targets the nucleocapsid antigen of SARS-CoV-2 in plasma samples. Previously analyzed SARS-CoV-2 positive samples (n=72), confirmed using Polymerase Chain Reaction (PCR), Luminex assay, and lateral flow devices were used as true positives while those that were negative in all the above were used as true negative samples (n=50) in addition to pre-coronavirus 2019 disease (COVID-19) plasma samples (n=100). Our in-house developed ELISA offers sensitivity and specificity of 96% and 100%, respectively, with the ability to detect anti-nucleocapsid antibodies above a cut-off concentration of 27.927 µg/ml. The efficiency of this ELISA in detecting individuals with the nucleocapsid antibody was assessed using the Receiver Operating Characteristics (ROC) curve and a 98.9% positive predictive value ($p = 0.00001$) was obtained. This implies that this SARS-CoV-2 antibody ELISA is an effective assay for COVID-19 seroprevalence studies and can be explored for mass surveillance to track transmission hotspots.

Keywords: Antibodies, nucleocapsid, ELISA, SARS-CoV-2

VR 009: SARS-CoV-2 seroprevalence and variant distribution during the Delta-Omicron transmission waves in Accra, Ghana

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Abstract:

A significant proportion of SARS-CoV-2 infections in Africa are identified as asymptomatic, facilitating the silent spread of the virus, especially in populated urban cities. With the surge of the highly transmissible Omicron variant, the inclusion of asymptomatics in epidemiological surveys is key in estimating true infections and seroprevalence in the population. The study aimed to determine seroprevalence, active infection and circulating variants in Accra, the capital city of Ghana during the Omicron wave. The study was a cross-sectional survey conducted in 22 municipalities in December 2021. Naso-oropharyngeal swabs and serum samples were collected from 1027 individuals aged 5 years and above, for detection of infection by RT-qPCR and estimation of total antibodies using the WANTAI ELISA kit. Our results show 10% SARS-CoV-2 prevalence, with the Omicron and Delta variants accounting for 44.1% and 8.8% of infections, respectively. Omicron was most prevalent (48.9.%) among the 20–39-year-olds. Asymptomatic individuals accounted for 75.2% of infections. Seropositivity within the population was 86.8%, with the 60+ year group having a significantly higher likelihood of exposure (OR 10.22: 95% CI: 3.51-29.73; p<0.001). This high seroprevalence appears to have been a result of increased vaccination among this group (OR 4.31: 95% CI 2.35-7.90, p < 0.001). The high seropositivity of SARS-CoV-2 in the capital could be a good indication of herd immunity among the population, while the low infection rate supports the role of vaccination in reducing viral transmission.

Keywords: SARS-CoV-2, Seroprevalence, Delta variant, Omicron variant

VR 010: SARS-CoV 2 infections amongst asymptomatic persons contributed to covid-19 cases: a cross-sectional study among prospective air travellers from Ghana

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Abstract:

Transmission of SARS-CoV-2 by asymptomatic individuals was reported early during the COVID-19 pandemic. However, data regarding the contribution of asymptomatic infections to the spread of SARS-CoV-2 in Ghana is limited. We analysed test data of prospective travellers from Ghana as a proxy for asymptomatic COVID-19. Persons, without clinical symptoms, who took the SARS-CoV-2 PCR test for "Travel" at Noguchi Memorial Institute for Medical Research (NMIMR) COVID-19 Walk-in Centre (NWC) from July 2020 to July 2021 were studied. Oro- and nasopharyngeal swabs were tested for SARS-CoV-2 by reverse-transcription quantitative PCR according to standardized protocols. Samples with cycle threshold (Ct) value <40 were Positive. Data were analysed in Microsoft Excel office 16 and STATA version 16 and summarised using descriptive statistics. Of 28,384 samples tested for "Travel" within the period, 1,900 (6.7%) were positive for SARS-CoV-2. Travel tests were requested predominantly by males (64.8%) and from the Greater Accra Region (83.3%). SARS-CoV-2 positivity was 6.9% among males and 6.4% among females. Positivity peaks were observed in July 2020 (11.1%), January 2021 (10.2%) and July 2021 (7%) mirroring

the different waves of infection. Eastern region recorded the highest SARS-CoV-2 positivity (8.35%), however, Greater Accra contributed 81% to the positive case count. We found SARS-CoV-2 in 6.7% of persons with no COVID-19 symptoms, who without travel requirements will not know their status, and may inadvertently spread the virus among their contacts. Our findings endorse enhanced tracing and testing of asymptomatic contacts of positive SARS-CoV-2 cases.

Keywords: Asymptomatic, Air travellers, SARS-CoV-2, COVID-19, Ghana

VR 011: SARS-CoV-2 variants among travellers entering Ghana through land borders

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Abstract:

New variations of the SARS-CoV-2 virus continue to appear, indicating ongoing mutation. With Ghana's land borders open, it is critical to monitor SARS-CoV-2 variations among people crossing these land borders. We present data gathered through surveillance at ten ports of entry into Ghana. Between February and July 2022, a cross-sectional survey of people (≥18 years) who crossed legally recognized land borders in ten different Ghanaian localities was carried out. In each region, prominent points of entry were chosen. We recruited and collected from 4,621 travellers oropharyngeal and nasopharyngeal swabs and bio data. Real-Time PCRs were used to evaluate samples for the presence of SARS-CoV-2. Using the Josh Quick methodology and Oxford Nanopore technology, we sequenced viruses we found. We detected up to 3.0% (170/4621) of SARS-CoV-2 positive cases and successfully sequenced 35 of them. Seventy-seven per cent (27/35) of the sequenced samples were categorized as Omicron (B.1.1.529), including subvariants (BA.2, BA.4, and BA.5). Alpha (3/35), Delta (3/35), and recombinants (Omicron BA.1 and B.2 recombinants) subtypes made up the remaining 23.0%. The majority of the sequenced samples (34.0%, 12/35) came from Côte D'Ivoire, 26.0% from Ghana (9/35), and Nigeria (9/35), while the remaining samples (3/35) and (1/35) were from Togo and Benin, respectively. Our research suggests that various SARS-CoV-2 subtypes might cross our boundaries. More initiatives to promote comprehensive vaccination should be implemented, and disease surveillance at land borders should continue.

Keywords: SARS-CoV-2, Ghana, points of entry

VR 014: Evaluation of Point of Care device and antigen kits for diagnosis of seasonal influenza infection in Ghana

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Abstract:

Rapid diagnosis of influenza is important for early treatment and the institution of control measures. We evaluated the performance of the UniCare Influenza A/B Antigen test kits and UniKoReader Smart Analyzer. Two strategies were adopted; the use of archived samples and freshly collected nasopharyngeal swabs. A total of 300 archived samples with influenza infection status previously determined by PCR assays (influenza A, n = 120; influenza B, n = 120; negative samples, n = 60) and 1241 (influenza A, n = 258; influenza B, n = 1; negative samples, n = 982) freshly collected nasopharyngeal swabs from patients were analysed. The UniCare kit was evaluated in comparison with the reverse transcription quantitative PCR (RT-qPCR). The overall sensitivity of the UniCare kit was significantly higher for the freshly collected nasopharyngeal swabs (66%, 171/259) than for the archived samples (48%, 115/240) [p-value<0.001]. With the archived samples, sensitivity was 57% (68/120) for influenza A and 39% (47/120) for influenza B. With freshly collected samples, sensitivity was 64% (166/258) for influenza A and 100% (1/1) for influenza B. Sensitivity by symptom duration between onset and date of sample collection showed 70% (126/179) for duration <4 days and 62% (32/52) for ≥4 days. Overall specificity was 83% (50/60) for archived samples and 77% (759/982) for the freshly collected samples. The field observations indicated that the kits and analyzer were user-friendly and with long battery-life. We conclude that the kit and analyzer are useful diagnostic tools for influenza infection screening during outbreaks.

Keywords: Influenza, rapid diagnostic testing, sensitivity, specificity

VR 013: Evaluation of direct RNA extraction method for detection of Poliovirus in stool samples

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Affiliations: [1]*Noguchi Memorial Institute for Medical Research. University of Ghana*

Abstract:

Poliovirus (PV) isolation has relied on cell culture which can be time-consuming. With eradication underway, a more reliable, sensitive, and faster method to reduce laboratory analysis time in PV identification has been developed by the Global-Polio-Eradication-Initiative (GPEI). This was a prospective study to analyze and compare the direct detection method with Zymo Quick RNA viral kit to the traditional virus isolation procedure in the

Ghana Regional Reference Polio Laboratory. Stool specimens from Acute Flaccid Paralysis (AFP) patients were received and processed following the WHO protocol. Faecal suspensions were tested, with the standard virus isolation employing RD and L20B cell lines and the direct RNA extraction method in parallel. Virus isolates and extracted RNA were identified using the Intratypic-Differentiation (ITD) rRT-PCR procedure and testing algorithm for polio. Of the 349 samples investigated from March-June 2022, 84 (24.1%) were positive by direct detection method, while 56 (16.1%) were positive by virus isolation. Besides, 262 (29 positive samples and 233 negative samples) gave concordant results with both methods. RNA extraction detected one more Sabin type 1 and Sabin type 3 PV than did virus isolation, and three specimens were PV positive by virus isolation but negative by RNA extraction; the differences were not significant. The direct RNA extraction method was similarly sensitive compared to virus isolation in culture in the identification of polioviruses. Combined with ITD rRT-PCR, the method can be utilized in the laboratory to rapidly detect and type polioviruses of programmatic importance to support the final stages of global polio eradication.

Keywords: AFP, Poliovirus, GPEI, ITD rRT-PCR, RNA

VR 015: SARS-COV-2 among healthcare workers in health facilities: identification of transmission routes using a phylogenetic-based model in Ghana

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Abstract:

Sever acute respiratory syndrome coronavirus 2 (SARS-CoV-2), remains a respiratory virus of international concern, causing over 604 million deaths globally. Ghana has confirmed over 168,000 cases and 1459 deaths. Healthcare workers are at the forefront of the fight against Covid-19 and are thus at an increased risk of being exposed to SARS-CoV-2. Therefore, they could potentially play a vital role in hospital transmissions of the virus from patient to healthcare worker as well as from healthcare worker to healthcare worker. WHO estimates that between 80,000 – 180,000 healthcare workers deaths from covid-19. This study aimed to identify the transmission of SARS-CoV-2 between healthcare workers in two major hospitals in Ghana. Oropharyngeal swabs were taken from 204 healthcare workers from the Greater Accra Regional Hospital and Cape Coast Teaching Hospital. The gender distribution analysis of this study showed significantly more females (60.78%) than males (39.22%). Participants sampled comprised of 5 departments: Covid ICU (10%), Paediatrics (31%), Neonatal intensive care unit (18%), Accident and emergency (25%) and General medicine (16%). Currently, 5 out of 204 participants tested positive throughout the study. This resulted in a total positivity rate of 2.5%. Weekly positivity showed that 40% (2) of positive samples were obtained during week 2, 40% (2) during week 3 and 20% (1) during week 6. 1 out of 5 positive samples was IgG positive at baseline showing reinfection. Results from this study so far have shown that HCWs were positive for SARS-CoV-2. Further phylogenetic analysis will enable the identification of transmission routes.

Keywords: SARS-CoV-2, Healthcare workers, Transmission, Phylogenetic, Nanopore

VR 016: Detection of SARS-CoV-2 among travellers vaccinated against COVID-19 entering Ghana through land borders.

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Abstract:

With the opening of the land borders in March 2022, it was important to monitor the importation of SARS-CoV-2 among travellers using these borders. We report here, SARS-CoV-2 positivity rates and variants among travellers vaccinated against COVID-19 who used Ghana's land borders from March to June 2022. A cross-sectional survey of travellers who crossed nine widely used recognized land borders in 10 different areas of Ghana was conducted. Structured questionnaires were used to obtain information on COVID-19 vaccination status and participant demographics. Oro/nasopharyngeal swabs were collected from 4,621 travellers. Samples were analyzed using rRT-PCR for the identification of SARS-CoV-2 and sequenced using the Josh Quick protocol with Oxford Nanopore technology. Half of the travellers, 49.08% (2268 /4621), had been vaccinated against COVID-19 disease. Of these, 2.9% (66/2268) tested positive for SARS-CoV-2. A majority, 69.69% (46/66) had received full doses, with the remaining 30.30% (20/66) having received half doses. We selected 15% (10/66) for sequencing and of these, 7 Omicron (B.1.1.529) including subvariants (BA. 2, BA.4, BA.5) and recombinant (XN) were detected among vaccinated travellers who had received full doses. The remaining 3 :1 Omicron, subvariant, and Delta (B.1617) were detected among travellers who had received more than one dose. This study detected the highly transmissible Omicron variant among fully vaccinated travellers. Whilst vaccines have proven effective against COVID-19, routine surveillance and vigorous public health measures remain important for reducing its spread.

Keywords: COVID-19, vaccination, Ghana, land borders

VR 017: Determining the spread of SARS-CoV-2 in Ghana through serologic testing: from evaluation of serologic kits to seroprevalence study in Tamale

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Abstract:

A SARS-CoV-2 seroprevalence investigation in a non-immunized population could help determine the true spread of SARS-CoV-2 in a population since serological tests can detect

past infections. This could provide information to map the transmission dynamics of the virus and in identifying high-risk populations. We evaluated the efficacy of several SARS-CoV-2 Rapid Diagnostic Test (RDT) kits using convalescent plasma from COVID-19 patients in Ghana to identify kits suitable for SARS-CoV-2 surveillance purposes. Using one of these kits, a seroprevalence study was conducted in Tamale Metropolis, Northern Region, to assess the spread of SARS-CoV-2 in Tamale. Six kits were identified to be suitable for surveillance purposes. SARS-CoV-2 infection was widespread in Tamale, with an exposure rate of 34% in residential areas and 54% in areas with commercial activities. Exposure in children (37.7%) and adults (34.5%) was similar. The most exposed individuals were 17-24 years old (53%). Infection risk was lower in males than in females (OR = 0.62, p = 0.02). Students (44%) and teachers (50%) were widely exposed. The seroprevalence study reveals a wide-spread of SARS-CoV-2 among adults and children in households and communities in Tamale, with a substantial rate of undetected COVID-19 cases in the population. Thus, the data suggest that COVID-19 cases in Ghana are substantially underestimated.

Keywords: SARS-CoV-2, COVID-19, Seroprevalence, non-immunized population

VR 018: First cases of Monkeypox virus recorded in Ghana.

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Abstract:

Monkeypox viral infection is a zoonotic disease caused by the Monkeypox virus (MPXV) from the family Poxviridae. Ghana is one of the West African countries that were yet to record a case even though the country is found in an endemic region. Here we report the first confirmed cases of MPXV in Ghana and the genetic variant of the isolated virus. Viral DNA was isolated from lesion exudate or crust on a swab and/or serum specimens of patients identified by clinicians to have met the case definition of an initial febrile prodrome accompanied by headache, and fatigue before rash development. Polymerase chain reaction (PCR) was then performed at the Noguchi Memorial Institute for Medical Research (NMIMR) to amplify the viral DNA and conduct a full-length sequencing with the Next Generation Sequencing (NGS) platform. To date, clinical samples from a total of 162 suspected MPXV cases have been received from health facilities across the country and tested. Nineteen out of the 162 (11%) have been confirmed to be MPXV cases whilst 60 out of 162(37%) were other Orthopoxviruses. Majority of patients presented with fever, general body pains, headache, and rashes on various parts of the body. Sequenced and characterized MPXV positives were found to belong to the West African clade. The genetic variant identified indicates a regional transmission and calls for case surveillance and other studies including seroepidemiology to establish whether is endemic.

Keywords: Monkeypox, Orthopoxvirus, NGS, Clade, PCR

VR 019: Impact of low-level viraemia on viral reservoir size among patients taking antiretroviral therapy in Ghana

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Abstract:

Antiretroviral therapy can achieve viral suppression and drastically improve clinical outcomes in the majority of HIV patients. However, the presence of latently infected cells, called the HIV reservoir, is the main obstacle to HIV eradication. Based on WHO recommendation, viral load (VL) <1000copies/ml is accepted as suppression in resource-limited settings (RLS) compared to 50copies/ml in developed countries. This low-level viraemia may favour continuous viral replication, drug resistance and an increase in reservoir size. However, these patients are regarded as virally suppressed and not given much attention to further reduce their viral loads. We, therefore, investigated the impact of persistent low-level viraemia (PLV) on the reservoir size by estimating the cell-associated DNA in patients with VL 50-999copies/ml and <50copies/ml. Ninety HIV-infected individuals were studied from two categories; 45 patients with PLV (VL = 50-999copies/ml) and 45 patients fully suppressed (FS) (VL <50copies/ml). HIV DNA was extracted from peripheral blood mononuclear cells and quantitative PCR was done to estimate and compare the reservoir size between the two groups. The median reservoir size was 682.65 viral copies (IQR: 451.04-1684.04) for the PLV group and 228.41viral copies (IQR: 149.42-475.61) for the FS group. The median reservoir size was three times larger in the group with PLV compared to the FS. This difference was statistically significant [p-value<0.001]. Our finding calls for a redefinition of viral suppression in RLS and targeted efforts at reducing viral load and in effect the reservoir size in these patients to enhance HIV cure.

Keywords: Reservoir, viral load, viraemia, HIV

VR 020: Molecular characterization of circulating viruses in an outbreak of Yellow Fever from October 2021 to February 2022 in communities in Ghana.

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Abstract:

Yellow fever (YF) is an acute viral hemorrhagic disease transmitted by infected Aedes spp. mosquitoes. Disease severity ranges from self-limited febrile illness to hemorrhagic

syndrome with jaundice, multiple organ failure and death. During outbreaks, severe cases are more likely to be detected and reported. From October 2021 to February 2022, an outbreak of Yellow Fever in some communities in Ghana resulted in 70 confirmed cases with 35 deaths (case-fatality, 50%). In all, a total of 188 clinical specimens of human sera were collected within the outbreak period and submitted to the Noguchi Memorial Institute for Medical Research (NMIMR) for testing. Large proportions (65%) of the cases were sent from communities within the Savannah region. Molecular amplification methods were used in the diagnosis and subsequently produced full-length sequences of three confirmed cases. Phylogenetic analysis characterized the three under the West African genotype II strains and they shared a close homology with sequences from Cote d'Ivoire and Senegal. The utility of the more sensitive advanced molecular diagnostic techniques deployed for laboratory testing during this outbreak investigation made it distinctive from the serological assays previously used. It enabled us to characterize the circulating strains and for the first time deposited YF strains from Ghana at the GenBank. To change the trend of YF outbreaks in-country and elsewhere, public health authorities must increase efforts to ensure that individuals and groups in difficult-to-access areas and at the highest risk of exposure are educated about the potential risk of YF infection and vaccinated.

Keywords: yellow fever, Hemorrhagic, Aedes, Genotype, Phylogenetic

VR 021: First-ever outbreak of Marburg virus disease declared in Ghana

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Abstract:

Marburg virus disease (MVD) is a dangerous life-threatening haemorrhagic fever with a case fatality rate of about 88%. Two suspected cases were received for viral haemorrhagic fevers (VHF) testing. The suspected cases were from 26- and 51-year-old males with symptoms such as fever, vomiting, diarrhoea, abdominal pains, difficulty in breathing and bleeding from the eyes and nose. The samples were subjected to viral nucleic extraction, purification, and amplification with molecular testing tools for the known endemic VHFs including Lassa, Ebola, Yellow Fever, Dengue and Marburg virus. The two cases were later confirmed as MVD. This may represent a serious public health threat as it is acute and often fatal. Clinical specimens of serum from 13 close contacts of the two index fatal cases tested negative on the 3rd of July, whilst 90 more contacts were kept under observation. Within three weeks of contacts observation, two showed symptoms, tested positive for MVD and subsequently expired. In total, Ghana has now confirmed four cases of MVD with 3 deaths. There was an immediate and swift response from the health authorities in proactively preparing to tackle an outbreak which prevented a difficult-to-control situation. This is the first time MVD has been reported in Ghana and it shows the capacity of the VHF testing system established in NMIMR is active and sensitive to detecting emerging pathogens for public health response. Resourcing of the facility and capacity building across public health laboratories is essential for responding to future emerging pathogens.

Keywords: Marburg Virus Disease (MVD), haemorrhagic, fatal

VR 022: Optimization of Real-Time systems for RT-qPCR detection of SARS-CoV-2 variants.

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Abstract:

Multiple variants of SARS-CoV-2 have been documented with each new variant having high transmissibility compared to the previous. The detection of these mutants is heavily reliant on sequencing, which is costly and time-consuming. Real-Time Polymerase Chain Reaction has become relatively more readily available since the emergence of COVID-19 as it is the gold standard method for detection. We aimed to optimize a Roche-validated RT- qPCR-based assay for detecting Omicron and Delta SARS-CoV-2 variants on three real-time systems; Light Cycler 480, ABI 7500 and Quantstudio-5, by assessing reagent compatibility, sensitivity and accuracy. Seven of each of the Omicron and Delta-confirmed SARS-CoV-2 positive samples were used for the assays. The manufacturer's recommended FAM fluorophore channel for the detection of Omicron was available on all three thermal cyclers, but HEX (for Delta) was only available on the Light Cycler 480 and had to be replaced with VIC for the ABI 7500 and Quantstudio-5 systems. In addition, our experiment showed that the manufacturer's reagents were only compatible with the Roche Light Cycler 480, and had to be replaced with a more universal reagent to obtain similar results on the other two pieces of equipment. The protocol we have developed therefore allows the detection of Omicron and delta variants on commonly available real-time machines and can be useful in medical settings.

Keywords: SARS-CoV-2, Delta, Omicron, thermal cycler, RT-qPCR.

VR 023: Serological evaluation of Lassa Fever in Ghana

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Abstract:

Lassa fever is a zoonotic and an arenaviral infectious disease characterized by acute haemorrhagic illness having the multimammate rat *Mastomys natalensis* as its reservoir. The disease is responsible for about 300,000 infections and 5000 deaths in Africa and symptoms include cough, sore throat, headache, nausea, and vomiting. The recent outbreak of Lassa fever in West Africa has raised concerns to survey Ghana and ascertain it epidemiological

status of the disease. The ReLASV Pan-Lassa NP IgG/IgM ELISA Kit was used to test pooled archived sera from seven regions in Ghana. Positive samples were determined by comparing the concentrations of each pool against the limit of detection (LOD) per plate. A total of 242 pools were screened for IgG/IgM antibodies. Overall, the IgG positives (57.9%) were higher than those of the IgM positives (38.4%). Brong Ahafo region recorded the highest IgG positivity (90.9%) followed by the Ashanti region (65.0%). Upper West had the least positivity (9.1%). The Northern (Savanna, North East) region had the highest IgM positivity (70.6%) followed by the Ashanti region (52.1%), and Greater Accra had the least recording (14.5%). No IgG and IgM positives were recorded in the Upper East and Brong Ahafo (Ahafo, Bono, Bono East) regions respectively. To overcome the gaps and challenges imposed by Lassa fever in Ghana, nationwide surveillance is needed to detect the presence of the virus. This will help determine hotspots and avoid a Lassa fever burden on the already suffocating health system.

Keywords: Lassa fever, seroprevalence, epidemic, transmission, surveillance

VR 024: First whole genome isolation of Crimean-Congo haemorrhagic fever virus (CCHFV) in ticks within Ghana and the risk of human exposure

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Abstract:

Ticks are blood-sucking arthropod vectors, that spread many severe diseases in animals and humans. In crowded trade areas, there could be an increased risk of zoonotic infections. This study, therefore, sought to identify the circulating tick species, determine the pathogens they carry, and assess the risk of exposure of primary animal handlers and the impact it may have on force health protection. The sites included military-owned kraals at Burma Camp (5 Infantry Battalion and 3 Mounted Squadron), Michel camp (1 Infantry Battalion) and Asutsuare within Greater Accra; and the abattoir, cow market and Nakong within Navrongo. In total, 705 ticks were collected from cattle (n=188) and horses (n=11). Three tick genera (*Hyalomma*, *Amblyomma* and *Rhipicephalus*) were observed in the study with the predominant species being *Hyalomma rufipes* (n=290, 41.13%), followed by *Amblyomma variegatum* (n=157, 22.27%) and the least, *Rhipicephalus sanguineus* (n=1, 0.14%). From the 705 ticks, CCHFV infection rates of 0.78% (95% CI, 0.02-3.96), 0.69% (95% CI, 0.08-2.4) and 0.64% (95% CI, 0.02-3.24) were recorded in *Hyalomma truncatum*, *H. rufipes* and *A. variegatum*, respectively. No infection was detected in the *Rhipicephalus* species. Further, a strain was successfully recovered using Next Generation Sequencing for PCR-positive tick

samples with analysis based on the complete open reading frame of the S-segment of the CCHFV genome. The strain belonged to genotype III (Africa 3) and shared 98.9% nucleotide identity with DQ211641_Mauritania_1984 and MF287636_Spain_2016. The preliminary analysis detected antibodies to CCHFV in 42.5% of the human serum (n=120) samples. Findings suggest the possible importation of the virus into the country, putting livestock and humans who may have primary contact with livestock at risk of infection.

Keywords: Ticks, CCHFV, Sequencing, Exposure, Ghana

VR 026: Application of survival analysis in the assessment of the timeliness of the measles surveillance system in Jasikan Municipality of Ghana

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Abstract:

Empirical evidence on the performance of surveillance systems in case detection, confirmation, and response remains lacking, particularly in the context of the COVID-19 pandemic. We assessed the timeliness of the measles surveillance system in Jasikan Municipality, Ghana. We conducted a cross-sectional study on measles surveillance data from 1st January 2022 to 31st August 2022. Data extracted were described by person, place and time. The timeliness of the surveillance system was defined by case detection (≤3 days), sample transportation (≤3 days) and case confirmation (<7 days). Kaplan-Meier survival estimator was used to estimate the duration of case detection, sample transportation and confirmation. Of the 35 measles cases suspected, 3 (8.6%) were IgM-positive. Males (60%), children <5 years (54.2%) and Baika-Ayoma sub-municipal (65.7%) were the most affected. Timely case detection was 51.4%. Late sample transportation and case confirmations were 88.6% and 85.7% respectively. The median delays in case detection, sample transportation and case confirmation were [7 (5-8)], [27 (15-36)] and [26 (15-36)] days respectively. The probability of late case detection for ≥4 days after onset was 76% [0.76, 95%CI (0.48-0.90)]. The probability of delay in sample transportation ≥7 days was 86% [0.86, 95%CI (0.69-0.94)] and late confirmation for ≥6 days after sample collection was 93% [0.93, 95%CI (0.76-0.98)]. The measles surveillance system was not timely in case detection and confirmation. Effective risk communication, an efficient sample transportation system and prompt laboratory feedback communication are critical to improving the timeliness of the surveillance system.

Keywords: Measles, Timeliness, Surveillance, Survival Analysis, Jasikan

VR 027: Seroprevalence of Chikungunya, Dengue, and West Nile virus infections among patients with febrile illness in some healthcare facilities in Ghana

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Abstract:

The re-emergence of vector-borne diseases has highlighted arboviruses, which include Chikungunya, Dengue, and West Nile viruses, as a major public health concern globally. They are known to be endemic in many parts of the world, including Ghana. Clinical manifestations are nonspecific, with fever being a major symptom, making the diagnosis of these infections very challenging. This study sought to determine the seroprevalence of Chikungunya, Dengue, and West Nile virus among febrile patients in select clinics in Ghana. Patients (5 to 65 years) with fever and/ or a history of fever were enrolled. Serum samples were tested for IgM and IgG antibodies using commercially available ELISA kits. Of the 280 samples tested, 132 (47.1%) demonstrated exposure to at least one or all three of the arboviruses tested. Ninety-nine (35.4%), 64 (22.9%), and 50 (17.9%) were exposed to Dengue, Chikungunya, and West Nile virus, respectively. Among the patients that were exposed, the most prevalent dual exposure observed as Dengue and West Nile virus 56 (20%). Adults were more likely to be exposed to Dengue (OR=6.7, 95%CI=3.3-3.8), Chikungunya (OR=2.8, 95%CI=1.3-6.3), and West Nile virus (OR=4.1, 95%CI=1.9-9.1) than children. The predominant arboviral infection detected among febrile patients in Southern Ghana was Dengue fever. These findings suggest the circulation of these arboviruses (Dengue, Chikungunya, and WNV), should be included during differential diagnosis of febrile patients in Ghana.

Keywords: Seroprevalence, Dengue, Chikungunya and WNV

VR 029: Syphilis and Latent Tuberculosis Co-infections in a Cohort of HIV-positive Individuals Receiving Anti-Retroviral Therapy in Ghana.

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Abstract:

Human Immuno-deficiency Virus (HIV) plays a critical role in increasing susceptibility to opportunistic infections such as M. tuberculosis and sexually transmitted infections (STIs) like syphilis. Unlike resource-rich settings, people living with HIV (PLWHIV) in Ghana are not routinely screened for STIs or latent tuberculosis (LTB). This study aimed to determine LTB and syphilis co-infections among a cohort of HIV-infected individuals in Ghana, to help guide future policies on routine screening. A total of 320 participants were tested for Syphilis using Rapid Plasma Reagin (RPR) and Treponemal pallidum Haemagglutination Assay (TPHA) whiles 71 were tested for LTB using QUANTIferon-TB Gold test. Demographic data including sex, gender, and years diagnosed with HIV were collected using questionnaires and their CD4 T cells and viral loads were measured. Out of 94 (29%) participants who tested positive

for RPR, 34% had CD4 count ≤500 cells/ul. In this group with CD4 ≤500 cells/ul, males, those diagnosed for > 5 years, and patients who had been on treatment for>6 years were at a higher risk of having syphilis co-infection. Out of twelve participants who tested positive for LTB (16.9%), there was an observed association between LTB infection to sex and years diagnosed with HIV. Males were more likely to be LTB positive compared to females (OR: 2.6 (0.8 - 9.4)) and participants diagnosed >5 years were likely to be LTB positive (OR: 3.0 (0.6 - 15.1)). Our findings show a high incidence of syphilis and LTB among PLWHIV and call for policy adjustment to initiate routine screening.

Keywords: HIV, Syphilis, *Mycobacterium tuberculosis*, Immunosuppression, routine-screening

VR 030: Phylogenetics and evolutionary analysis of Cameroon 2017-2018 dengue virus serotypes 1 outbreak strains

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Abstract:

Dengue fever continues to be one of the main public health threats globally. For the past few decades, Cameroon has continued to experience sporadic outbreaks of arboviral infections including dengue fever. Here, we describe the origins of evolutionary lineages, the potential of emergence/re-emergence and predict vaccine efficacy to the Cameroon DENV outbreak strains. Samples collected between 2017-2018 during DENV outbreaks in Cameroon were screened for DENV using reverse transcription polymerase chain reaction (RT-PCR), followed by whole genome sequencing of positive samples. Bayesian inference phylogenetic approach based on the Bayesian Markov chain Monte Carlo (MCMC) method was used evolutionary analysis. Sample analysis yielded six near-complete DENV-1 genomes. Phylogenetics analysis revealed that the strains from the current study belong to an emerging sub-lineage of DENV-1 genotype V and form a monophyletic taxon with a 2012 strain from Gabon. The time of the most recent common ancestor (TMRCA) of the Cameroon and Gabon strains was estimated to have existed around 2009. Compared to the Dengvaxia vaccine strain, 3 and 19 amino acid substitutions were observed in the immuno-protective prM and E protein segments respectively. These new DENV strains constitute a conserved genomic pool of an emerging sub-lineage that needs prospective monitoring to track local viral evolution. This study highlights the importance of ongoing vector surveillance efforts to provide accurate and actionable data for the DoD and the global public health community and to enhance global health security by coordinating a surveillance network for vector-borne diseases.

Keywords: Dengue virus, Cameroon, Phylogenetics, Dengvaxia vaccine

VR 031: Avian influenza in backyard poultry in Ghana: A five-year secondary data analysis.

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Abstract:

Avian influenza viruses (AIVs) are a major health threat that causes significant economic loss to poultry farmers globally. The constant circulation and mutation of AIVs pose a potential health threat to humans. Periodic outbreaks in West Africa motivated Ghana's AIV surveillance which has been conducted biannually since 2017. This study analyzed AIVs surveillance data to determine Avian Influenza (AI) prevalence and distribution amongst farm animals in Ghana. Secondary data analysis was conducted using AI surveillance data from 2017 to 2021. Logistics regression was used to determine factors associated with AI detection. Overall, AI prevalence was 1.9% (103/5319) with subtype AH5 strains dominating at 83.5% (86/103), AH7 at 1.9% (2/103), and AH9 at 14.6% (15/103). Most, 58.9% (79/3130) of the AI cases occurred in the coastal belt, followed by 19.6% (9/1024) from the northern belt. AI detections increased gradually from 2017 (1.1%, 3/265) to 2019 (3.3%, 8/930) and declined in 2020 (0.1%, 1/1238). However, after an AI outbreak in July 2021, was an increase in AIV detection (3.4%, 87/2581). The high prevalence of AI in the coastal belt of Ghana may be attributable to the number of Ramsar sites for migratory birds. This information on key factors associated with avian influenza occurrences in poultry guides appropriates One Health interventions and targeted surveillance.

Keywords: Avian Influenza, Poultry, Birds, Ghana

VR032: Validation of cheap sample processing methods and LAMP assays for COVID-19 diagnosis

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Abstract:

The gold-standard RT-qPCR-based diagnostics, although sensitive, is costly and unavailable to many under-resourced healthcare facilities, especially in rural settings in low-and-middle-income countries. This study aimed to evaluate a loop-mediated isothermal amplification (LAMP) assay that used lyophilized reaction beads and crude viral isolation methods that would allow relatively cheaper detection of SARS-CoV-2 infection. We evaluated the performance of the assay using 30 archived naso/oropharyngeal swabs stored in 0.9% saline, and then 324 freshly collected samples collected into sterile nuclease-free water. Different

sample treatment methods including heat treatment, the addition of BSA and proteinase K were also explored for crude viral isolation. Against the gold-standard detection method, heat treatment with or without the addition of BSA produced the best crude isolation of the virus from saline-stored swabs giving an assay sensitivity of 65% compared with using RNA samples (80%). However, saline as a collection medium impacted the expected colour changes for the LAMP assay. Similar processing of swabs collected in water showed 39.7% sensitivity compared to paired swabs analysed with standard RT-qPCR (78 positives). Improvements to this assay will explore other cheap viral isolation techniques, quantification of colour intensity and generation of colour charts for standardization.

Keywords: LAMP, SARS-CoV-2, Diagnosis, Rural Settings

VR 033: Using digitalization to optimize data collection during an epidemic: the case of a population-based age-stratified seroprevalence survey of SARS-CoV-2 in Cotonou, Benin

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Abstract:

In response to COVID-19, age-stratified, population-based seroprevalence surveys are of utmost importance to assess the magnitude of the epidemic and are designed to provide key epidemiological and serological characteristics of SARS-CoV-2. A digital technology-based system was implemented for data collection during two of these surveys conducted in Cotonou, Benin as part of the ARIACOV project. Electronic forms were designed via the SurveyCTO mobile data collection platform and deployed on smartphones running the Android operating system and included a barcode identification system to avoid misidentification, facilitates anonymization and secure linking of field and laboratory data of participants after serological testing. Once data are collected on the field, automatically sent to the server and securely stored in a back-end database, the summary statistics and KPI are viewed on a front-end functionality via a real-time dashboard developed for monitoring purposes. This contributed to adjusting data collection orientations and verifying if the objectives of the data collection were achieved. At the same time, as part of data quality control, statistical quality control programs are automatically running on the database to detect inconsistencies and errors. As the system offers bi-directional synchronization, forms with errors are returned to the field officers for correction. Globally, in the context of a health emergency such as COVID-19, this system optimized data collection in several points as reducing data collection time, facilitating identification through barcodes, offering real-time monitoring and continuous data quality control. And then, quality data are quasi-immediately available for statistical analysis and decision-making.

Keywords: digitalization, epidemic, COVID-19, data, technology

VR 034: Evaluating the sensitivity of nose masks as a non-invasive sample collection method for covid-19 diagnosis

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Abstract:

Naso-oropharyngeal swabbing is widely accepted for COVID-19 testing. However, they are often uncomfortable procedures, with reports of the overly cranial direction of the swab, excess use of force by personnel, and epistaxis in some cases. We investigated the use of nose masks, which are highly recommended in preventing respiratory droplet transmission of SARS-CoV-2 from human-to-human, as a non-invasive alternative for collecting samples for testing. We collected paired samples of oro/nasopharyngeal swabs and used nose masks (Old) from 102 consenting adults. Before the oro/nasopharyngeal swab collections, each participant was asked to produce three strong coughs while wearing a new sterile nose mask (New). The inner lining of each nose mask was swabbed with wet swabs and returned into viral transport media (VTM). Viral isolation and detection of SARS-CoV-2 from nose mask swabs were performed according to standard protocols and results compared to results from naso-oropharyngeal swabs ('gold standard). Swabs from Old and New masks matched 12 and 17 positives respectively of 83 positives detected from the gold-standard swabs. Sensitivity was 13.6% and 18.2% for the new and old nose masks, respectively, while the specificity was high (78.9% and 88.9% respectively). We observed increased sensitivity of the nose mask swabs at Ct-values below 30 for the gold standard for some samples; which suggests that the nose mask sampling method is sensitive when the viral load is high. We discuss factors that explain these results and steps that could potentially improve the probability of isolating and detecting the virus from nose masks.

Keywords: Nose mask, covid-19 testing, non-invasive

VR 035: Sensitivity and specificity of WANTAI and Luminex ELISA assays in detection of exposure to SARS-CoV-2

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Abstract:

Testing and identifying cases of COVID-19 relies on molecular-based methods. However, sample processing is lengthy, especially with a large number of samples, and costly. Serological surveillance is relatively less expensive and provides an opportunity to assess the severity and extent of disease transmission. Currently, laboratory-based serological and rapid diagnostics tests for IgG/IgM have been validated and provide valuable information on the extent of transmission of SARS-COV-2. In this study, we compared the sensitivity and specificity of two antibody-based ELISA: WANTAI and Luminex ELISA assays. 1259 serum

samples were screened using WANTAI ELISA and Luminex ELISA that was coupled with four different antigens (Receptor Binding Domain (RBD) 1, Receptor Binding Domain (RBD) 2, Viral Replication Complex (VRC), and Viral Replication Complex (VRC) Prep 2) to determine the presence or absence of SARS-CoV-2 antibodies. We compared the performance of the four antigens against the WANTAI ELISA. The WANTAI assay had a sensitivity of 94% and specificity of 100% while the Luminex assay had a sensitivity of 66% and specificity of 80% (McNemar:1.82, CI: 95% p=0.1771) for the RBD 1, 32% and 82% for RBD 2, 67% and 79% (McNemar: 0.22, CI: 95% p=0.639) for VRC, and 96% and 59% (McNemar: 283.18, CI: 95% p<0.001) for VRC Prep 2 respectively. Luminex assay with a combination of the RBD 2 and VRC Prep 2 antigens is the best for detecting the presence or absence of SARS-CoV-2 antibodies since RBD 2 and VRC Prep 2 had high specificity and sensitivity respectively.

Keywords: SARS-CoV-2, Sensitivity, Specificity, ELISA

VR 036: The emerging threat of invasive mosquito species in Ghana: implications for the vector control landscape

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Abstract:

Vector-borne diseases remain a major public health challenge in Africa. Although the outbreak of Aedes-borne arboviruses such as Dengue, Chikungunya and Zika has not been reported in the country, there have been reports of the outbreak of these diseases in neighbouring countries with Aedes aegypti implicated as the main vectors. Yellow fever is endemic with sporadic outbreaks in some parts of the country and *Aedes aegypti* is widely distributed in the country. Aside from the major challenge of insecticide resistance in limiting the malaria control efforts in most African countries, there is a recent threat of the invasion of *An. stephensi* in some areas in Africa including Djibouti, Ethiopia and the Republic of Sudan and recently in Nigeria as well as *Aedes albopictus* in many West African countries including Ghana. These two species are known to have different behaviours and inhabit different ecological niches and have been responsible for increased urban malaria and outbreak of Zika in some countries. This presentation will discuss the implications of the introduction of invasive mosquito species in Ghana within the context of the formulation of vector control strategies in Ghana.

Keywords: Malaria, Arboviral Diseases, Invasive species

VR 038: Expression of neutralizing SARS-CoV-2 antibodies in the plasma of COVID-19 patients in Ghana

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Abstract:

The advent of the COVID-19 pandemic has left most people concerned about the potency of the immune response to the virus in preventing/minimizing subsequent infections, particularly against emerging variants. Immune response to COVID is not fully understood but with most infections, the expression of neutralizing antibodies is very important in inhibiting re-infection and thus an important step in disease control. Our study aims at determining SARS-CoV-2 neutralizing antibody kinetics after infection and/or vaccination. In this ongoing study, we are testing the presence and breadth of neutralizing antibodies against SARS-CoV-2 in plasma samples of COVID-19 patients. Patient-isolated live SARS-CoV-2 virions are used for the live virus assays. Following neutralization, virus infectious titers are measured using a TCID50-based assay. We observed the expression of neutralizing antibodies (nAbs) against the wildtype SARS-CoV-2 predominantly in patients infected during the later waves of the pandemic but not during waves 1 and 2 when the wildtype was dominantly circulating. We also observed an association between nAb expression and vaccination. A more comprehensive analysis and interpretation of data can be made upon testing for nAbs against other SARS-CoV-2 variants especially by employing the pseudovirus system to include a wider breadth of variants. Our data will aid in understanding the cross-neutralizing capacity of SARS-CoV-2 sera from different variants. It will also provide an understanding of factors that contribute to the expression of neutralizing antibodies in individuals exposed to SARS-CoV-2 antigens either via a natural infection or vaccination.

Keywords: SARS-CoV-2, neutralizing-antibodies, COVID-19, virus, immune-response

VR 039: Potential role of wastewater in the transmission of SARS-CoV-2 in Ghana

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Abstract:

Since the beginning of the COVID-19 pandemic, the presence of the causative agent, Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2), in wastewater has been reported. Monitoring SARS-CoV-2 genomes in wastewater can be a potential source of epidemiological data. This study investigates the potential role of wastewater from hand washing in the transmission of SARS-CoV-2 in Ghana. A total of 342 water (171 reservoir water and 171 wastewater) samples from hand wash stations were collected and analyzed from selected public places such as schools, banks and hospitals in Ghana, between June 13, 2022, and August 8, 2022. Samples were collected in the morning and afternoon from the same hand wash stations for a day. From the RT-PCR analysis, a total of 17 samples (4.97%) were positive for SARS-CoV-2. All 17 positive samples were wastewater samples with no reservoir water samples (0 out of 342) testing positive for SARS-CoV-2. This could be an indication that current wastewater treatment methods used in Ghana are effectively eliminating viral RNA from water. Samples from schools had the highest positivity rate (15 out of 17) followed by hospitals (2 out of 17). All samples from banks tested negative (0 out of 17) for SARS-CoV-2. This result suggests that schools maybe the hotspots for viral spread. These preliminary findings show wastewater could provide information on viral dynamics in the community.

Keywords: SARS-CoV-2, wastewater, hand wash stations

VR 040: Population-based seroepidemiological investigation of the dynamics of SARS-CoV-2 infections in the Greater Accra Region of Ghana

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Abstract:

The COVID-19 pandemic has devastated countries worldwide and resulted in a global shutdown. Because not all infections are symptomatic, the extent of SARS-CoV-2 infection in the community is unknown. To address this in Ghana, the paper presents the dynamics of the SARS-CoV-2 epidemic in the Greater Accra metropolis, describing the evolution of seroprevalence through time and stratified by age group. Three (3) repeated independent population-based surveys with six-week intervals were conducted to determine the dynamics of SARS-CoV-2 seroprevalence in four (4) districts within the epicentre of Ghana's outbreak from November 2020 to July 2021. The global and by age-group weighted seroprevalences were estimated, and the risk factors for SARS-CoV-2 seropositivity were assessed using logistic regression. The overall age-standardized SARS-CoV-2 seroprevalence for both SP and NC in Accra increased from 13.8% (95% CI: 11.9, 16.1) in November 2020 to 39.6% (95% CI: 34.8, 44.6) in July 2021. After controlling for other factors such as gender, marital status, education level, and occupation, the older age group over 40 had a higher odd of seropositivity than the younger age group (OR: 3.0 [95% CI 1.1-8.5]) in the final survey. Pupils or students had 3.3-fold increased odds of seropositivity (OR: 3.2 [95% CI 1.1-8.5]) compared to individuals who had never attended school. This study reinforces that, SARS-CoV-2 infections in Africa have been significantly higher than reported.

Keywords: SARS-CoV-2, COVID-19, Sero-epidemiological, Population-based, Ghana.

VR 041: COVID-19 in patients presenting with malaria-like symptoms at the Korle Bu Polyclinic, Accra.

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Abstract:

Malaria is one of Ghana's most frequent illnesses and the most common cause of febrile sickness. Most infectious diseases including COVID-19 and arboviral infections mimic malaria due to the overlapping of non-specific symptoms they both share. This study investigated COVID-19 in patients presenting with malaria-like symptoms at the Korle Bu Polyclinic, Accra. This study enrolled 300 patients presenting with malaria-like symptoms

aged ≤ 18. After consent was obtained from study patients, two to three millilitres of whole blood, nasopharyngeal and oropharyngeal swab samples were collected for screening of Plasmodium falciparum using malaria rapid diagnostic test, microscopy and nested PCR and SARS-CoV-2 using SARS-CoV-2 antigen test and Real-time PCR respectively. The whole blood sample was also used for the COVID-19 antibody test and full blood count using a haematological analyser. The detection of SARS-CoV-2 by COVID-19 Rapid Antigen Test and Real-time PCR were 60/300 (20%) and 26/300 (8.7%) respectively. Delta variant was reported in most SARS-CoV-2 positives with CT values below 30. The prevalence of malaria by microscopy, RDT and nested PCR were 7/300 (2.3%), 7/300 (2.3%) and 8/300 (2.7%) respectively. The most common symptom was headache (95%; 57/60). Comorbidities were hypertension, diabetes, Asthma, hypertension and diabetes. Most of the study patients had been previously exposure to SARS CoV-2 (113/300) and 66.7% (34/51) of AstraZeneca vaccinated patients had no antibody. Due to the synergy of symptoms, screening for COVID-19 in patients presenting with malaria-like symptoms is vital for immediate diagnosis and treatment.

Keywords**:** Malaria, COVID-19

VR 043: A longitudinal look at liver health among chronic Hepatitis B virus (HBV) infected persons in Ghana

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Abstract:

Although Hepatitis B virus (HBV) infection is known to compromise liver integrity, the extent of damage over time and their drivers are unclear. We compared liver function between chronic HBV patients not needing treatment with healthy controls every quarter over one year to ascertain liver integrity and factors that could influence it. Ninety-one pairs of cases and controls have been recruited. HBV infection was confirmed by screening for viral antigens and antibodies. HBV was quantified in cases at the study baseline and 7 months later. Additionally, liver enzymes were quantified quarterly over one year, compared between cases and controls, and the correlation with viral load was determined. At the start of the study, 11.8% of cases exhibited replicating HBV but this decreased to 3.6% at the end. Additionally, viral load at baseline did not significantly change after seven months ($p = 0.73$). The liver enzymes, Alanine transaminase (ALT) and Aspartate transaminase (AST) were significantly higher in cases than in controls at each time point although there was no significant change within the cases and controls from baseline to the end of the study. In contrast, Alkaline phosphatase (ALP) and gamma-glutamyl transferase (GGT) significantly decreased with time among both cases and controls. Also, an association between high viral load (>2000 IU/ml) and ALP levels ($p<0.001$) was found. Our findings point to an ongoing hepatocyte injury in cases which does not seem to change overtime. Furthermore, viral load not significantly changing with time may point to other drivers of liver injury.

Keywords: HBV, Liver-function, Viral load, Hepatocyte, Liver

VR 044: Dietary quality of HIV-exposed children aged 6 - 18 months and associated factors in the Greater-Accra Region of Ghana

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Abstract:

HIV-exposed children are at greater risk of malnutrition and to an extent, slower motor and cognitive development than their HIV-unexposed counterparts. WHO guidelines for infant and young child feeding recommends that children aged 6-23 months be fed meals at an appropriate frequency (Minimum Meal Frequency, MMF) and in sufficient variety (Minimum Dietary Diversity, MDD) to ensure that energy and nutrient needs are met (Minimum Acceptable Diet, MAD). This study aimed at assessing the dietary quality of HIV-exposed children 6-18 months in the Greater-Accra region of Ghana as part of a supplementation trial conducted by the Department of Nutrition, Noguchi Memorial Institute for Medical Research. A total of 648 mother-infant dyads were recruited from 19 facilities. Dietary quality for each child enrolled was assessed using the IYCF practice questionnaire. The percentage of infants who met the MDD by eating from more than five food groups was 11.1% and infants with MMF (2-4 meals in a day) were 53.9%. Children who achieved the MAD were 10.5%. Children born to older and employed mothers were more likely to meet their MAD as compared to younger mothers (OR=2.96, 95%CI [1.491, 5.875], p=0.002). HIV-exposed children in the Greater Accra region have a lower MAD (10.5%) compared to the national prevalence (13%). Also, having a younger mother puts a child at an increased risk of not achieving MAD.

Keywords: Dietary diversity, Minimum acceptable diet

VR 045: SARS-CoV-2 seropositivity amongst pregnant women attending a routine antenatal clinic or delivering at a general hospital in Ghana

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Abstract:

Viral infections during pregnancy predispose pregnant women to severe disease and adverse perinatal outcomes. With the coronavirus disease 2019 (COVID-19) pandemic, studies suggest prenatal infection with the Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) could increase the risk of severe symptoms and adverse birth outcomes. However, it is not clear how prenatal SARS-CoV-2 infection modulates existing immunity in pregnancy and impacts the efficiency of the maternofetal transfer of immunoglobulins. In sub-Saharan Africa, there are limited studies to estimate the burden of SARS-CoV-2 infection amongst pregnant women and related perinatal outcomes. In a hospital-based cross-sectional study, we determined SARS-CoV-2 positivity amongst pregnant women attending the antennal clinic and those admitted for delivery at a general hospital in Accra.

We screened oro/nasopharyngeal swabs from 600 pregnant women (400 antenatal and 200 at delivery) for SARS-CoV-2 by real-time RT-PCR from March to May 2022. Plasma from 185 of the participants (110 from ANC; 75 from delivery) was screened for SARS-CoV-2-specific IgG antibodies by ELISA. All samples tested negative for SARS-CoV-2 by RT-PCR indicative of no active SARS-CoV-2 infection. However, ELISA showed 93.2% of delivery and 96.4% of antenatal care had SARS-CoV-2-specific antibodies (IgG). This high seropositivity shows earlier exposure to or infection with the virus and is not vaccine-induced since less than 5% of our study population had taken the COVID-19 vaccine. Thus, pregnant women should be a priority population for education on COVID-19 transmission, vaccination and preventive measures to help reduce the risk of infection.

Keywords: SARS-CoV-2, seropositivity, pregnancy, vaccine

VR 046: Isolation and characterization of rotavirus strains that grow efficiently in the baby hamster Kidney BSR-T7 Cell Line

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Abstract:

Rotaviruses are a major cause of acute gastroenteritis in infants and young children. The recent development of a plasmid-based reverse genetics (RG) system that allows modification of the rotavirus genome represents critical progress in probing rotavirus biology and pathogenesis. A key step in the RG is the transfection of baby-hamster kidney cells expressing T7 RNA-polymerase (BHK-T7) with rotavirus T7 transcription vectors. BHK-T7 are inefficient in supporting rotavirus spread and amplification, therefore they are overseeded with MA104 cells to promote recovery of recombinant viruses. To avoid overseeding, we sought to identify and generate rotavirus strains capable of efficient growth on BHK-T7 cells. We created 8 inoculum pools (A – H), each containing 10 unique rotavirus strains. The pools were serially passaged on BHK-T7 cells. Only three pools (E, F, and H) caused CPE in BHK-T7 cells after 6-rounds of passage. Electrophoresis suggested that each pool contained only a single rotavirus strain. Next Generation Sequencing detected a chicken rotavirus CH2 (E), a simian-bovine (VP4) reassortant SA11-4F rotavirus (F), and a rhesus RRV rotavirus (H). The serially passaged CH2, SA11-4F, and RRV grew better on BHK-T7 cells than the same viruses used in preparing initial inoculums suggesting serial passaging selected for mutations favouring replication. These results suggest that it may be possible to modify the RG system such that overseeding with MA104 cells is not required either through the use of viruses adapted to the BHK-T7 cell line or through the inclusion of sequence determinants in viral genes that favour replication on BHK-T7 cells.

Keywords: Rotavirus; Reverse genetics; BHK-T7 cells

VR 047: Whole genome sequence analysis of historical AU-1-like Rotavirus A strains: evidence for direct interspecies transmission of rotavirus between humans and cats

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Abstract:

Occasional interspecies transmission events have contributed to the expansion of the genetic diversity of Rotavirus A strains. Available ample whole genome sequences from historical and contemporary Wa-like (genotype 1) and DS-1-like (genotype 2) RVAs have facilitated the establishment of robust evidence for direct interspecies transmission in these constellations. However, limited full genome sequences of strictly AU-1-like (genotype 3) strains exist with five strains of human origin and three strains of feline origin. In this study, the full genome sequences of 23 historical Japanese human and feline AU-1-like strains, including the prototype AU-1 strain were sequenced by the Illumina Miseq platform and analyzed to define the extent of genetic diversity within the RVA strains possessing strictly the AU-1-like genotype constellation. When the AU-1-like constellation is represented by AU-1-wt, 26 strictly AU-1-like strains (G3-P[9]-I3-R3-C3-M3-A3-N3-T3-E3-H3) were identified, of which 22 were determined in this study and four of which were previously published in the GenBank database. The 26 AU-1-like strains belonged to five lineage constellations each of which consists of two or more strains. Thus, even within the strict AU-1-like constellation, the genetic diversity at the sub-genotype level was higher than it was predicted from limited whole genome sequence data available before this study. Notably, two strains isolated from stray cats were >99.0% identical to a human AU-1-like strain in every genome segment. This observation provides robust molecular evidence for direct interspecies transmission of a rotavirus strain between cats and children.

Keywords: Rotavirus; AU-1-like; NGS; Phylogeny; Interspecies transmission

VR 048: Stability of homologous and heterologous sequence insertions in the rotavirus genome

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Abstract:

The rotavirus genome consists of eleven segments of double-stranded-RNA. Previous studies showed that viable recombinant rotaviruses with heterologous-sequence insertions can be made by reverse genetics. The heterologous-sequences are sometimes genetically unstable and are lost from the engineered genome during serial passage. In contrast, naturally occurring rotaviruses with sequence duplications exist which are genetically stable during serial passage. To understand factors connected to the genetic instability of foreign sequences in the rotavirus genome, we made a recombinant rotavirus (rSA11/NSP3-NSP3) that contained a segment-7/RNA with a head-to-tail partial duplication of the NSP3 coding sequence. The segment-7/RNA duplication was engineered such that only the first

copy of the NSP3 open reading frame (ORF) was expressed. Serial passage of rSA11/NSP3-NSP3 showed that, despite the long insertion, the virus was genetically stable. Competition growth experiments performed by mixing rSA11/NSP3-NSP3 and rSA11/wildtype showed that segment-7 (NSP3-NSP3) was preferentially packaged into progeny virus. This result suggests that duplicated rotaviral sequences may provide a pathway for increasing the genetic stability of long RNA insertions. To further explore this possibility, the segment-7 NSP3-NSP3 cassette was fused to a 2A element and UnaG or mRuby ORF immediately downstream of the first NSP3 ORF. Viruses with 1.5-kb NSP3-2A-UnaG-NSP3 and 1.8-kb NSP3-2A-mRuby-NSP3 RNAs were recovered, expressed UnaG and mRuby fluorescent proteins and were stable upon serial passaging. Taken together, these results suggest that placement of duplicated NSP3 sequences in rRVs containing long heterologous sequences may enhance genetic stability, a property critical for the development of rotavirus as a vaccine expression vector.

Keywords: Rotavirus; Genetic stability; NSP3; heterologous sequence

VR 049: Intragenotype reassortment events account for the apparent diversifying nature of the Rotavirus A G2P[4] NSP4 gene

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Abstract:

The Rotavirus NSP4 has come under scrutiny in recent years with a few studies exploring its diversity at the nucleotide and amino acid levels. This study explored the extent of G2P[4]/NSP4 genetic diversity at the phylogenetic/lineage level and provided insight into the evolutionary processes responsible for the observed diversity. Whole genome sequences of G2P[4] strains detected before and after vaccine introduction in Ghana-(2008-2013) were sequenced and compared to global G2P[4] strains by maximum likelihood and Bayesian phylogenetics using MEGA6 and BEAST v1.1.8, respectively. Their genotype constellation was G2-P[4]-I2-R2-C2-M2-A2-N2-T2-E2-H2. All genes except the NSP4 gene of strains detected in 2009, belonged to G2P[4] lineages - IVa(VP7, VP4, VP2, NSP1, and NSP5) and V(VP6, VP1, NSP2, and NSP3). Their VP3 genes changed lineages from V to VII just around the time of the countrywide rotavirus vaccine introduction in 2012. High genetic diversity among the NSP4 genes resulted in divergence into distinct lineages – V, VI and X shared with Ghanaian G2 strains detected during a RotaTeq vaccine trial and a few African RVA strains possessing G2P[6] and G3P[6]. Phylogenetic history and the time of the most recent common ancestor revealed sharing of a larger lineage with African G8 strains that have traces of animal-like genotype-2 genes as part of their genomes. In summary, the G2P[4] NSP4 gene diversified more frequently than other genes at the lineage level as a result of the recent acquisition of the NSP4 gene from non-G2P[4] DS-1-like strains by intragenotype reassortment.

Keywords: Rotavirus; NSP4; whole genome; genetic reassortment

VR 050: Dynamics of SARS-CoV-2 transmission in the Greater-Accra Region of Ghana

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The severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is gradually becoming an endemic pathogen in most populations. Naturally acquired immunity and vaccine-induced antibodies against SARS-CoV-2 variants may have contributed to the current decline in transmission intensity across different populations. However, the threat of novel SARS-CoV-2 variants emerging with better immune evasive and enhanced transmissibility features remains real and calls for continuous genomic surveillance. We assessed the transmission dynamics of SARS-CoV-2 in the Greater-Accra region of Ghana which was the epicentre of the outbreak in the country. Lineages were assigned using the Pangolin COVID-19 Lineage Assigner to identify the circulating variants in the population. The genomic sequencing data identified the major waves of transmission being primarily driven by the introduction of novel variants into the population. This underscores the need for sustained SARS-CoV-2 genomic surveillance to promptly identify and mitigate such threats and to inform related health policies in Ghana.

VR 051: Title: FCGR gene polymorphisms and reservoir size in HIV patients in Ghana

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Fc gamma receptors (FcγR) are cell surface glycoproteins that bind to the Fc portions of immunoglobulin IgG antibodies to elicit diverse effector functions. Polymorphisms in different FcγR genes have been associated with HIV infection and vaccine trial outcomes. Some studies have suggested that FcγRIIa may be a marker of latent reservoir size, however, this remains controversial. Hence whether FcγRIIa and other Fc receptors have functional consequences on the size or reactivation capacity of the reservoir needs to be investigated. In this pilot study, single-nucleotide polymorphisms (SNPs) in FcγRIIIa, FcγRIIa, and FcγRIIb genes were determined by Sanger sequencing in 50 HIV-infected ART-suppressed individuals. HIV reservoir size was determined by quantifying total HIV DNA (vDNA) and cell-associated unspliced (US) HIV RNA by qPCR. Association analysis was performed using three

coding SNPs, one per gene (FcγRIIIa-rs396991, FcγRIIa-rs1801274, and FcγRIIb-rs1050501). The median reservoir size as estimated by vDNA copy number was 116 (range, 1 - 5798) copies/million cells and US RNA was detectable in 15 out of the 50 samples. Our analysis found the reservoir size was almost 6 times larger in males compared to females who are suppressed. Reservoir size was observed to be larger in younger patients compared to those older, however, not statistically significant. However, there were no significant associations between the FcγR SNPs and HIV vDNA or US RNA. Studies in larger cohorts are necessary to explore associations between FcγR polymorphisms and HIV reservoirs.

VR 052: Surveillance for Dengue and Chikungunya viruses in selected health facilities in Ghana, 2018 - 2020

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Abstract

Cases of dengue fever and chikungunya virus disease, which are mosquito-borne tropical diseases, have been globally appreciated. These infections are characterised by febrile illness in addition to headache, body pains and a rash in some cases. In Ghana, patients presenting with symptoms of these diseases are usually screened and treated for malaria, typhoid, or Yellow Fever virus, without investigating for other possible causative viruses. This study sought to establish a differential diagnostic system for dengue and chikungunya Viruses and other endemic arboviruses and to identify these viruses that may be in circulation in selected health facilities in Ghana. The study enrolled patients who met the case definition. Human whole blood samples collected were screened with the use of serological kits and analysed for anti-Dengue and anti-Chikungunya viral antibodies.

A total of 1,105 participants were recruited for the 30 months serology prevalence study across the country in the years 2018 to 2020. Out of the 1105 study participants, the seroprevalence of the Dengue virus was estimated to be 61.63% (681/1105; 95%; 58.71 – 64.46). Out of the 1,053 study participants, the seroprevalence of the chikungunya virus was estimated to be 40.27% (424/1053; 95%; 37.34 – 43.26). For effective prevention and control strategies for dengue and chikungunya, it is vital to understand the various social, economic, and demographic risk factors that increase the odds of these infections in the population and the adoption of measures addressed to epidemic impact alleviation in most geographical areas

VR 053: The presence of SARS-CoV-2 on frequently touched surfaces in selected areas in Accra

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Severe Acute Respiratory Syndrome coronavirus type 2 (SARS-CoV-2), the virus that causes COVID-19 disease, has infected 594,590,450 million people leading to 6,453,982 million

deaths worldwide. Though transmission is mainly through respiratory droplets, surfaces contaminated with respiratory secretions containing the virus particle could be a possible transmission source. To understand indirect transmission dynamics of SARS-CoV-2 in Ghana and implement effective infection control measures, it is imperative to investigate the presence of SARS-CoV-2 on frequently touched surfaces at selected places like treatment centres, schools, and banks in Ghana. We present preliminary data on the presence of SARS-CoV-2 on some frequently touched surfaces. We swabbed and analysed 588 frequently touched surfaces at banks, schools, COVID-19 treatment centres, and a research laboratory for the presence of SARS-CoV-2. We categorized these into clinical and non-clinical settings. Surfaces were swabbed in the morning and afternoon. A total of 37 surface samples tested positive for SARS-CoV-2 RT-PCR. The results also revealed clinical settings had a majority (31/37) of surfaces contaminated with SARS-CoV-2 than non-clinical settings. Samples collected in the afternoon showed a higher positivity rate (25/37) than those collected in the morning (12/37), an indication that viral RNA could persist on these surfaces for some time. Our findings confirm the presence of SARS-CoV-2 on frequently touched surfaces and could be a possible transmission source. This supports the need for strict adherence to hand and environmental hygiene.

Key Words: SARS-CoV-2, frequently, touched, surfaces

DRUG DISCOVERY

DD 001: LC-MS Profiling and molecular docking analysis of bioactive compounds from Dissotis rotundifolia as new potential antifolate compounds against malaria

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Abstract:

Malaria is a major health issue in Africa and Asia contributing significantly to high morbidity and mortality. The major setback in eradicating the disease is marked by low effectiveness and increased resistance of parasites to antimalarial drugs. Medicinal plants such as Artemisia continue to be a potential source for identifying new antimalarial drugs. Amongst such is *Dissotis rotundifolia*, an ethnopharmacological plant used in West Africa to treat malaria. This study aimed at identifying new potential antimalaria drugs for *Plasmodium falciparum* by virtual screening of phytochemicals characterized from a whole plant extract of *D. rotundifolia* against *P. falciparum* Dihydrofolate Reductase using Molecular docking and molecular dynamics studies. A total of 30 phytochemical compounds from various classes were identified in the entire *D. rotundifolia* plant. Out of the 30 phytochemicals, 16 had binding energies less than or equal to -8.0 kcal/mol. CID 1286, CID 342737, CID 73571 and CID 71944 were identified among the top hits after molecular docking with binding energies of -8.4, -8.9, -8.6 and -8.9 kcal/mol respectively. ADMET analysis conducted revealed that the potential 4 compounds were bioavailable and were also predicted to be antiprotozoal. MD simulation and MM-PBSA calculation were performed to elucidate the stability and the binding free energy of the complexes. These compounds will further be investigated by in vitro and in vivo techniques to determine their potential efficacy against *P. falciparum*.

Keywords: Malaria, Dihydrofolate Reductase, molecular dynamics simulation

DD 002: Re-purposing of anti-infectives for the management of Onchocerciasis using machine learning and protein docking studies

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Abstract:

The discovery of new drugs for the treatment of Neglected Tropical Diseases (NTDs) has been significantly hampered due to the lack of financial reward associated with their development. These diseases are endemic in largely deprived populations who have little or no means to purchase them. Onchocerciasis is among the few that are yet to be eradicated and considering that there are a small number of drugs available for treating the disease, drug resistance is gradually becoming a major concern. Drug repurposing is a relatively

inexpensive strategy to overcome challenges and speed up drug development by taking advantage of the various existing compounds that have already established safety in humans. With the help of machine learning models and protein docking software, anti-infective drug agents which may be repurposed for treating onchocerciasis were investigated. A variety of unsupervised and supervised machine learning algorithms were employed to generate a meaningful model toward this goal. Among these algorithms, some of the best-performing ones included Random Forests, Bagged Decision Trees, Stochastic Gradient Boosting, the Multi-Layer Perceptron and Support Vector Machines. Our results indicated that 15 compounds may have some relevance in the management of Onchocerciasis. The drug interactions of these compounds with known protein targets of ivermectin, moxidectin and diethylcarbamazine were then investigated in silico via blind docking using the Python Prescription Virtual Screening tool (PyRx) and visualized with the BIOVIA Discovery Studio Client. The activity of these drugs may be further investigated in vitro.

Keywords: Machine Learning, Neglected Tropical Diseases

DD 003: Identification of potential SARS-CoV-2 main protease inhibitors from compounds isolated from reported anti-influenza effective plants via an integrated in-silico approach

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Abstract:

The coronavirus disease 2019 (COVID-19) pandemic has ravaged global populations causing deaths and exacerbating disease conditions. This is due to the highly infectious and drug-resistant nature of the causative agent SARS-CoV-2. Consequently prompting, an urgent need to identify compounds capable of inhibiting SARS-CoV-2. The main protease of SARS-CoV-2 (Mpro) has been identified as an important protein which contributes to the infectious nature of the virus as well as implicated in its viral replication cycle. We report here studies that used computational methods to identify potential inhibitors of Mpro from compounds extracted from anti-influenza effective plants. A library of 66 compounds was docked against the Mpro using AutoDock Vina. The molecular docking studies revealed two compounds 12795683 and 16142 with binding affinities -8.7 and 7.9 kcal/mol respectively, against Mpro which were higher than those of known antiviral drugs, lopinavir and remdesivir, undergoing clinical trials. The area under the curve of the receiver operating curve used to validate the docking protocol was 0.781, which was considered to be fairly good. The compounds exhibited good binding mechanisms against Mpro and were pharmacologically profiled to have tenable efficacies as well as negligible toxicity. Molecular dynamics simulations coupled with molecular mechanics Poisson-Boltzmann surface area (MM/PBSA) calculations on the Mpro-12795683 complex were used to analyze the conformational changes caused by protein-ligand interactions. Five compounds with PubChem compound identification numbers (CIDs), namely 12795683, 16142, 44387915, 46229104 and 5280961 were found

to be potential inhibitors worthy of further development as Mpro biotherapeutic agents.

Keywords: SARS-COV-2, Main protease, Molecular docking

DD 004: Molecular docking and molecular dynamics simulations studies identify potential cytochrome p540 17A1 inhibitors; abiraterone structurally similar compounds

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Abstract:

Prostate cancer is one of the leading causes of cancer-related deaths among males. The androgen receptor pathway is the target for most chemotherapeutic drugs. Abiraterone, an FDA-approved drug, is used to treat advanced prostate cancer via the inhibition of CYP 17 from producing testosterone, which drives a cascade of activities resulting in prostate cancer growth and its metastases. This work aims to identify potential inhibitors of CYP 17, that are structurally like abiraterone using computational approaches. Compounds structurally similar to abiraterone were prefiltered and virtually screened against CYP 17. The top three compounds, estazolam, 3-O-acetylepisamarcandin and 11beta,13-dihydrolactucopicrin, with binding energies -9.4, -10.0 and -10.1 kcal/mol, respectively, were selected since the binding energy of abiraterone was -9.4 kcal/mol. The interactions between CYP 17 and the compounds depicted that estazolam and 3-O-acetylepisamarcandin formed a hydrogen bond with Arg440 while 11beta,13-dihydrolactucopicrin formed hydrogen bonds with Ile371 and Arg96. All three compounds interacted with residues Ala113 and Ala302, which are the critical residues involved in the CYP 17 activity. A 20 ns molecular dynamics simulation was carried out to determine the stability and the mechanism of the CYP 17 and the CYP 17 – ligand complexes. In vitro analysis will be required to corroborate the results obtained. These compounds can therefore be used as scaffolds to design new inhibitors of CYP 17.

Keywords: Prostate cancer, CYP 17, Abiraterone, Simulation

DD 005: Computational identification of potential natural bioactive compounds targeting the immunomodulatory protein ancylostoma secreted protein -2 of the human hookworm

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Abstract:

Hookworm is a soil-transmitted helminth (STH) and one of the most common roundworms, with serious consequences for the human host. Anthelmintic medications have become less effective as a result of emerging resistance, according to recent research. The *ancylostoma*-secreted protein-2 (ASP-2) of the *Necator americanus* (Na-ASP-2) is a potential therapeutic

target because it is required for host survival. Furthermore, the functional properties of natural products have been identified as potent sources of novel anthelmintics. In silico methods for identifying potential inhibitors are quick and cost-effective. The study sought to identify natural bioactive compounds that could inhibit the expression of Na-ASPs. A total of 1470 pre-filtered compounds were screened against Na-ASP-2. The results of molecular docking were validated by an excellent Receiver operating curve (ROC) value. Seven compounds, Retusolide F, Epicocconigrone B, Nobilisine, Seneciphylline, Strigol, Cossonine, Glutinosine, Sarcophine, and ZINC000014780240 were predicted to have plausible pharmacological properties. Four of the compounds, Epicocconigrone B, Strigol, Sarcophine and ZINC000014780240 were predicted to have anthelmintic properties. Extensive research further revealed these compounds belonged to classes of molecules which are constituents of plants known to possess anthelmintic activity. These compounds shared some structural similarities to known anthelmintics compounds found in Drugbank. Molecular Mechanics Poisson-Boltzmann calculations helped gain a novel understanding of the binding mechanisms of the protein, culminating in the identification of Phe142, Met183, ARG94, HIS88, LEU97, GLU99 as critical residues required for binding and ligand design.

Keywords: Hookworm; Terpenoids; anthelminthics; Molecular docking, ASP-2

DD 006: The antiviral effect of Ghanaian herbal extracts and isolated compounds on SARS-CoV-2

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Abstract:

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), causes the coronavirus disease 2019 and threatens human health and public safety. Available SARS-CoV-2 vaccines reduce disease severity; however, effective drugs against SARS-CoV-2 infection are lacking. Since antiquity, medicinal plants have been used to prevent and/or treat infectious diseases. In Ghana, claims of herbal plants' curative, preventative, and immune-boosting potentials against COVID-19 were reported but with limited scientific data. We, therefore, screened 11 herbal extracts and 7 isolated compounds for their ability to inhibit SARS-CoV-2 replication in vitro. Vero-TMPRSS2 cells propagated in Dulbecco's Minimum Essential Medium containing 10% Fetal Bovine Serum, 1% L-Glutamine, sodium pyruvate and penicillin-streptomycin were infected with SARS-CoV-2. The MTT (3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyl tetrazolium bromide) assay was used to determine cytotoxicity levels of the test products, and TCID50 of virus isolate was determined. Test products were then added in varying dilutions to SARS-Cov-2 infected cells and incubated for 72h at 37˚C with 5% CO_2, alongside cell and virus controls. To determine virus inhibition, the culture supernatant was

harvested for RNA extraction and RT-qPCR analysis in duplicates. The neutralization effect was assessed via crystal violet staining of infected cells in triplicates. Six extracts (CPM01, CPM02, CVD2, Y1, MABP+, MACP+, and MAFP+) and 2 compounds (C3 and C4) showed inhibition of virus replication with a 2-6 log reduction in viral copies. The highest inhibitory activity of 6 log reduction was observed with MACP+, and CPM01 neutralized SARS-CoV-2 at titre 1:512. Our study provides evidence of the antiviral activity of herbal extracts against SARS-CoV-2.

DD 007: Epigenetic-modifying compounds identified as HIV latency-reversing agents in vitro

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Abstract:

The persistence of the latent reservoirs has prevented the eradication of the human immunodeficiency virus (HIV). They are the source of viral rebound after cessation of anti-retroviral therapy (ART). Latency reversing agents (LRAs) can be used to reverse latent reservoirs. HIV remains in latency during ART due to the modifications of the chromatin around the virus. We, therefore, screened a library of 150 epigenetic-modifying compounds to determine their latency-reversing ability using the JLAT 10.6 cell line which contains one copy of HIV-green fluorescent protein (GFP) reporter. The cells were incubated with 1uM or 10 uM of the compounds at 37°C with 5% CO2 for 24 hours. TNF alpha and Vorinostat were used as positive controls and DMSO as the negative control. Fluorescent-activated cell sorting (FACS) was performed to measure HIV reactivation from latency determined by GFP expression in the cells. Out of the 150 epigenetic compounds screened, 18 were positive hits with GFP expression ranging from 11% to 91%. Seventeen (17) compounds reactivated HIV at 1um while one (1) compound reactivated at 10um. Of the 18 positive hits, 9 were histone deacetylase inhibitors, 3 targeted epigenetic reader domains, 3 histone methyl transferase inhibitors, 1 dual phosphoinositide 3-kinase (PI3K) and pim inhibitor. The compound (MC1568) with 91% GFP expression is a class 2 HDACI. We report the establishment of a low throughput drug screening system and the identification of epigenetic compounds for HIV latency reversal. Further work will determine the ability of the positive hits to reactivate HIV in a primary cell latency.

Keywords: Epigenetic-modifying, Reactivate, Latency Reversing Agents, Reservoir

DD 017: Cryptosporidiosis: A potential anti-diarrhoeal natural product drug discovery journey in Ghana, West Africa

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Abstract:

The overwhelming resistance to current drugs and the exhaustion of drug development interventions, as well as synthetic libraries, have compelled researchers to resort to the use of novel drug candidates derived from natural products. Cryptosporidium, the causative organism of Cryptosporidiosis, is no exception. The diarrhoea-causing parasite is known to be the leading cause of death in children below age 5 in developing countries such as Ghana and second to rotavirus as the causative agent for diarrhoea in new-born calves and infants. Currently, the only FDA-approved drug for the treatment of Cryptosporidiosis is Nitazoxanide. It is, therefore, needful to develop novel alternative candidates as it could aid in the decrease in child mortality and malnutrition in developing countries. Even though there have been significant limitations to anti-cryptosporidial drug development in vitro and in vivo, essential advancements are being made and this review article addresses the need for research into natural products. Some studies discussed in this paper have stated potential plant extracts showing anti-cryptosporidiosis efficacy. With the wealth of medicinal plant products and Cryptosporidium in vitro culture expertise available in our labs at the Noguchi Memorial Institute for Medical Research, we are certain of making significant strides in the world of natural product Cryptosporidium drug discovery in Africa.

Keywords: Drug discovery, *Cryptosporidium*, natural products, drug

DD 008: In silico identification of potential inhibitors against lytA-encoded major autolysin (N-acetylmuramoyl-l-alanine amidase) of Streptococcus pneumoniae

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Abstract:

Pneumococcal meningitis is the inflammation of the meninges. If not treated and cured early, it can have long-term neurological and neurocognitive anomalies that affect the quality of life, lead to encephalitis and eventually cause death. It is caused by *Streptococcus pneumoniae*), one of the 12 priority pathogens listed by the World Health Organization. There are presumptions of toxicity, variations with mutations, chemo-resistance and poor efficacy of current therapeutic options. Therefore, there is a need to find novel active compounds to be used to design highly effective inhibitors against *S. pneumoniae*. In this report, computational techniques were employed to identify four molecules as a novel, potential lead compounds against the major autolysin, LytA of *S. pneumoniae* by screening African natural products and traditional Chinese medicine libraries. Structure-based molecular docking was used to identify these compounds: ZINC000056874331(picrasin B), (-)-6alpha-hydroxy-5alpha,8alpha,9alpha,10alpha-cleroda-3,13-dien-16,15-olid-18-oic acid, ZINC000095912784 and pinocembrin to have binding energy ≤ -7.0 kcal/mol against LytA and have the potential to inhibit the lytic activity of LytA. The compounds were predicted to have favourable binding characteristics, and pharmacological profiles and possess antibacterial, anti-inflammatory and anti-fungal activities with pinocembrin also predicted to possess anti-mutagenic and antioxidant. These compounds have the propensity to disrupt the release of toxins to hamper nasopharyngeal entry and colonization of S. pneumoniae,

however, further in vitro investigation is recommended to corroborate the findings of this study.

Keywords: Meningitis; lytA-encoded; autolysin; molecular docking; anti-inflammatory

DD 009: Computational approach to identify natural products as potential inhibitors of the Hepatitis C virus

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Abstract:

Hepatitis C virus (HCV) is a global health problem, resulting in liver inflammation that can develop into hepatocellular carcinoma. The NS5B polymerase of HCV is the most potent target for antiviral therapy against HCV because it plays a vital role in the replication of the virus. The adaptability of the HCV genome to vary its composition and the existence of multiple strains makes it more difficult to combat the emergence of drug-resistant HCV infections. HCV genotype 3 (GT3) has turned out to be the most difficult genotype to treat causing a financial burden on infected people. To search for new potent compounds against the HCV NS5B polymerase, modelling and docking techniques were performed followed by molecular dynamics (MD) simulations for a period of 100 ns. This study modelled a high-quality 3D structure of HCV NS5B GT3b using the crystal structure of NS5B genotype 1b (PDB ID: 3hkw) as a template. The potential inhibitors of the NS5B were screened out from an integrated library of 2049 compounds. The docking results obtained from AutoDock Vina were validated with Hepa acceptable area under the curve (AUC) of 0.738. The binding energies of the potential compounds were higher than that of the inhibitor Sofosbuvir. Gly557, Ser407 and Lys141 were predicted as key residues critical for ligand binding in the ATP binding pocket of the NS5B. This study identified six potential compounds after ADME analysis and were also predicted to have anti- hepatitis activity. Therefore, in vitro validation will be used to augment their potential as candidate biotherapeutic moieties.

Keywords: Molecular dynamics simulation, ADME, NS5B, Hepatitis

DD 010: Machine learning guided repurposing of anti-infectives for neglected tropical diseases; the case of onchocerciasis

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Abstract:

The discovery of new drugs for the treatment of neglected tropical diseases (NTDs) has been significantly hampered due to the lack of financial reward associated with their development. These diseases are endemic in largely deprived populations who have little or no means to purchase them. Onchocerciasis is among the few that are yet to be eradicated

and considering that there are a small number of drugs available for treating the disease, drug resistance is gradually becoming a major concern. Drug repurposing is a relatively inexpensive strategy to overcome challenges and speed up drug development by taking advantage of the various existing compounds that have already established safety in humans. With the help of machine learning models and protein docking software, anti-infective drug agents which may be repurposed for treating onchocerciasis were investigated. A variety of unsupervised and supervised machine learning algorithms were employed to generate a meaningful model toward this goal. Among these algorithms, some of the best-performing ones included Random Forests, Bagged Decision Trees, Stochastic Gradient Boosting, the Multi-Layer Perceptron and Support Vector Machines. Our results indicated that 15 compounds may have some relevance in the management of Onchocerciasis. The drug interactions of these compounds with known protein targets of ivermectin, moxidectin and diethylcarbamazine were then investigated in silico via blind docking using the Python Prescription Virtual Screening tool (PyRx) and visualized with the BIOVIA Discovery Studio Client. The activity of these drugs may be further investigated in vitro.

Keywords: Machine-Learning, Neglected Tropical Diseases, Onchocerciasis

DD 011: High-profiled drugs inhibiting Plasmodium falciparum dihydroorotate dehydrogenase: early drug discovery

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Abstract:

Antimalarial drug resistance has emerged as a threat to global malaria control efforts, underscoring the need for a continuous pipeline of new drugs to combat malaria. Malaria parasite relies exclusively on de novo pyrimidine biosynthesis to supply precursors for DNA and RNA biosynthesis. *Plasmodium falciparum* dihydroorotate dehydrogenase (PfDHODH) is an extensively studied class of enzymes that catalysis L-dihydroorotate to orotate in the de novo pathway. This study focused on identifying inhibitors of the substrate-binding activities of the PfDHODH using. using comparative in silico analyses. The parasite and human DHODH were extensively characterised. High throughput virtual screening of PfDHODH against 13,200 compounds from the Drugbank database was done. Ligands interacting with important substrate binding site residues were identified and subjected to molecular dynamics (MD) simulations to assess protein-inhibitor complex stability. Overall, parasite and human DHODH shared a sequence identity of 38.52%. Substrate binding residues Tyr169, Leu172, Gly181, Phe188, Asn195, Leu197, Leu501, Val502, Met506 in parasite differed from the human protein except for His185, Leu189, Phe171 and Arg265. 29 compounds bound tightly at the substrate binding site of PfDHODH making several hydrogens, polar, and Pi-alkyl interactions with functional residues. 23 of the 29 exhibited the highest stability during 100 ns MD simulations. In conclusion, inhibitors of the PfDHODH were discovered. These compounds are approved drugs used in the treatment of other infectious diseases and will be explored in laboratory assays for their potential activity.

Keywords: *Falciparum*, dehydrogenase, drug bank, docking, simulations

DD 012: Prophylactic effect of a quinone compound from Ōmura natural compound library against schistosomula migration in Schistosoma mansoni infected-mice.

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Abstract:

Praziquantel is the approved treatment drug for human schistosomiasis but has limited activity against juvenile worms. Also, the sole dependence on it raises concerns about the potential for increased drug resistance, which warrants the search for alternative drugs, ideally among natural compounds. In this study, the efficacies of three quinone compounds (namely 22, 31 and 32) from the Ōmura natural compound library, were assessed against *Schistosoma mansoni* worms, using in vitro and in vivo assays. Our results showed that the 3 quinone compounds exhibited activity against schistosomula with limited toxicity against mammalian cells. Additionally, prophylactic and treatments of compound 31 in experimental schistosomiasis showed significant inhibition of lung-stage schistosomula but not adult worms. The fluorescent microscopic analysis also revealed the ROS-inducing capability of compound 31. Further RT-qPCR analysis of compound 31-treated parasites revealed elevated expressions of some selected antioxidant enzymes including TGR, SOD, GST, PRx and GPx. These results suggest that compound 31 may kill schistosomula by inducing oxidative stress either via ROS production and/or antioxidant enzyme inhibition, thereby offering a protective effect at the onset of infection. This may be important since praziquantel is known to exhibit limited activity against schistosomula. However, to fully elucidate the mechanism of action of compound 31, and to understand in detail the parasite's response to the compound, a complete transcriptomic analysis of treated-parasite is currently ongoing using RNA-seq technology.

Keywords: Quinone, Ōmura natural library, *S. mansoni*,

DD 015: Anti-hyperglycaemic activity of Synedrella nodiflora (L) Gaertn (Asteraceae) whole plant extract in streptozotocin-induced diabetes in rats

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Abstract:

Synedrella nodiflora is a common weed in Ghana used for the treatment of epilepsy and pain. The ethanolic extract of the whole plant has demonstrated an anti-inflammatory, antioxidant, anticonvulsant, and hypoglycaemic effect in murine models. This study presents the anti-oxidant and anti-hyperglycaemic effects of the ethanolic extract of *S. nodiflora* in a diabetic rat model. Type-1 diabetes was induced in Sprague-Dawley rats by an intra-peritoneal injection of streptozotocin (STZ) (55 mg/kg). The diabetic rats were divided into seven groups (n=5) and administered SNE (100, 300, 1000 mg/kg, p.o), insulin (0.1, 0.3, 1.0 IU/kg, subcutaneous) or vehicle (untreated diabetic groups), respectively for 8 weeks. Bodyweight and fasting blood sugar were measured twice weekly. Serum biochemistry, haematological indices, organ histopathology, MDA and SOD assays were assessed. SNE (1000 mg/kg) significantly ($p < 0.05$) decreased the hyperglycaemia by 62% with a corresponding 4% increase in weight of the rats after 4 weeks. The extract also significantly decreased liver enzymes such as AST, ALT, and ALP and increased albumin levels when compared to the vehicle group ($p < 0.01$). SNE high dose (1000 mg/kg) showed a significant in SOD by 6.2% ($p < 0.05$) and a decrease in MDA levels by 18.1% ($p < 0.01$), indicating antioxidant activity. The ethanolic extract of the whole plant of *S. nodiflora* possesses anti-oxidant and anti-hyperglycaemic effects in diabetic rats.

Keywords: *Synedrella nodiflora*, anti-hyperglycaemic, anti-oxidant, diabetes

DD 016: Analgesic effects of Synedrella nodiflora (L) Gaertn (Asteraceae) whole plant extract in streptozotocin-induced diabetic neuropathy in rat

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Abstract:

Diabetic neuropathic pain is a painful condition caused by chronic progressive nerve disease resulting from long-standing hyperglycemia. Although conventional drug therapy for diabetic neuropathic pain is effective, they present with severe untoward side effects. This study was conducted to determine the possible analgesic effect of the ethanolic

extract of *Synedrella nodiflora* whole plant (SNE) in attenuating hyperalgesia and allodynia in STZ-induced diabetic neuropathy. Diabetes and diabetic neuropathy were induced by intraperitoneal injection with 55 mg/kg of freshly prepared streptozotocin (STZ) in female Sprague Dawley rats. The effects of SNE on behavioural indices, biochemical parameters, anti-nociceptive effect, histological alterations, and oxidative stress were investigated SNE significantly improved the behavioural indices of the experimental groups compared to the control group ($P < 0.001$). Serum biochemical parameters were not adversely affected. Lipid profile and kidney function tests showed no changes in the parameters measured; however, the higher doses (SNE 300 mg/kg and 1000 mg/kg) showed a significant decrease in urea levels ($P= 0.008$). The level of albumin was significantly elevated with the lower doses of the extract (100 mg/kg, $P= 0.0429$). SOD activity was lowered dose-dependently but did not lower malondialdehyde concentration in vitro ($P < 0.05$). There was improved myelination in the cerebral cortex of all treatment groups. SNE thus has analgesic activity against hyperalgesia and cold allodynia in diabetic neuropathy in rats. The study also suggests a potential therapeutic strategy for diabetic-induced demyelination as observed in the photomicrographs of the cerebral cortex of the rat's brain within the treatment groups.

Keywords: Diabetic, Neuropathy, Chronic, streptozotocin, Allodynia

BACTERIAL INFECTIONS OF PUBLIC HEALTH IMPORTANCE

BA 001: Evaluation of the surveillance system for the detection of new cases of tuberculosis in the Ga North Municipality.

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Abstract:

Tuberculosis contributes to about 5% of total deaths in Ghana annually, with as much as 70% of people unable to access treatment. The backbone of TB surveillance is case notification at national and subnational levels. This study assessed the TB surveillance system in the Ga North Municipality based on selected attributes and for its effectiveness in achieving its objectives. The updated CDC guidelines for evaluating public health surveillance systems served as the framework for this study. The study was conducted from January to March 2022 using face-to-face interviews with selected stakeholders, a semi-structured questionnaire and a document review at treatment and diagnostic facilities. Data analysis was performed using Epi Info 7 and Microsoft Excel. The primary goal of the TB surveillance system in the municipality was to increase case detection (target of 80% in 2020 and 95% in 2021). The surveillance system in the Ga North municipality achieved 83% case detection in 2020, which decreased to 57% in 2021. About 83% of respondents considered the surveillance system to be useful, 85% considered it to be simple, and 89% considered it acceptable. Challenges with diagnostics and screening strategies accounted for most of the outcomes observed. Tuberculosis surveillance plays a key role in case notification, reporting and subsequent treatment. The goal to end the TB epidemic in Ghana can only be reached through improved investment in diagnostics and targeted screening strategies.

Keywords: Tuberculosis, Surveillance, Evaluation, Accra

BA 036: Variable physiology of West Africa specialist Mycobacterium tuberculosis complex genotypes

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Abstract:

Tuberculosis (TB) is caused by a group of bacilli called *Mycobacterium tuberculosis* complex (MTBC). The human-adapted MTBC is the ubiquitous *M. tuberculosis sensu-scricto* or Mtbss (lineages (L)1-4 & 7) and the West Africa-restricted *M. africanum* or Maf (L5 and L6). Studies into carbon and nitrogen metabolism of the pathogen are paving way for the discovery of novel biomarkers for the development of new effective control tools. However, all these efforts are based on *Mtbss* to the neglect of *Maf* (causing over 40% TB in some countries). We used West Africa dominant MTBC genotypes to determine the potential influence of genomic diversity on growth physiology when using specified sources of carbon and

nitrogen. We carried out a comparative-mutational analysis of genes encoding specific carbon and nitrogen metabolism enzymes among the isolates. We observed at the lineage level that L4 grows significantly better followed by L5 and then L6 irrespective of the source of nitrogen or carbon. This observation is also supported by the number of lineage-specific mutations identified from our in silico comparative mutational analysis supported by the SIFT analysis. At the sub-lineage, we observed a very high within-lineage diversity among the five L5 and 3 L6 genotypes used in the study whereas the 3 L4 genotypes (including H37Rv) were the same. The slow growth of *Maf* irrespective of carbon/nitrogen sources may negatively impact the generalised treatment-regimen targeting rapidly dividing MTBC cells. *Maf*-associated TB cases might require a longer period of therapy compared to TB caused by *Mtbss*.

Keywords: Physiology, *Mycobacterium tuberculosis*, *M. africanum*

BA 037: Macrophage susceptibility to infection by Ghanaian Mycobacterium tuberculosis complex lineages 4 and 5 varies with self-reported ethnicity

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Abstract:

We sought to investigate the early phase of tuberculosis (TB) infection upon in vitro infection of macrophages derived from the blood of Ewe and Akan volunteers with *Mycobacterium tuberculosis* complex lineages 4 and 5. The study participants consisted of 16 controls among which Akan and Ewe self-reported ethnicity was equally represented as well as 20 cured TB cases consisting of 11 Akans and 9 Ewes. Peripheral blood mononuclear cells were isolated from both healthy controls and cured TB cases. CD14 monocytes were isolated and differentiated into monocyte-derived macrophages (MDMs) before infection with L4 or L5 endemic strains. The bacterial load was assessed after 2 hours (Uptake) as well as 3, 5, 7 and 14-days post-infection. We observed a significantly higher intra-cellular growth of L4 strains within control MDMs of Ewe participants compared to L5 ($p<0.001$) whereas within Akan macrophages, we observed a significantly higher growth of L5 compared to L4 ($p<0.001$). Although there was no significant difference in the growth assessment of the cured TB cases, the bacterial load at Day7 showed both L4 ($p=0.02$) and L5 ($p=0.02$) grew faster in Ewe macrophages compared to Akan macrophages. Analysis of the donors' white blood cell composition showed significantly higher CD4+ cell counts ($p=0.02$) and proportions ($p=0.02$) for Akan controls compared to the Ewes. Our results suggest that host genetic diversity influences the susceptibility of macrophages to MTBC infection in a lineage-dependent manner.

Keywords: Tuberculosis, *Mycobacterium tuberculosis*, macrophage, ethnicity, lineage

BA 005: Diagnosis of tuberculosis among covid-19 suspected cases in Ghana

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Abstract:

Symptoms of Coronavirus disease 2019 (COVID-19) include fever, cough, and shortness of breath similar to synonymous several viral and bacterial diseases. This, thence, requires differential diagnoses to ascertain the etiological cause of such symptoms. During the early stages of COVID-19 in Ghana, we used sputum collected as part of the national COVID-19 response system from the Greater Accra region to concurrently diagnose TB using GeneXpert MTB/RIF. TB-positive results were immediately communicated to the National Tuberculosis Control Programme (NTP) for follow-up and the commencement of anti-TB drug therapy. Seven hundred and seventy-four samples were analyzed from COVID-19 cases and 95 contacts out of which, 111(14.3%) tested positive for COVID-19. Six (0.8%) out of the 774 suspected COVID-19 individuals tested positive for TB. One TB-positive sample was also resistant to rifampicin. Two samples tested positive for both TB and COVID-19. Half (3/6, 50%) of the TB-positive samples came from the Ayawaso District, a known hotspot of community transmission of TB. This study harbingers the untold stories of undiagnosed TB in our communities. The detection of TB among COVID-19 suspected cases further emphasizes the need for differential diagnosis for appropriate management. Misdiagnosis of respiratory diseases often leads to improper patient care and mismanagement of treatable infections. This pilot study provides valuable information calling on the NTP to intensify community engagement and active case search to promote early detection and treatment of TB to ensure positive outcomes as most unfavourable outcomes of TB control are associated with late diagnosis and mismanagement.

Keywords: COVID-19, Tuberculosis, Coinfection

BA 007: Early life microbiome of Ghanaian infants

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Abstract:

Early development of the microbiome has long been associated with the general health and physical development of the infant. The use of antibiotics for pre-term infants, coupled with their underdeveloped immune systems, promotes intestinal bacterial communities that are less diverse and enriched with potential pathogens. We examined faecal samples from pre-term infants (cases) and full-term infants (controls) for the presence of bacteria. Samples were cultured and isolates were confirmed by the matrix-assisted laser desorption ionization-time of flight mass spectrometry (MALDI-TOF MS). Antimicrobial susceptibility testing of isolates was done using disk diffusion and interpreted according to a standard guideline (CLSI or EUCAST). Six hundred and seventy samples (262 meconium and 414 faecal samples) have been analyzed so far. Findings revealed that the most abundant genera in

all the tested samples were *Escherichia coli*, *Staphylococcus* and *Klebsiella pneumoniae*. *E coli* predominated in meconium and 1st week's faecal samples. Whilst the second-week samples were dominated by other Gram-positive (belonging to the genera *Corynebacterium* and *Rothia*), and Gram-negative bacteria belonging to the genera *Enterobacter, and Pseudomonas*, as well as some yeasts. Distinct differences were observed among the two groups, whilst preterm babies were dominated by Gram-positive bacteria, full-term babies were dominated by Gram-negative bacteria. Our study revealed diverse bacteria communities with the potential to impact physical and neurocognitive development and life course disease risk. Understanding these influences on life development will inform newborn care and parental education to identify microbial intervention strategies to promote the health of infants.

Keywords: Early childhood, gut microbiome, bacteria,

BA 008: Analysis of commonalities across the mucosal pathogens, Streptococcus agalactiae and Streptococcus pneumoniae.

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Abstract:

Streptococcus agalactiae and *Streptococcus pneumoniae* are implicated in pneumonia, sepsis, and meningitis in newborns. Pneumococcal conjugate vaccines face issues of serotype replacement/switching. *S. agalactiae* vaccines are in clinical trials. We proposed to look for conserved capsular polysaccharide biosynthetic genes and surface proteins with high similarities within their sequences. 2001 African genomes were used in this study. Amino acid sequence analysis was performed on the Linux command line. Pangenome analysis was performed using Prokka and roary command line software. Capsular polysaccharide biosynthetic genes similarity check showed regulatory and processing genes and glycosyl transferases as conserved genes across the pneumococcal strains that found good matches within the various strains of the GBS genomes. GBS-conserved genes with good similarity matches within the pneumococcal genomes were tyrosine-protein phosphatase, tyrosine-protein kinase, sugar transferase and acetyltransferase. Amino acid similarity check showed that some of the pneumococcal surface proteins that are currently being formulated for pneumococcal vaccines have found good matches with the GBS. Similarly, GBS Alp family proteins previously shown to be immunogenic have found good matches with the pneumococcus. The core genome analysis showed mainly genes involved in metabolic processes rather than immunogenicity or antigenicity. In conclusion, there is the possibility of finding common vaccine targets between pneumococcus and GBS. However, this will require more in vitro and in vivo studies.

Keywords: Vaccine, Target, Capsule, Pangenome, Serotype

BA 009: Genomic features of Extended-Spectrum Beta-lactamase producing Escherichia coli and Klebsiella pneumoniae recovered from surgical site infections in Accra, Ghana

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Abstract:

Extended-Spectrum beta-lactamase (ESBL) producing bacteria from surgical site infection (SSI) in Ghana has mainly been characterized using phenotypic methods. Using whole genome analysis, this study investigated ESBL-positive Klebsiella *pneumoniae* and *Escherichia coli* recovered from SSI. Isolates were identified using MALDI-TOF-MS; Antibiotic testing was interpreted according to the CLSI guideline (2021). Whole-genome sequencing was performed using the Illumina Miseq platform. Genomic characteristics of isolates were determined using the Center for Genomic Epidemiology and Pathogen watch online tools. Out of 73 ESBL-positive isolates recovered, 36 comprising *E. coli* (42%) and *K. pneumoniae* (58%), have been sequenced. These isolates are resistant to cefuroxime (100%), ciprofloxacin (n=35; 97%), cefotaxime (94%), sulfamethoxazole/trimethoprim (94%), tetracycline (96%), chloramphenicol (78%), and gentamicin (72%). Genomic analysis revealed diverse *E. coli* serotypes/ clones: O101:H4:ST2 (4), O8:H9:ST410 (4), and O25:H4:ST131 (3), O8:H9:ST471 (1), O102:H6:ST405 (1), O1:H25:ST1722 (1), O1:H8:ST38 (1). High-risk ST15 (4), ST39 (3), ST22 (2), ST530 (2), ST16 (1), ST133 (1), ST25 (1), ST147 (1), ST512 (1), ST323 (1), ST242 (1), ST307 (1), novel sequence type ST6243 (1), and O-serotype O1 (43%) were present among *K. pneumoniae* isolates including *K. quasipneumoniae* with sequence type ST414. Beta-lactam CTX-M-15 (94%), quinolone gyrA (94%), aminoglycoside aac(6')-Ib-cr (75%), antiseptics (69%) resistance genes, virulence genes encoding for siderophores, fyuA (75%), and iutA (78%) were detected. The presence of ST16 *K. pneumoniae*, an emerging high-risk clone and the *E. coli* pandemic ST131 clone underscores the importance of continuous surveillance.

Keywords: WGS, SSI, ESBL, *K pneumoniae*, *E. coli*

BA 032: Genomic analysis of Staphylococcus aureus isolated from clinical sources from eight hospitals in Ghana

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Abstract:

Staphylococcus aureus is a common pathogen isolated from clinical infections and can be resistant to a wide range of antimicrobials. Using whole genome sequencing (WGS) and bioinformatic analysis, the epidemiology, resistance, and virulence genes of 95 *S. aureus* isolated from clinical sources from eight hospitals across Ghana were investigated. WGS performed on *S. aureus* revealed 43% as methicillin-resistant *S. aureus* (MRSA). ST152 (37%,) was the predominant clone with the majority (80%) being MRSA. Other MRSA clones detected were ST5, ST121, ST15, ST1, ST852 and ST2021. Twenty-six different genes encoding resistance to 11 antimicrobial classes were observed with blaZ which confers resistance to beta-lactams (96%) as the most prevalent. Others resistance genes include beta-lactams [mecA, mecA1], phenicol [cat(pC221), cat(pC194)], tetracycline [tet(K)], macrolide [erm(C), fexB, erm(B)], diaminopyrimidine [dfrG], aminoglycoside [aph(3')-III, aac(6')-aph(2''), aac(6')-Ib-cr, aph(2")Ia, aadD], lincosamide [msr(A), erm(B), sal(A)], quinolone [aac(6')-Ib-cr, qnrD3], fosfomycin [fosD], and sulphonamide [sul1]. Virulence genes for enterotoxin, exfoliative and toxic-shock-syndrome toxins, hemolysins, siderophores, aerolysin, leukotoxins, serine-protease, and staphylokinase were also detected. A total of 17 replicon-type and 4 colicin-type plasmids were found to harbour resistance and virulence genes. The study provides valuable information for understanding the population structure and genomic content of *S. aureus* from clinical sources; the finding of isolates harbouring multiple resistance and virulence genes necessitates the need for continuous surveillance.

Keywords: *Staphylococcus aureus*, Whole-genome sequencing, Methicillin-resistant S. aureus

BA 010: Genomic investigations of Multi-Drug Resistant Enterococcus species recovered from raw meat and livestock

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Abstract:

Enterococcus species are notable opportunistic pathogens due to their inherent antimicrobial resistance (AMR) ability and virulence potential. *Enterococcus species* recovered from livestock and raw meat were investigated by MALDI-ToF mass spectrometry and antimicrobial susceptibility testing. Whole genome sequencing was performed on the multidrug-resistant (MDR) isolates. Sequence types, resistance and virulence gene content of isolates were determined using the Center for Genomic Epidemiology online platform. *Enterococcus species* were predominantly *E. faecalis* (96/236) and *E. faecium* (89/236) and overall, showed resistance to erythromycin (175/236), ciprofloxacin (127/236), tetracycline (74/236), linezolid (43/236), vancomycin (35/236), chloramphenicol (21/236) and ampicillin (5/236). MDR was observed in 23% (54/236) isolates. Detected AMR genes included vancomycin (VanC1XY, VanC2, VanXY), streptogramins (Isa(A), Isa(E), msr(C)), aminoglycosides (aac(6')-Ii, aph(3')-III, ant(6)-Ia, aac(6')-aph(2"), aac(6')-Iid, str), macrolides (erm(B), erm(T), msr(C)), tetracyclines (tet(M), tet(L), tet(S)) and lincosamides (Isa(A), Isa(E), Inu(B)). Virulence genes for biofilm formation, adhesins, sex pheromones, cytolysins,

hyaluronidase, oxidative stress resistance, quorum-sensing and anti-phagocytic activity were found among the isolates. Unlike *E. faecium*, sequence types associated with *E. faecalis* belong to nosocomial clones: ST4, ST16, ST480 and ST116. Close genetic relatedness was observed between isolates from meat and livestock. This study sheds more light on clones of MDR *Enterococcus species* circulating in raw meat and livestock and their potential to harbour multiple virulences and AMR genes.

Keywords: Whole-genome sequencing, multi-drug resistance, *Enterococcus* species

BA 011: Occurrence and antimicrobial resistance of Beta-Lactamase Producing Gram-Negative bacteria from clinical infections in Southern Ghana.

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Abstract:

Beta-lactamase-producing Gram-negative bacteria (GNB) are a public health concern due to their frequent resistance to a wide range of antibiotics. This study sought to investigate the antimicrobial resistance and occurrence of beta-lactamases: AmpC-, Extended-Spectrum Beta-Lactamase (ESBL)- and carbapenemases among a collection of archived GNB recovered from clinical infections. Isolates were investigated by Matrix Assisted Laser Desorption Ionization Time of Flight – Mass Spectrometry, Antimicrobial susceptibility testing, and multiplex Polymerase Chain Reaction. The 182 GNB analyzed originated from urine (n=114, 63%), wound (n=38, 21%), blood (n=22, 12%), throat (n=4, 2.2%), stool (n=3, 1.6%), and ear (n=1, 0.5%). *Escherichia coli* (45.6%) and *Klebsiella pneumoniae* (16.4%) were frequent among the isolates. Resistance to ampicillin (50%) cefuroxime (53%), norfloxacin (21%), ertapenem (21%), and cefoxitin (8%) were observed. Resistance to 3rd generation of cephalosporins was found in 58% of the isolates. Beta-lactamases found among the isolates (29%) include AmpC (6%), ESBLs (19%) and carbapenemase (4%). ESBL genes such as blaCTX-M (72%), blaSHV (66%), and blaTEM (46%) were predominant, followed by blaDHAM and blaFOXM (36%) of the AmpC family. Carbapenemase genes such as blaOXA-48 (3%), blaKPC and blaOXA396-like genes (1%) were also detected. One *K. pneumoniae* isolate was found to co-harbour AmpC (blaFOX+EBCM) and carbapenemase (blaKPC+blaOXA-48) genes. The finding of beta-lactamase-producing GNB harbouring multiple antimicrobial resistance genes, calls for continuous surveillance to inform treatment decisions in clinical settings.

Keywords: Beta-lactamases, Antimicrobial-resistance, 3rd generation cephalosporin-resistance

BA 012: Genome sequencing of Pseudomonas aeruginosa revealed multidrug-resistant global clones from surgical site infections

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Abstract:

Pseudomonas aeruginosa is difficult-to-treat in many infections. Genomic data available on this important pathogen is however scarce, particularly from surgical site infections (SSI). In this ongoing study, MALDI-ToF-mass spectrometry, antimicrobial susceptibility testing and whole genome sequencing (WGS) were used to investigate a collection of *P. aeruginosa* recovered from SSIs. Antibiograms of the isolates (n=61) showed resistance to amikacin (n=5; 8.2%), meropenem (n=9; 14.8%), cefepime (n=10; 16.4%), ceftazidime (n=10; 16.4%), piperacillin-tazobactam (n=10; 16.4%), gentamicin (n=15; 24.6%) and ciprofloxacin (n= 17; 27.9%). Multi-drug resistance (MDR) was observed in ten isolates (16.4%). WGS of 29 isolates revealed: O4 (n=2;6.90%), O5 (n=5;17.2%), O6 (n=3; 10.4%), and O11(n=16; 55.2%) as key serotypes. The collection also comprised global clones: [ST773 (n=3;10.4%), ST308 (n=4;13.8%), ST446 (n=2; 6.90%), ST357 (n=1;7.7%), ST654(n=1;3.85%), ST235 (n=1;3.45%), and ST244 (n=1; 3.45%)]. Genes encoding resistance to carbapenems [VIM-5, IMP-15, GES-1], beta-lactams [PAO, CTX-M-15, TEM-1B, OXA-50], aminoglycosides [APHs, AACs, AADs, ANTs], fluoroquinolones [qnrVC1, crpP], fosfomycin [fosA], and heavy metals [qacE] were detected. The finding of MDR global clones/serotypes threatens therapeutic options and existing infection prevention and control strategies.

Keywords: *Pseudomonas aeruginosa*, global-clones, multi-drug resistance, WGS

BA 033: Ticks and zoonotic tick-borne pathogens of livestock in the Kassena-Nankana Districts, Ghana.

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Abstract:

Ticks play a significant role in the transmission of infectious pathogens that affect both animals and humans, including U.S. military personnel whose medical readiness is affected due to increased morbidity. Even though tick-borne infections continue to increase globally, there are no effective measures to prevent infection spread. The Upper East Region of Ghana is a conducive environment for the proliferation and spread of disease-causing pathogens, especially those of zoonotic origin due to the high dependence on livestock production by inhabitants. With the trade of livestock across borders, there is an increased risk of zoonotic infections. This study focused on identifying tick species within selected sites in the Kassena-Nankana Districts and sought to determine infectious zoonotic pathogens in livestock. A total of 1,550 ticks were collected from 448 livestock that included cattle, sheep, and goats, with tick infestations recorded as 78.60%, 25% and 5.88%, respectively. *Amblyomma variegatum* (62.98%) was identified as the most predominant tick species. Out of the 491 tick pools screened, the tick-borne pathogens identified were *Rickettsia africae* (39.72%), *Rickettsia aeschlimannii* (14.66%), *Coxiella burnetii* (3.67%), *Theileria orientalis* (3.05%), *Babesia sp. Lintan* (2.04%), *Babesia bovis* (1.43%), *Theileria parva* (1.43%), Crimean-Congo haemorrhagic fever virus (0.41%) and *Babesia sp.* Xinjiang (0.2%). From the 276 livestock dry blood spots screened, tick-borne pathogens identified were *Babesia sp. Lintan* (8.7%), *Rickettsia spp* (3.26%), *Theileria orientalis* (2.17%) and *Theileria parva* (0.36%). The findings suggest an increased risk of zoonotic infections in animal handlers and livestock populations.

Keywords: Ticks, Livestock, zoonosis, Kassena-Nankana

BA 006: Molecular epidemiology and drug susceptibility profiles of Mycobacterium tuberculosis complex isolates from Northern Ghana

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Abstract:

A cross-sectional study was conducted in Northern Ghana to determine the population structure and regional prevalence of *Mycobacterium tuberculosis* complex (MTBC) sub/lineages and their susceptibility to isoniazid (INH) and rifampicin (RIF). Sputum specimens were cultured on Lowenstein-Jensen slants. Mycobacterial isolates obtained were confirmed as members of the MTBC by PCR amplification of IS6110 and rpoß and assigned lineages and sub-lineages using spoligotyping. Isolates were screened for their susceptibility to isoniazid (INH) and rifampicin (RIF) and MDR using the Genotype MTBDRplus. Of 294 mycobacterial isolates recovered, MTBC species identified were: 241 (82.0%) *M. tuberculosis sensu stricto* (Mtbss), 41 (13.9%) *M. africanum* and 4 (1.4%) *M. bovis* with 8 (2.7%) unidentified. The human-adapted lineages (L) identified (N=279) were L1 (8/279, 2.9%), L2 (15/279, 5.4%), L3 (7/279, 2.5%), L4 (208/279, 74.5%), L5 (13/279, 4.7%) and L6 (28/279, 10.0%) with three unidentified lineages. Among the 208 L4, the dominant sub-lineages in the region were Cameroon 120/208 (57.7%) and Ghana 50/208 (24.0%). We found 4.4% (13/294) and 0.7% (2/294) of the patients infected with MTBC isolates resistant to INH only and RIF only, respectively, with 2.4% (7/294) being infected with MDR strains. Whereas L6 was associated

with the elderly, we identified that the Ghana sub-lineage of L4 was associated with both INH and MDR ($p<0.05$), making them important TB pathogens in Northern Ghana and a growing public health concern.

Keywords: Northern Ghana, Spoligotype, *Mycobacterium*

BA 014: Diarrhoea-causing bacteria and their antibiotic resistance patterns among diarrhoea patients from Ghana

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Abstract:

Diarrhoea remains a major global health concern, particularly among children under five years with antimicrobial-resistant (AMR) strains of causative pathogens threatening to stymie control efforts, particularly in settings where treatment options are limited. A surveillance study was conducted between 2017 to 2021 to determine the prevalence and antimicrobial susceptibility profile of diarrhoea-causing bacteria in Ghana. Diarrhoeic stool samples were collected from patients and cultured on standard differential/selective media. The isolates were identified using MALDI-TOF bio-typing and serology. Antimicrobial susceptibility of the characterized isolates was done using Kirby-Bauer disk-diffusion and MicroScan autoScan4 MIC panels for extended-spectrum beta-lactamase (ESBL). Bacteria were isolated from (772/792) stool samples, and 167 of the isolates were diarrheagenic and met our inclusion criteria for AMR analysis. *Escherichia coli* (49.1%, 82/167), *Salmonella spp* (23.9%, 40/167), *Vibrio spp* (16.8%, 28/167), and *Shigella spp* (10.2%, 17/167) were among the species identified. We found resistance to cefotaxime (21/24, 87.5%), and ciprofloxacin (6/24, 25%) in 24 *Vibrio spp*, isolates including four multi-drug resistant isolates. Cefazolin resistance was found in all 13 *V. parahaemolyticus* isolates. Tetracycline resistance was found in all 17 *Shigella* isolates, as well as resistance to shigellosis drugs such as norfloxacin and ciprofloxacin. The *Salmonella spp* were resistant to norfloxacin (40/40, 100%). Two ESBL-producing *E. coli* were detected along with strains highly susceptible to gentamicin (66/72, 91.7%) and amikacin (57/72, 79.2%). These findings highlight the need for differential diagnosis to ensure appropriate management of diarrhoea cases.

Keywords: antimicrobial, bacteria, diarrhoea, resistance, susceptibility

BA 016: Evaluation of the use of automated urine analysers as screening tools for urinary tract infections in Ghana.

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Abstract:

Urinary Tract Infections (UTIs) are of great public health concern in Ghana due to their negative impact on health and livelihood as well as being a great contributor to antimicrobial resistance. This study sought to evaluate Automated Urine Analysers (AUAs) as predictive tools of positive urine culture using biochemical and cellular urinary markers; to improve rapid diagnosis and treatment of UTIs and ensure antimicrobial stewardship. A cross-sectional analysis of 357 urine samples was conducted measuring all biochemical and cellular markers of urine using an AUA. Standard laboratory culture of urine samples was performed on each sample concurrently to serve as the study reference. Results from culture showed 26.6% [95/357] samples being positive with prevalent uropathogens including *E. coli*, *Enterococcus sp.* and *Citrobacter sp*. Meanwhile, measures of biochemical markers were expressed as percentages of positive counts. Univariate logistic regression analysis revealed that the presence of nitrites, leukocyte esterase and blood in urine were significantly associated with the odds of UTI; while multivariate logistic regression analysis showed that nitrite (AOR= 15.80 (1.89-131.84), 95% CI, p<0.0001) and leukocyte measurement of 3+ (AOR= 2.71 (1.01-7.28), 95% CI, p<0.0001) were independently associated with increased odds of UTI. At a standard reference value of 58 bacteria cells/µL, the AUA could predict the probability of positive urine culture with 88.4% sensitivity and a specificity of 40.2%. This assessment proved that automated urine analysers could be very good screening tools for UTIs; cutting down diagnosis time and aiding antimicrobial stewardship.

Keywords: Antimicrobial Stewardship, Urine Analysers, UTIs

BA 017: Sepsis among neonates in a Ghanaian Tertiary Military Hospital: culture results and turnaround times

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Abstract:

In this study, we described the bacterial profile, antibiotic resistance pattern, and laboratory result turnaround time (TAT) in neonates with suspected sepsis from a tertiary-level, military hospital in Accra, Ghana (2017-20). This was a cross-sectional study using secondary data from electronic medical records. Of 471 neonates clinically diagnosed with suspected sepsis in whom blood samples were collected, the median TAT from culture request to report was three days for neonates who were culture-positive and five days for neonates who were culture-negative. There were 241 (51%) neonates discharged before the receipt of culture reports, and of them, 37 (15%) were culture-positive. Of 471 neonates, 29% (n = 139) were bacteriologically confirmed, of whom 61% (n = 85) had late-onset sepsis. Gram-positive bacterial infection (89%, n = 124) was the most common cause of culture-positive neonatal sepsis. The most frequent Gram-positive pathogen was coagulase-negative *Staphylococcus* (55%, n = 68) followed by *Staphylococcus aureus* (36%, n = 45), of which one in two were multidrug resistant. The reasons for large numbers being discharged before the receipt of

culture reports need to be further explored. There is a need for improved infection prevention and control, along with ongoing local antimicrobial resistance surveillance and antibiotic stewardship to guide future empirical treatment.

Keywords: Neonatal sepsis; bacteria; turnaround time

BA 018: Assessment of anti-tuberculosis chemotherapy response among TB only and TB-diabetes cases using different microbiological methods

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Abstract:

Tuberculosis is a global health emergency and resistance to available medication is hindering global control efforts. Reduction in viable bacterial burden has been the marker for monitoring treatment response in tuberculosis. We evaluated tuberculosis-molecular bacterial load assay (TB-MBLA) which estimates bacterial colony forming units based on the expression of 16S rRNA, culture and microscopy for monitoring treatment response among TB only and TB-diabetes (TBDM) cohorts. Serial sputa collected at days 0, 3, 7, 14, 28 and 56 during first-line anti-TB treatment were analyzed by microscopy, TB-MBLA and culture. A total of 324 serial sputa collected from 54 cases (43 TB and 11 TBDM cases) were analyzed using the 3 different methods. Both TB and TBDM cohorts had similar average bacterial loads at Day0 (p=0.27), but TBDM participants had significantly higher average bacterial loads at day14 (p=0.04) using MBLA. However, using microscopy and culture, we did not observe any significant difference in the bacterial load at the different time points for the two cohorts. We found the average time-to-culture positivity for TBDM longer (median=21) than that of TB (median=19, p=0.08) cohorts). However, there was no correlation between microscopy and culture (r=-0.004, 95% CI -0.26-0.26, p=0.97). Our findings suggest delayed Mtb clearance among TBDM cohorts and suggest TB-MBLA as the most reliable tool for monitoring TB treatment.

Keywords: Tuberculosis, MBLA, TB-Diabetes, 16S rRNA, Culture

BA 019: Molecular epidemiology of bovine tuberculosis in Northern Ghana identifies several uncharacterized bovine spoligotypes and suggests possible zoonotic transmission

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Abstract:

We conducted an abattoir-based cross-sectional study in the five administrative regions of Northern Ghana to determine the distribution of bovine tuberculosis (BTB) among slaughtered carcasses and identify the possibility of zoonotic transmission. Direct smear microscopy was done on 438 tuberculosis-like lesions from selected cattle organs and cultured on Lowenstein-Jensen media. Acid-fast bacilli (AFB) isolates were confirmed as members of the *Mycobacterium tuberculosis* complex (MTBC) by PCR amplification of IS6110 and rpoß and genotyped by spoligotyping. Data obtained were compared to Spoligotype patterns of clinical *M. bovis* isolates from the same regions to identify similarities. A total of 319/438 (72.8%) lesion homogenates were smear positive out of which, 84.6% (270/319) had a microscopic grade of at least 1+. Out of the 265, 60.5% (438) were culture positive, and 212 (80.0%) were MTBC. Two hundred and three isolates were identified as *M. bovis* (198, 97.5%), *M. caprae* (3, 1.5%), *M. tuberculosis* (Mtbss) lineage (L) 4 Cameroon sub-lineage, (1, 0.5%), and *M. africanum* (Maf) L6 (1, 0.5%). A total of 53 unique spoligotype patterns were identified across the five administrative regions with the most dominant spoligotype being SIT1037/ SB0944 (77/203, 37.93%). Analysis of the bovine and human *M. bovis* isolates showed 75% (3/4) of human *M. bovis* isolates sharing the same spoligotype pattern with the bovine isolates. Our findings suggest possible zoonotic transmission and highlight the need for BTB disease control in Northern Ghana

Keywords: Zoonotic transmission, *M. bovis*, spoligotyping, TB

BA 020: Gut microbiome variation in pulmonary TB patients with diabetes or HIV comorbidities

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Abstract:

The gut microbiota plays a critical role in shaping the host immunity, and metabolism and influences the onset and progression of both communicable and non-communicable diseases. This study assessed the gut microbiome of tuberculosis (TB) cases with diabetes mellitus (DM) or HIV comorbidities before anti-TB therapy and after the intensive phase of anti-TB therapy. Ninety cases comprising 60 TB-only, 23 TB-DM, and 7 TB-HIV were recruited, among which 35 TB-only, 10 TB-DM, and 5 TB-HIV were also sampled after 2 months of anti-TB treatment. The total gut microbiome was detected by 16S rRNA gene sequencing of DNA extracted from the collected stool specimen. The taxonomic and functional diversity

of the different groups were compared in addition to changes that could occur after 2 months of antibiotic use. Compared to the healthy controls, the gut microbiome of all the TB cohorts was characterized by a significantly decreased alpha diversity and significant compositional changes. All three TB cohorts were enriched with inflammatory-related microorganisms of the genera *Escherichia-shigella*, *Streptococcus*, *Enterococcus* and *Erysipelatoclostridium* with depletion in beneficial taxa of the genera *Faecalibacterium*, *Bifidobacterium* and *Clostridium*. In pairwise comparison with the healthy controls, the TB-only cohort was enriched with Streptococcus and *Erysipelatoclostridium*, the TB-DM enriched with Bacteroides, and TB-HIV enriched with *Escherichia-shigella*, *Dialister* and *Erysipelatoclostridium*. After the intensive phase of anti-TB therapy, there was general enrichment of the genera *Erysipelotrichaceae*_UCG 003, *Veillonella* and *Fusobacterium*. Our findings show a dysbiotic gut microbiome and associated upregulation of inflammation-related microorganisms in the gut microbiome of TB individuals with or without comorbidity

Keywords: Gut, Microbiome, TB, TB-DM, TB-HIV

BA 021: Evolution of glycated haemoglobin in tuberculosis patients with without diabetes: a longitudinal prospective cohort study

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Abstract:

We explored changes in glycated haemoglobin (HbA1c) among newly diagnosed TB patients with/without diabetes mellitus (DM) during and after TB treatment. TB patients with random blood glucose (RBG) ≥ 7mmol/L at baseline (t0), underwent an HbA1c test and were categorized into three groups: TB-only (HbA1c<6.5%) and diabetic group (HbA1c≥6.5%) consisting of those on DM treatment (TBDMt) and those without DM treatment (TBDMnt). Blood samples were taken for serum biochemistry, and HbA1c test at; baseline(t0), 3 months(t1), and 6 months(t2) during standard TB treatment, and 9 months(t3), which is 3 months post-treatment. Out of 559 TB patients recruited, 95 had RBG≥ 7mmol/L. 60 out of the 95 patients were TB-only, and 8 and 27 were TBDMnt and TBDMt respectively. The TBDMt showed fluctuations in median-HbA1c, although not significant from t0 (9.6% to t1(8.1% p=0.57; & t3(8.5% p=0.18). However, TBDMnt showed a significant decline in median-HbA1c from t0 (6.7% to t1(6.0% p=0.001; & t3(5.7% p=0.002). The TB-only cohort demonstrated a slight decline (not significant) in median-HbA1c from t0 (5.6%) to t1(5.4%) & t3(5.5%) p=0.37. The mean serum levels of ALT (73 vs 18, p=0.02), AST (51 vs 23, p=0.01), and urea (4.2 vs 3.3, p=0.04) at t0 were higher among the TBDMnt vs TBDMt cohorts, and increases were significant. Our study demonstrates the bidirectional relationship between TB and DM.

Keywords: glycated haemoglobin, diabetes, TB, treatment

BA 022: Genetic analysis of TB susceptibility variants in Ghana reveals candidate protective loci in SORBS2 and SCL11A1 genes

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Abstract:

Despite advancements made toward diagnostics, tuberculosis caused by *Mycobacterium africanum* (Maf) and *Mycobacterium tuberculosis sensu stricto* (Mtbss) remains a major public health issue. Human host factors are key players in tuberculosis (TB) outcomes and treatment. Research is required to probe the interplay between host and bacterial genomes. Here, we explored the association between selected human/host genomic variants and TB disease in Ghana. Paired host genotype datum and infecting bacterial isolate information were analysed for associations using multinomial logistic regression. *Mycobacterium tuberculosis* complex (MTBC) isolates were obtained from 191 TB patients and genotyped into different phylogenetic lineages by standard methods. Two hundred and thirty-five (235) Non-diseased participants were used as healthy controls. A selection of 29 SNPs from TB disease-associated genes with high frequency among African populations was assayed using a TaqMan® SNP Genotyping Assay and iPLEX Gold Sequenom Mass Genotyping Array. Using 26 high-quality SNPs across 326 case-control samples in association analysis, we found a protective variant, rs955263, in the SORBS2 gene against both Maf and Mtb infections (P BH = 0.05; OR = 0.33; 95% CI = 0.32-0.34). A relatively uncommon variant, rs17235409 in the SLC11A1 gene was observed with an even stronger protective effect against Mtb infection (MAF = 0.06; PBH = 0.04; OR = 0.05; 95% CI = 0.04-0.05). These findings suggest SLC11A1 and SORBS2 as potential protective genes of substantial interest for TB, which is an important pathogen in West Africa, and highlight the need for in-depth host-pathogen studies in West Africa.

Keywords: TB, SORBS2, SCL11A1, Mass Genotyping Array

BA 023: A molecular and epidemiological study of Vibrio cholerae isolates from cholera outbreaks in southern Ghana

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Abstract:

Cholera remains a major global public health threat. We conducted a molecular epidemiological study to detect virulence markers and antimicrobial resistance patterns of *Vibrio cholerae* isolates obtained from the 2012-2015 outbreaks in Ghana. Archived clinical isolates obtained from 2012, 2014 and 2015 cholera outbreaks in Ghana were revived by culture and subjected to microscopy, biochemical identification, serotyping, antibiotic susceptibility testing, molecular detection of distinct virulence factors and MLVA. Of 277 isolates analysed, 168 (60.6%) were confirmed to be *V. cholerae* and 109 (39.4%) isolates constituted other bacteria (*Escherichia coli*, *Aeromonas sobria*, *Pseudomonas aeruginosa*, *Enterobacter cloacae* and *Enterococci faecalis*). Serotyping the *V. cholerae* isolates identified 151 (89.9%) as Ogawa, 3 (1.8%) as Inaba and 14 (8.3%) as non-O1/O139 serogroup. The O1 serogroup isolates (154/168, 91.7%) carried the cholera toxin ctxB gene as detected by PCR. Additional virulence genes detected include zot, tcpA, ace, rtxC, toxR, rtxA, tcpP, hlyA and tagA. The most common and rare virulence factors detected among the isolates were rtxC (165 isolates) and tcpP (50 isolates) respectively. All isolates from 2014 and 2015 were multidrug resistant against the selected antibiotics. MLVA differentiated the isolates into 2 large unique clones A and B, with each predominating in a particular year. Identification of several virulence genes among the two different genotypes of *V. cholerae* isolates and resistance to first- and second-line antibiotics, calls for the scaleup of preventive strategies to reduce transmission, and the strengthening of public health laboratories for rapid antimicrobial susceptibility testing to guide accurate treatment.

Keywords: Cholera, MVLA, V. cholerae, virulence factors

BA 024: Staphylococcus aureus surgical site infections: insights from two hospitals in Accra, Ghana

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Abstract:

In Ghana, antimicrobial resistance is a growing concern and poses a challenge to treating surgical site infections (SSIs). Characterization of bacteria species causing infections is key in combating this problem. In this study, *S. aureus* isolates recovered from patients' SSI were investigated using MALDI-TOF-MS, Kirby Bauer disk diffusion, and whole genome sequencing. From a total of 452 patients, *S. aureus* isolates (7%; 31/452) recovered were all resistant to penicillin but susceptible to vancomycin. The majority of the isolates were also susceptible to rifampicin (97%; 30/31), trimethoprim-sulfamethoxazole (97%; 30/31), linezolid (90%; 28/31) and clindamycin (87%; 27/31). Eighteen (58%; 18/31) isolates were positive for the Panton-Valentine leukocidin (pvl) gene and 12 (39%) for the mecA gene. These mecA-positive isolates were resistant to tetracycline (58%; 7/12) and erythromycin (42%; 5/12) but all susceptible to rifampicin, trimethoprim-sulfamethoxazole and vancomycin. Thirteen

(four MRSA and nine MSSA) isolates sequenced showed that three related MRSA isolates belonged to PVL-positive t355 (ST152) with SCCmec type Iva and one PVL-negative to t002 (ST5) with SCCmec type Vc. MSSA isolates had varied STs with ST152 (3/9) being the highest. One isolate was also positive for the tst gene. Among all 13 isolates, there were several enterotoxin genes detected, with sei (31%; 4/13) being the most prevalent. The study reports for the first time pvl positive ST152-t355 MRSA clone from SSI in Ghana. This underscores the importance of proper surveillance as this community-acquired clone is associated with significant infections in patients without any risk factors.

Keywords: Surgical Site Infections, Whole Genome Sequencing

BA 025: Solid waste motor tricycle operators in Kumasi, Ghana, harbour respiratory pathogens; a public health threat

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Abstract:

The use of motor tricycles in transporting solid waste within urban centres in Ghana is on the increase. This activity often leads to the introduction of pathogen-containing bioaerosols into the environment, as well as to the tricycle operators. We sought to investigate the prevalence and associated risk factors of respiratory pathogens among waste tricycle operators. A cross-sectional study was conducted among 155 waste transporters who use motor tricycles using semi-structured interviews. Nasopharyngeal swabs were obtained from participants and screened for respiratory pathogens using Polymerase Chain Reaction. Pathogens detected in participants were SARS-CoV-2 (6.5%) and *Streptococcus pneumoniae* (6.5%), constituting an overall prevalence of 12.9% and a co-infection rate of 1.3%. The most common self-reported symptoms were cough (n = 67, 43.2%), sore throat (n = 44, 28.4%) and difficulty in breathing (n = 22, 14.2%). Adherence to the use of gloves (75.5%) and nose mask (71.0%) was high. The use of gloves, use of more than one PPE, and exposure to other pollutants ($p < 0.05$) were significantly associated with the detection of respiratory pathogens and individuals who were exposed to "other pollutants" significantly had lower odds of becoming infected with respiratory pathogens (Adj. OR (95% CI): 0.119(0.015,0.938). Although the prevalence of respiratory pathogens is generally low, strict adherence to Personal Protective Equipment use could further reduce these rates to even lower levels. Governmental health institutions

and informal solid waste transporters should address challenges related to exposure to pollutants, the use of gloves, and multiple PPE.

Keywords: Motor tricycle operators, respiratory pathogens

BA 026: Molecular surveillance uncovers methicillin-resistant Staphylococcus aureus dynamics in the burns unit of a tertiary care hospital

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Abstract:

Molecular surveillance is an important tool for the detection of disease outbreaks and outbreaks caused by antimicrobial-resistant pathogens. The study aimed to perform routine laboratory surveillance for methicillin-resistant *Staphylococcus aureus* in the Burns unit of a tertiary teaching hospital. Whole genome sequencing was performed on *S. aureus* isolates obtained from clinical samples from burn patients, healthcare workers and visitors of the patients. The study identified MRSA sequence types ST5, ST8 and ST152 circulating in the Burns unit. The change of MRSA genotype from ST250 previously to ST5, ST8 and ST152 highlight the importance of molecular routine surveillance. This is important for the detection of potential outbreaks caused by MRSA and the detection of new resistance genes.

Keywords: Molecular surveillance, *Staphylococcus aureus*, antimicrobial resistance

BA 027: Assessment of pathogenic bacteria in bushmeat in Ghana

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Abstract:

The handling, processing and consumption of wild animals (bushmeat) increase the risk of contracting zoonotic diseases. Management of bacterial zoonosis is further complicated when the etiological agent is resistant to commonly used antibiotics. Resistance observed in wild animals is of major concern to both human and animal health. We investigated the occurrence and antibiotic resistance patterns of several bacterial species identified in wild animal carcasses being processed for human consumption. Oral and anal swabs, and faecal and tissue samples were obtained from the carcasses of 60 wild animals (Grasscutters, Bush bucks, African Civets and Duikers) in the Ashanti region of Ghana. Bacterial load was determined by serial dilution and total plate counts. Bacteria were identified using MALDI-TOF biotyping and isolates were subjected to antimicrobial susceptibility tests (AST) against 12 antibiotics using the Kirby Bauer disk diffusion method. The mean coliform, Enterobacteriaceae and fungal counts were 9.79 log/cfu/g, 9.78 log/cfu/g and 11.8 log/

cfu/g respectively. A total of 522 isolates belonging to 20 genera were identified including *Escherichia coli* (18.0%), *Klebsiella sp* (15.5%), *Serratia sp.* (7.5%), *Pseudomonas sp.* (6.7%), *Yersinia ruckeri* (6.1%), *Enterobacter sp.* (5.0%), and *Acinetobacter sp.* (2.9%). Of 60 isolates tested for AST, the majority were resistant to Ampicillin (97.1%), Cefotaxamine (84.10%), Cefuroxime and Tetracycline (78.8%), Vancomycin (76.8%) and Meropenem (63.8%). The prevalence of pathogenic and multidrug-resistant bacteria in bushmeat is a serious food safety challenge that must be addressed with a one-health approach.

Keywords: Bushmeat, bacteria, antimicrobial resistance

BA 028: The burden of extensively drug resistance and pre-extensively drug resistance tuberculosis among multidrug-resistant Mycobacterium tuberculosis patients in Ghana

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Abstract:

The emergence of Extensively Drug-Resistant (XDR) and Pre-extensively drug-resistant (Pre-XDR) tuberculosis (TB) is threatening the management of multidrug-resistant tuberculosis patients worldwide. The first case of XDR-TB in Ghana was reported in 2018. The study sought to provide baseline data on the burden of pre-XDR-TB and XDR-TB in Ghana and the associated mutations. One hundred and seventy-one (171) archived MDR-TB isolates collected from patients across Ghana between January 2016 to December 2020 were retrieved. The isolates were retested to confirm their phenotypic and genotypic drug susceptibility to the first- and second-line anti-TB drugs using the BACTEC MGIT system, MTBDRplus 96, and MTBDRsl 96-line probe assays respectively. Of the 171 archival isolates collected, 81 (47.4%) were confirmed to be MDR, 12 (14.8%) were Pre-XDR-TB and no XDR-TB was detected. The katG S315T1 (73.3%) and rpoB S531L (42.5%) were the common mutations observed among isoniazid and rifampicin-resistant isolates respectively. Majority of the mutations that caused pre-XDR-TB were D94A (gyrAWT3+gyrAMUT3A and gyrAMUT3A) (50.0%) for fluoroquinolone and C1402T (rrsWT1) (50.0%) for aminoglycosides. The other detected mutations were A90V, D94G and S91P (16.7%) each for fluoroquinolones and rrWT2 (33.3%) and G1484T (16.7%) for the aminoglycosides The proportion of pre-XDR-TB among MDR-TB patients in Ghana was 14.8% and no XDR-TB was detected. Nonetheless, sustained surveillance of pre-XDR-TB and XDR-TB is advocated.

Keywords: Extensively Drug-Resistant Tuberculosis, Pre Extensively Drug-Resistant Tuberculosis, Multi-Drug Resistant Tuberculosis, Ghana, Mutations

BA 029: Gene expression and cytokine profile of extrapulmonary tuberculosis patients in Ghana

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Abstract:

Extrapulmonary tuberculosis (EPTB) is mostly paucibacillary and usually requires the use of complex invasive methods to obtain samples for diagnosis. We sought to identify potential diagnostic biomarkers for EPTB in blood. We measured and compared the serum levels of 25 analytes comprising cytokines, chemokines and growth factors among 20 EPTB and 10 pulmonary TB (PTB) patients and 10 healthy controls using Human Magnetic Luminex Immunoassay. The diagnostic potential of differentially significant cytokines was determined by receiver operating characteristic (ROC) curve analysis based on area under curve (AUC) values. Additionally, differentially expressed genes (DEGs) in five EPTB, two PTB and two healthy controls (HC) were determined using microarray (Agilent Gene Expression 8x60K Chip). Gene Ontology and Reactome Pathway analysis were used to determine the biological relevance of DEGs. The concentrations of IL-1Ra, IL-2R, IL-6, IL-10, IL-15 and MIG were significantly higher in EPTB patients compared to HC. Similarly, there were significantly higher concentrations of IL-4, IL-10 and IL-15 in EPTB patients relative to PTB patients. IL-1RA [AUC=0.81, (0.61-1.00)] and IL-10 [AUC= 0.84, (0.70-0.98)] showed the greatest potential to discriminate EPTB from HC and EPTB from PTB respectively. A total of 30 DEGs were uniquely identified in EPTB. The majority of the DEGs encoded proteins associated with transport, immune response and cell migration. Our results suggest that IL-1RA and IL-10 may be potential biomarkers for diagnosing EPTB relative to HC and PTB respectively. Also, DEGs including NUP107, GALR3, POLR2I, STEAP3, RCL1, CD177, USP42, ND2 could be candidate genes for EPTB diagnosis.

Keywords: Extrapulmonary tuberculosis, cytokines, microarray, Ghana

BA 030: The burden of extensively drug resistance and pre-extensively drug resistance tuberculosis among multidrug-resistant Mycobacterium tuberculosis patients in Ghana.

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Abstract:

The emergence of Extensively Drug-Resistant (XDR) and Pre-extensively drug-resistant (Pre-XDR) tuberculosis (TB) is threatening the management of multidrug-resistant tuberculosis patients worldwide. The first case of XDR-TB in Ghana was reported in 2018. The study sought to provide baseline data on the burden of pre-XDR-TB and XDR-TB in Ghana and

the associated mutations. One hundred and seventy-one (171) archived MDR-TB isolates collected from patients across Ghana between January 2016 to December 2020 were retrieved. The isolates were retested to confirm their phenotypic and genotypic drug susceptibility to the first- and second-line anti-TB drugs using the BACTEC MGIT system, MTBDRplus 96, and MTBDRsl 96-line probe assays respectively. Of the 171 archival isolates collected, 81 (47.4%) were confirmed to be MDR, 12 (14.8%) were Pre-XDR-TB and no XDR-TB was detected. The katG S315T1 (73.3%) and rpoB S531L (42.5%) were the common mutations observed among isoniazid and rifampicin-resistant isolates respectively. Majority of the mutations that caused pre-XDR-TB were D94A (gyrAWT3+gyrAMUT3A and gyrAMUT3A) (50.0%) for fluoroquinolone and C1402T (rrsWT1) (50.0%) for aminoglycosides. The other detected mutations were A90V, D94G and S91P (16.7%) each for fluoroquinolones and rrWT2 (33.3%) and G1484T (16.7%) for the aminoglycosides The proportion of pre-XDR-TB among MDR-TB patients in Ghana was 14.8% and no XDR-TB was detected. Nonetheless, sustained surveillance of pre-XDR-TB and XDR-TB is advocated.

Keywords: Extensively Drug-Resistant Tuberculosis, Pre Extensively Drug-Resistant Tuberculosis, Multi-Drug Resistant Tuberculosis, Mutations, Ghana

BA 031: Identification of plasma cytokine/chemokine biomarkers for discriminating between active Tuberculosis and latent Tuberculosis infection

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Abstract:

Latent tuberculosis (LTB) is an asymptomatic stage of tuberculosis infection defined based on the cellular immune response to mycobacterial antigens. Individuals with LTB are not infectious; however, they remain potential reservoirs of active TB (ATB) thus being a barrier to the global eradication of TB. Diagnostic assays that can discriminate between ATB and LTB, identify individuals at risk of developing ATB or monitor response to LTBI treatment are required. However, the tuberculin skin test (TST) and the single cytokine-based interferon-gamma release assay (IGRA) currently used for the diagnosis of LTB cannot perform these functions. Alternate single or multiple cytokine biomarkers are needed. We quantified and compared the plasma levels of pro-inflammatory cytokines (TNF-α, IFN-γ, IL 12p70, IL-17A, Granzyme B) and anti-inflammatory cytokines (IL-10, IL-6, IL-4) among 71 individuals with LTB (13), ATB (46), and 12 healthy controls (HC) using the Human Magnetic Luminex™ 200 system. The plasma levels of the same set of cytokines were also assessed at four-time points during treatment for ATB. IFN-γ, IL-6, IL-10, IL-4, and IL-17A levels were higher in LTB compared to ATB patients. A 21-fold increase in IL-12p70 levels was observed in ATB compared to LTB. Of the 8 cytokines, IL-4 and IL-12p70 had the greatest predictive potential to differentiate between ATB and LTB (AUROC 100%). A significant increase in IL-12p20 levels was observed from baseline up to treatment completion (month 6). The quantitative estimation of IL-12p20 may be a very useful marker to discriminate ATB from LTBI as well as monitor treatment success.

Keywords: Latent/Active TB, cytokines, Luminex Assay

BA 032: Multi-drug Resistant E. coli from urban environmental sources in Ghana: A public health concern

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Abstract:

In most low-income countries, the discharge of partially treated or untreated wastewater into water bodies and pollution of the environment by other anthropogenic activities may be an important factor in the spread of antibiotic-resistant bacteria. Here, we characterized environmental *E. coli* isolated from effluents from three hospitals, a wastewater treatment plant, and its receiving waters. The hospital ($9.9x10^3$), sewage ($1.4x10^4$) and receiving ($8.4x10^3$) water samples collected were positive for *E. coli*. Isolates were frequently resistant to ampicillin (64%), meropenem (47%), azithromycin (46%), sulfamethoxazole-trimethoprim (42%), ciprofloxacin (32%), cefotaxime (24%), cefuroxime (17%) and ceftriaxone (15%). The 23 MDR isolates recovered were sequenced on the Illumina MiSeq platform. Genomic analysis showed that 10 (47%) isolates were extended spectrum beta-lactamase (ESBLs) producers with *blaTEM1B*, *blaOXA-1 blaTEM-1C*, *blaCTX-M-15*, *blaOXA-181*, and *blaDHA-1* as common resistant genes. The prevalent *E. coli* clones include: ST21, ST845, ST342, ST19, ST866, ST446, ST137, ST492, ST390 and ST700. A total of 116 virulence genes were identified including those responsible for adhesion, invasion, and toxins. The study provides insights and baseline information on characteristics of MDR *E. coli* isolates from environmental sources to inform surveillance intervention to reduce the spread antibiotic resistant bacteria species in the environment.

Key words: *Escherichia coli*, antibiotic resistance genes, whole genome sequencing, environment

MALARIA/OTHER PROTOZOAN INFECTIONS

MA 001: Simian Malaria in Humans; A study of communities inside Mole National Park.

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Abstract:

Zoonotic malaria is an emerging public health concern since there have been dozens of reports of *Plasmodium knowlesi* being responsible for several severe malaria cases in Malaysia, Singapore and the Philippines. Therefore, studies on simian malaria in human populations is very essential especially if malaria is ever to be eradicated. In this study,172 samples obtained from asymptomatic individuals living in the Mole National Park were analysed using microscopy, rapid diagnostic tests (RDTs), and polymerase chain reaction (PCR). Microscopy and RDT had a comparable result of 20.3% (35/172) of Plasmodium-infected participants. Using PCR, the proportion of the participants that were found to harbour *Plasmodium falciparum*, *Plasmodium malariae*, and *Plasmodium ovale* as mono and mixed infections were 52.3% (90/125), 16.9% (29/125) and 39% (67/125), respectively. The majority of the *P. falciparum*, *P. malariae* and *P. ovale* infections were detected as mixed infections. Analysis across age groups indicates that Plasmodium species infection was highest (46.4%) among individuals above 20 years and lowest (2.40 %) in the age group of 0 - 5 years. No study participant was found to harbour any of the five simian *Plasmodium* parasites- *P. knowlesi*, *P. cynomolgi*, *P. inui*, *P. coatneyi or P. fieldi*. Although no simian malaria parasite was detected among our participants, the recent reports on the increasing prevalence of non-falciparum *Plasmodium* species underscore the need for continuous surveillance of these parasites among both asymptomatic and symptomatic individuals as we aim towards zero malaria transmission.

Keywords: Asymptomatic, *Plasmodium*, Zoonotic, Detection, non-falciparum

MA 002: Characterization of IgG subclasses against Plasmodium malariae Reticulocyte Binding Protein 1a (PmRBP 1a)

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Abstract:

The biased focus of vaccine and drug development programs on *Plasmodium falciparum* and *Plasmodium vivax* at the expense of other human malaria-causing Plasmodium spp. has an evolutionary impact on non-falciparum and non-vivax spp that could stymie global malaria elimination and eradication efforts. As a result, there is rising support for the development of a species-transcending vaccine against human malaria parasites. *Plasmodium malariae* is one of the neglected species whose prevalence is believed to be underestimated due to its characteristic low parasitemia presentation. Though it causes mild malaria, it is implicated in nephrotic syndrome and other complications such as anaemia, convulsion and death. *P. malariae* reticulocyte binding protein (PmRBP1a) has

been shown to potentially be a major player during the invasion of erythrocytes by *P. malariae*. This calls for the need to assess this antigen as a potential vaccine candidate. Hence, this study will evaluate the functional affinity of naturally acquired IgGs to *P. malariae* reticulocyte binding protein, a potential vaccine candidate and assess the differential pattern of IgG subclass responses to this antigen. An ELISA-based avidity and subclass typing will be employed for the evaluation. The results will provide insights into the poorly understood transmission dynamics of *P. malariae* and inform the vaccine candidacy of PmRBP1a.

Keywords: Vaccines, Antigens, *Plasmodium malariae*, Immunology, Pathogens

MA 067: Effect of environmental factors on mosquito larval abundance in some selected larval sites in the Kintampo area of Ghana

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Affiliations: [1]*Kintampo Health Research Centre,Ghana;* [2]*Presbyterian University Ghana*

Abstract:

The abundance of malaria vectors is influenced by micro-ecology, rainfall, and temperature patterns. The main objective of the study was to identify mosquito larval breeding sites for future larval surveys and possible intervention programs. The study was conducted in Kintampo located in the middle belt of Ghana. Twenty larval sites were surveyed. Larval density was determined per cm2 of water from each of the various sites. The dipper was used to fetch larvae from the larval sites and a Global positioning system (GPS) was used to identify larvae locations. There was a negative linear relationship between humidity, temperature, ph, and mosquito larval density. GPS of larval sites were taken for easy larval identification. There was the presence of Anopheles mosquito larvae in all polluted waters with *Culex* larval presence. This shows that *Anopheles* mosquito larvae are beginning to adapt to survival in polluted waters. The identified breeding sites are going to be useful for future larval surveys and will also help in intervention programs

Keywords: larvae, Culex, Anopheles, GPS, Dipper

MA 003: Baseline susceptibility of Anopheles gambiae to clothianidin in northern Ghana

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Abstract:

Clothianidin, an insecticide with a novel mode of action, has been deployed in the annual indoor residual spraying programme in northern Ghana since March 2021. To inform pragmatic management strategies and guide future studies, baseline data on local Anopheles gambiae s.l susceptibility to the clothianidin insecticide were collected in Kpasolgu, a village

in the Northern Region, of Ghana. The phenotypic susceptibility of *Anopheles* mosquitoes to clothianidin was determined using the WHO insecticide resistance monitoring bioassay. The WHO cone bioassay was conducted on mud and cement walls sprayed with Sumishield 50 WG (with clothianidin active ingredient). Mortality rates were observed up to 168 hours. Species of the An. gambiae complex present in the area and the detection of insecticide target-site mutations (knockdown resistance [kdr] and Acetylcholinesterase [Ace-1]) were determined by PCR. The WHO susceptibility bioassay revealed a delayed killing effect of clothianidin. Mosquitoes exposed to the cone bioassays for five minutes died 120 hours after exposure. Slightly higher mortalities were observed in mosquitoes exposed to clothianidin-treated cement wall surfaces than in mosquitoes exposed to mud wall surfaces. The kdr mutation occurred at very high frequencies (0.89-0.94) across all vector species identified whereas the Ace-1 mutation occurred at moderate levels (0.32-0.44). An. gambiae s.s was the most abundant species observed at 63% whereas *An. arabiensis* was the least observed at 9%. *An. gambiae* s.l. mosquitoes in northern Ghana were susceptible to clothianidin. They harboured kdr and ace-1 mutations at high frequencies

Keywords: Anopheles gambiae, Insecticide Resistance, Clothianidin

MA 004: The impact of haemoglobinopathies on Plasmodium falciparum infection among children in Northern Region, Ghana

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Abstract:

The effect of human erythrocyte variants encoding for most haemoglobinopathies on *P. falciparum* parasite carriage has been reported only on a few variants. In this study, we investigated the prevalence of Hb A, S, C, and F variants and alpha thalassaemia on the risk of *Plasmodium falciparum* infection among children in Ghana. A cross-sectional study was conducted among 1,045 children (1-14 years) in 13 malaria-endemic communities in the Northern Region of Ghana. *P. falciparum* infection and Hb phenotypes were diagnosed by malaria rapid diagnostic (RDT) and SickleSCAN tests, respectively, and confirmed with PCR. IgG responses against malaria antigens (CSP, GLURP, MSP3, *Pf*s230, and two *Pf*EMP1 proteins) and crude asexual blood-stage antigens were measured by ELISA. Our findings indicated that the wild-type Hb (HbAA) was most frequent (70.2%), followed by HbAC (17.8%) and HbAS (8.5%). Other phenotypes (HbCC and HbSS) were less frequent (< 1%). Overall, 29% were heterozygous and 5.6% were homozygous mutants for alpha-thalassaemia. HbAC and HbAS were co-inherited with alpha-thalassaemia. *P. falciparum* infection risk was about three times higher among homozygous alpha thalassaemia individuals carrying HbAC (OR=2.97, p=0.09) and heterozygous carriers with HbAS variants (OR=2.86, p=0.09). HbAS individuals had significantly lower anti-*Pf*EMP1 and higher anti-CSP antibodies. Co-inheritance of haemoglobinopathies observed among the children increased their risk of *P. falciparum* infections in HbAC and HbAS carriers, suggesting an epistatic mechanism. Antibody responses against non-*Pf*EMP1 antigens were higher among homozygous carriers, an indication of enhanced immune responses due to exposure to parasites.

Keywords: Haemoglobinopathies, *Plasmodium falciparum*, malaria, alpha-thalassaemia

MA 005: Burden of anaemia and its association with asymptomatic malaria among pregnant women in antenatal clinic in a malaria endemic setting

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Abstract:

Anaemia remains a serious concern among pregnant women, and thus, it is closely monitored from the onset of pregnancy through to delivery to help prevent adverse maternal and neonatal outcomes. In malaria endemic-settings, continuous low-level carriage of P. falciparum parasites is common and its contribution to maternal anaemia cannot be underestimated. In this study, we evaluated the adherence to antenatal care (ANC) protocols (e.g. the number of antenatal visits, intake of malaria prophylaxis, folic acid supplementation, use of insecticide-treated bednets) and the association with anaemia and asymptomatic malaria among women on ANC visits in Hospitals in the Central region of Ghana. The study was conducted between two seasons; October-November 2020 (dry season, n=124) and May-June 2021(rainy season, n=138). Among the women, there was a high adherence to the ANC protocols, and these did not differ between the two seasons. The occurrence of anaemia was high for both seasons (57.3% for the dry season; 66.7% for the rainy season) and was associated with the carriage of P. falciparum parasites. Despite the high adherence to ANC protocols, asymptomatic *P. falciparum* infection was common among pregnant women and contributed to the high burden of maternal anaemia. These findings prompt the need to increase the effectiveness of malaria control measures targeting pregnant women.

Keywords: Anaemia, asymptomatic malaria, pregnant women

MA 006: Prevalence of structural haemoglobin variants and alpha-thalassaemia in the Nanton, Tolon and Kumbugu Municipalities of Northern Region, Ghana

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Abstract:

Certain hemoglobinopathies, such as HbS, HbC, and alpha-thalassaemia, are disproportionately higher in areas currently or historically exposed to P. falciparum (P. f) malaria due to the relative protection they confer against malaria. Despite this fitness advantage, they confer against malaria, these hemoglobinopathies, under certain circumstances, have been observed to cause severe genetic disorders, like the homozygote state of HbS that results in sickle-cell disease (SCD). As a result, genetic screening has become a mainstay of clinical practice to eliminate the transmission of severely debilitating diseases like SCD. In this study, we carried out a genetic screening to determine the prevalence of hemoglobinopathies among children in selected rural communities in Northern Ghana. A total of 1060 healthy children between the ages of 1-18 years were screened for structural haemoglobin variants and alpha-thalassaemia during a cross-sectional study in 13 rural communities in the Tolon (n=466), Nanton (n=338) and Kumbugu (256) Municipalities of Northern Region, Ghana. Screening of structural haemoglobin variants was carried out in situ with the SickleSCAN RDT and retrospectively confirmed with Hb electrophoresis, and alpha-thalassaemia screening was carried out with PCR. Normal Hb (HbAA) was the most frequent phenotype (71.7%), followed by HbAC (16.7%) and HbAS (8.1%). Other phenotypes, including HbCC and HbSS, were less frequent (< 1%).

Keywords: Malaria, Sickle cell, protection, prevalence, Ghana

MA 007: Mechanisms underlying spontaneous Plasmodium falciparum clearance in the post-partum period

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Abstract:

African pregnant women with peripheral *P. falciparum* parasitemia spontaneously lose the parasites a few hours after delivery. We characterized var-gene transcript profiles and VAR2CSA-specific and non-VAR2CSA-specific antibody responses among Ghanaian women from a period near delivery through to the post-partum period to help explain rapid postpartum parasite clearance. Additionally, we genotyped parasite populations (merozoite surface protein 1&2; msp1&2) to identify alleles that can persist and serve as a source of malaria rebound during the postpartum period. Seventeen (17) out of 377 pregnant women in-labour with peripheral malaria parasitemia and 10 un-infected women were followed longitudinally (8-16 hours, 24-48 hours, and 48-72 hours post-partum). Within 24-48 hours post-delivery, peripheral parasitemia declined by 99.3%-99.7%. Var-gene transcription analysis revealed a heterogeneous population of pre-delivery parasites; var2csa predominated in 9/17 women while ABC var-genes predominated in 8/17 women. Within the post-partum period, both var2csa and ABC var-group transcripts declined significantly. Non-VAR2CSA-specific IgG responses were boosted in infected women relative to un-infected women. Prior-to-delivery, women were infected with multiple *P. falciparum* clones (3-17 clones), however, the complexity of the clones declined significantly by 24-48 hours post-

delivery. K1-type alleles between 150-300bp of msp1 persisted in the postpartum period. Put together, our data suggest the absence of a placental sequestration focus and placental malaria-induced boosting of non-VAR2CSA PfEMP1-specific immunity could help explain the rapid clearance of parasites in the post-partum period. Also, low or undetectable levels of K1-type alleles of *P. falciparum* could be drivers of the high risk of postpartum malaria.

Keywords: *P. falciparum*, Var genes, postpartum malaria

MA 008: Bio-products from Serratia marcescens reduce Plasmodium falciparum burden in Anopheles gambiae mosquitoes.

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Abstract:

Novel control ideas for mosquito-borne diseases are being tailored towards the use of microbiomes to reduce transmission. A potential limitation of *Plasmodium* intensity in the Anopheles vector has been demonstrated using bacteria from the family Enterobacteriaceae including *Enterobacter cloacae* and *Serratia marcescens*. It however remains uncertain whether this impact on the parasite is a direct bacteria-parasite cell-cell interaction or indirect through bacterial secreted products. This study investigated if naturally-occurring bacteria release substances that can disrupt mosquito stages of *P. falciparum* development. *Enterobacter cloacae* and *Serratia marcescens* bacterial species were isolated from field-caught *Anopheles gambiae* mosquitoes. Media from liquid cultures of these bacteria were filtered to remove microbial cells, lyophilized and dissolved in sterile 1X phosphate buffered saline (PBS). Their impact on the prevalence and intensity of infection of P. falciparum in the mosquito was assessed by membrane-feeding of mosquitoes with gametocytaemia blood mixed with the bacterial spent-media. Mosquitoes were dissected 10-11 days post-infection and oocysts were counted. We observed a significant reduction in *P. falciparum* prevalence (P=0.001) and infection intensity (P=7.85 x10-12) in mosquitoes that fed on an infectious blood meal containing *S. marcescens* product compared to control groups which contained no bacterial spend-media. The experimental set-up with *E. cloacae* did not show a strong negative impact on the parasite (P<0.05). These products released by symbiotic bacteria can be used as potential transmission-blocking agents and should be further explored for their use in reducing the burden of malaria.

Keywords: Microbiota, *P. falciparum*, *Serratia marcescens*, *Anopheles*

MA 010: Genotypic glucose-6-phosphate dehydrogenase (G6PD) deficiency protects against Plasmodium falciparum infection in individuals living in Ghana

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Cape Coast, Cape Coast, Ghana; [3]National Malaria Control Program, Accra, Ghana

Abstract:

The global effort to eradicate malaria requires a drastic measure to terminate relapse from hypnozoites as well as transmission via gametocytes in malaria-endemic areas. Primaquine has been recommended for the treatment of *P. falciparum* gametocytes and P. vivax hypnozoites, however, its implementation is challenged by the high prevalence of G6PD deficient (G6PDd) genotypes in malaria-endemic countries. The objective of this study was to profile G6PDd genotypic variants and correlate them with malaria prevalence in Ghana. A cross-sectional survey of G6PDd genotypic variants was conducted amongst suspected malaria patients attending health care facilities across the entire country. Malaria was diagnosed using microscopy whilst G6PD deficiency was determined using restriction fragment length polymorphisms at positions 376 and 202 of the G6PD gene. The results were analyzed using GraphPad Prism software, version 8.4.3. A total of 6108 subjects were enrolled in the study with females representing 65.59% of the population. The overall prevalence of malaria was 36.31%, with malaria prevalence among G6PDd genotypic variants were 0.07% for (A-A-) homozygous deficient females, 1.31% and 3.03% for (AA-) and (BA-) heterozygous deficient females respectively and 2.03% for (A-) hemizygous deficient males. The odd ratio (OR) for detecting *P. falciparum* malaria infection in the (A-A-) genotypic variant was 0.0784 (95% CI: 0.0265–0.2319, p<0.0001). In conclusion, G6PDd genotypic variants, (A-A-), (AA-) and (A-) protect against *P. falciparum* infection in Ghana.

Keywords: G6PD deficiency, *Plasmodium falciparum*, Ghana, malaria

MA 011: Nationwide Surveillance of Pfhrp2 Exon 2 Diversity in Plasmodium falciparum Circulating in Symptomatic Malaria Patients Living in Ghana

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Abstract:

Reports of increasing false-negative Histidine-Rich Protein-2 (HRP2-based) rapid diagnostic test results across Africa require constant monitoring of factors associated with these false-negative outcomes, as a failure of this diagnostic tool will have severe consequences on malaria treatment and control programs. This study characterized the extent of genetic diversity in the Plasmodium falciparum histidine-rich protein 2 (Pfhrp2) gene in P. falciparum isolates from symptomatic malaria patients across the regions of Ghana. Exon 2 of Pfhrp2 was amplified from gDNA using a polymerase chain reaction. All Pfhrp2-negative samples were subjected to Pf18S rRNA and Pfmsp2 gene amplifications. The amplified Pfhrp2 exon 2 fragments from clonal samples were sent for commercial Sanger sequencing. The type and number of PfHRP2 repeats, classified based on repeat types previously reported, were estimated from the sequence data and compared among geographical regions. About 81% (2,333/2,890) of the original microscopy-positive dried blood spot (DBS) samples were available and used in this study. The Pfhrp2 exon 2 amplification was successful in 98.5% (2,297/2,333) of the tested samples, with band sizes ranging from 400 bp to 1,050 bp. A total of 13 out of the 24 previously reported repeat types were identified among the samples, with three samples lacking both type 2

and type 7 repeat motifs. This study suggests that the genetic diversity of Pfhrp2 exon 2 identified in P. falciparum circulating in symptomatic malaria patients in Ghana is unlikely to influence the sensitivity and specificity of HRP2 RDT-based diagnosis.

Keywords: Malaria, Rapid diagnostic test, Pfhrp2, Diversity

MA 012: Genetic co-deletions and high diversity of Plasmodium falciparum histidine-rich proteins 2 and 3 genes in malaria parasite populations in Ghana.

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Abstract:

Rapid diagnostic tests (RDTs) are used to diagnose malaria in endemic countries. Plasmodium falciparum histidine-rich protein 2 (PFHRP2)-based RDTs are widely used. The deletions of the pfhrp2 gene in some parasites gave false negative test results. Monoclonal antibodies of PFHRP2 cross-react with PFHRP3 because they share structural similarities, and this complements the detection of the parasites by RDT. The pfhrp2 and pfhrp3 genes were investigated in parasite populations to detect deletions and polymorphisms. Parasites from children ≤12 years (2540) with uncomplicated malaria from 2015-2020 were used. Genes were amplified using nested PCR, no amplification indicated deletion of genes and amplified genes were sequenced. Deletions were observed in 30.7% (780/2540) and 17.2% (438/2540) of the samples for pfhrp2 and pfhrp3 respectively with increasing trends over the three time periods ($\chi 2$ - 10.305, p = 0.001). Pfhrp2 repeat polymorphisms were of predominantly types 2 (AHHAHHAAD) and 7 (AHHAAD). For pfhrp3, types 16 (AHHAAN), 17 (AHHDG) and 18 (AHHDD) were the dominant types. Repeat types 1-8, 11, 13, 15-16 and 19 were shared by both genes. The haplotype diversity of both genes ranged between 0.872 and 1 indicating high diversity of the polymorphisms in the isolates. The implication of the findings of the frequencies of the pfhrp2 and pfhrp3 deletions as well as the variants of the main epitopes of the monoclonal antibodies for the RDT (types 2 and 7) in our isolates, is an indication of the decreased sensitivity of the RDTs in diagnosing malaria infections in Ghana.

Keywords: malaria, RDTs, histidine-rich proteins 2/3

MA 013: Population Genetic Analyses of Pfs230 in Malaria Parasite Isolates Among Ghanaians Suggests High Field Efficacy of Current Vaccine Candidates.

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Abstract:

The Prodomain plus the first cysteine motif domain (CMD1) of Pfs230 (herein referred to as the 'vaccine region') are components of transmission-blocking vaccines (TBV) under development, whose designs are mostly based on the 3D7 laboratory strain. This design strategy neglects the possible impact of parasite population genetics on the efficacy of future field vaccine trials. This study assessed the genetic diversity of the vaccine region of Pfs230 in Ghanaian parasite isolates and any associations with MSP2 clone diversity. DNA was extracted from a total of 118 venous whole blood samples from malaria patients from southern, central and northern divisions of Ghana followed by Pfs230 vaccine region gene amplification and deep sequencing as well as PfMSP2 genotyping. A total of 9 variants consisting of one deletion and 8 SNPs were identified. The Prodomain of the vaccine region had the highest nucleotide diversity and there was no sequence differentiation between sequences collected from different parts of the country. No destabilizing mutation was identified within the binding site of a recently reported binding site of a human monoclonal antibody with potent transmission-blocking activity. Out of 13 identified haplotypes, the 3D7 haplotype was the 3rd most prevalent and neutrality tests suggested the vaccine region was not under selection. Furthermore, none of the identified Pfs230 vaccine region haplotypes was unique to an MSP2 clone. These findings suggested that the current Pfs230 vaccine candidates are expected to have high efficacy with very minimal influence of genetic diversity of the antigen on efficacy.

Keywords: Malaria, Population-genetics, vaccine, Pfs230, transmission

MA 014: Nationwide Surveillance of Pfhrp2 Exon 2 Diversity in Plasmodium falciparum Circulating in Symptomatic Malaria Patients Living in Ghana

Bredu Dorcas G[1] Ahadzi George K[2] Dickson Donu[1] Peprah Nana Y[3] Asamoah Alexander[3] Asumah George A[3] Abuaku Benjamin[1] Asare Kwame K[4*] Obiri-Yeboah Dorcas[2] Ford Colby T[5] Lo Eugenia[6] Malm Keziah L[3] Amoah Linda E[1]

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Abstract:

Reports of increasing false-negative HRP2-based rapid diagnostic test results across Africa require constant monitoring of factors associated with these false-negative outcomes, as the failure of this diagnostic tool will have severe consequences on malaria treatment and control programs. This study characterized the extent of genetic diversity in the Plasmodium falciparum histidine-rich protein 2 (Pfhrp2) gene in P. falciparum isolates from symptomatic

malaria patients across the regions of Ghana. Exon 2 of Pfhrp2 was amplified from gDNA using a polymerase chain reaction. All Pfhrp2-negative samples were subjected to Pf18S rRNA and Pfmsp2 gene amplifications. The amplified Pfhrp2 exon 2 fragments from clonal samples were sent for commercial Sanger sequencing. The type and number of PfHRP2 repeats, classified based on repeat types previously reported, were estimated from the sequence data and compared among geographical regions. About 81% (2,333/2,890) of the original microscopy-positive DBS were available and used in this study. The Pfhrp2 exon 2 amplification was successful in 98.5% (2,297/2,333) of the tested samples, with band sizes ranging from 400 bp to 1,050 bp. A total of 13 out of the 24 previously reported repeat types were identified among the samples, with three samples lacking both type 2 and type 7 repeat motifs. This study suggested that the genetic diversity of Pfhrp2 exon 2 identified in P. falciparum circulating in symptomatic malaria patients in Ghana is unlikely to influence the sensitivity and specificity of HRP2 RDT-based diagnosis.

Keywords: Malaria, Rapid diagnostic test, Pfhrp2, Diversity

MA 015: Molecular markers of antimalarial drug resistance in Ghana.

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Abstract:

Malaria continues to be a major public health problem globally with high rates of morbidity and mortality in disease-endemic areas. Treatment of the disease with artemisinin (ART) and its derivatives and partner drugs in artemisinin-based combination therapy (ACT) has seen a reduction in parasite susceptibility in some countries in Southeast Asia and Africa. In Ghana, ACT regimens used in the treatment of uncomplicated malaria are artemether-lumefantrine, artesunate-amodiaquine and dihydroartemisinin-piperaquine. For intermittent preventive treatment in pregnant women (IPTp) and seasonal malaria chemoprevention (SMC) in children, sulfadoxine-pyrimethamine (SP) is used. Molecular markers of antimalarial drug resistance have been monitored in Treatment Efficacy Studies (TES) conducted in the country in collaboration with the National Malaria Control Program. Using molecular methods involving PCR followed by Sanger sequencing, markers of parasite drug resistance for the ACT regimens and SP have been observed in Ghanian malaria parasites. The known markers of ACT resistance and as well as variants observed include pfk13 C580Y/R/V, R539I, I543S/V, N585H/I, M579T/Y; pfcoronin R100K/R; pffp2 V511, S59F; pfarps10 V127M; pfnfs S62N, E67G; pfubp1 E1528D; pfap2mu S160N; pfmrp1 I876V; pfpm2 and pfpm3 increased gene copy numbers; pfmdr1 increased gene copy number. For SP, pfdhfr N51I, C59R, S108N, I164L/R/K; pfdhps A437G, A581G, A613S. Some of these markers of drug resistance are showing increasing trends in their prevalence in the parasite population in Ghana over the years due to selection pressure of drug use. The implications of the presence of these molecular markers on antimalarial drug efficacy/resistance in Ghana are further discussed.

Keywords: antimalarial drug resistance, molecular markers

MA 016: Evaluating the Susceptibility of Static and Suspension Cultures of P. falciparum parasites to antimalarials

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Abstract:

The advent of in vitro culture techniques has played a key role in the discovery and development of new antimalarials, as also the identification of novel drug targets, and the elucidation of the mechanisms of drug action and resistance. Despite the utility of the in vitro culture system in the numerous breakthroughs in malaria research, this system does not completely reflect the in vivo settings. This has been attributed to several physical, nutritional and immunological factors that affect the phenotypic and genetic makeup of parasites in vivo, which differs from those adapted to in vitro culture conditions. Our previous studies showed that growing P. falciparum parasites (Dd2 and W2mef strains) in moving suspension contrary to static culture conditions resulted in host-independent changes in invasion phenotypes with corresponding changes in gene expression. Therefore, using in vitro growth inhibition assays and ring survival assay, this study evaluated the response of Dd2 and W2mef strains of P. falciparum parasites cultured under static and moving suspension conditions to Dihydroartemisinin and Artesunate. Preliminary data from the study showed increased susceptibility of the Dd2 and W2mef parasites in suspension culture to the antimalarials compared to those in static culture conditions. Additional studies are ongoing to screen other antimalarials, and also evaluate the effect of gene expression in the two P. falciparum strains cultured under static and moving suspension conditions to antimalarials. The outcomes of this work will throw more light on how moving suspension culture conditions affect the response of P. falciparum parasites to antimalarials.

Keywords: Antimalarials, *P. falciparum*, Suspension, Static, Susceptibility

MA 017: Histological Diagnosis of Placental Malaria in Women with and without pre-eclampsia at the Korle-Bu Teaching Hospital

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Abstract:

Pre-eclampsia is a global health syndrome with major effects in sub-Saharan Africa. Malaria in pregnancy results in placental malaria, which is associated with pre-eclampsia. This study assessed and compared subclinical placental Plasmodium infections between women diagnosed with and without pre-eclampsia.

The study recruited 50 pregnant women; consisting of 25 who were diagnosed with pre-eclampsia (cases) and 25 without pre-eclampsia (controls). Their placentas were collected after delivery and a portion was processed histologically for the diagnosis of placental malaria.

All the 50 placentas examined were exposed to Plasmodium infections with 84% of the case placentas recording a parasitaemia <10%, whilst 16% recorded a parasitaemia between 10 – 40%. On the other hand, 88% of the control placentas examined showed parasitaemia <10%, with 8% showing parasitaemia between 10 – 40%, and 4% showing parasitaemia above 40%.

The presence of *Plasmodium* parasitaemia in both groups indicates that pre-eclampsia might have developed due to other factors other than placental malaria. However, we recommend that further studies be conducted employing a larger sample size to support our findings.

Keywords: Histology, placental malaria, preeclampsia, parasitaemia

MA 018: Genetic diversity and population structure of asymptomatic P. falciparum carriers living in varying transmission settings in Ghana

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Abstract:

Asymptomatic parasite carriage has become a major hindrance to achieving the total elimination of malaria globally. This study employed Merozoite surface protein 2 (Msp2) and 12 polymorphic microsatellites markers to determine the diversity and population structure of asymptomatic *P. falciparum* carriers living about 90 km apart with varying transmission settings in the Greater Accra, Ghana. Methods: The study recruited 160 asymptomatic volunteers in Obom and Asutsuare ages 8 to 60 years old. Nested Polymerase Chain Reaction (nPCR) was used to genotyped Msp2 before clonal samples were subjected to 12 polymorphic microsatellite genotyping. Results: Asymptomatic parasite carriage in Obom was higher (mean PD 318.8) than in Asutsuare (below statistical estimation). Asutsuare and Obom recorded 100% and 65% via Msp2 genotyping but this declined to 50% and 5% respectively when microsatellites markers were employed, high genetic diverse clones accompanied by moderate to low population structure were observed in Obom relative to Asutsuare. Conclusion: High diverse P. falciparum asymptomatic infections with moderate to low population structure in Obom than in Asutsuare, however TA40 and TA87 were useful markers in estimating Multiplicity of Infection from varying malaria settings.

Keywords: microsatellites, asymptomatic, diversity, P. falciparum, malaria

MA109: The impact of repeated administration of Artesunate-Amodiaquine and Artemether-Lumefantrine on lipid peroxidation and antioxidant levels.

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Abstract:

In endemic countries, malaria treatment is often focused on symptoms rather than a parasitological diagnosis; therefore, people repeatedly take Antimalarial without malaria. This study evaluated renal oxidative stress induced by repeated treatment with Artemether-Lumefantrine A/L and Artesunate-Amodiaquine A/A. One hundred mice were equally distributed into 20 groups of non-infected and Plasmodium berghei-infected mice treated with either A/L or A/A therapeutically 1,2,3 and 6 times. Kidney lipid peroxidation and antioxidants were examined after the treatment regimen. Kidney Malondialdehyde (MDA) concentration significantly increased in Infected mice treated with A/L or A/A 1, 2,3, and 6 times compared to the non-infected and control group, the highest in A/L infected treated groups. MDA levels increased in Non-infected groups treated with A/L and A/A 3- and 6-times compared to the control. Glutathione peroxidase (GPx), Superoxide Dismutase (SOD), and Catalase (CAT) activities highly increased in Non-Infected and Infected groups treated with A/L and A/A for 2, 3 and 6 times compared to the control group, with highest in Infected AL treated group. The finding revealed that malaria Infected and Non-infected repeatedly treated with A/L or A/A increased the lipid peroxidation in the kidney, with a high increase when malaria-infected and highly increased when infected and treated with A/L. However, this increase was counteracted by an increase in GPx and, SOD, CAT production; this suggests that Therapeutic intake of A/L and A/A when not infected could lead to less stress in the kidney.

Keywords: Malaria, Antimalaria, Lipid peroxidation, Antioxidant, Kidney

MA 020: Seasonal variation of malaria vector distribution and insecticide resistance genes in a Coastal Forest community of Ghana.

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Abstract:

In high malaria transmission settings, insecticide resistance and the high prevalence of mosquitoes may play a crucial role in perpetuating malaria transmission. In this study, the seasonal variation in anthropophilic mosquitoes and insecticide resistance genes was characterized in Simiw, a rural community in the Central Region of Ghana. The human Landing Catching (HLC) technique was used to collect adult mosquitoes from both

indoors and outdoors during the off-peak and peak rainy seasons in 2021. Mosquitoes were identified by morphology and by PCR which was also used to determine Anopheles species knockdown resistance genes (Kdr east and Kdr west). A total of 4133 adult mosquitoes were collected from the study, of which 3216 (77.81%) mosquitoes were *Anopheles gambiae*, 620 (15%) *Mansonia* sp., 255(6.17%), 25(0.6%) *Culex* sp. and 17(0.41%) *Anopheles funestus*. Out of 3216 *Anopheles gambiae* collected, 1631(50.7%) were caught in the dry season and 1590(49.3%) in the wet season. In the off-peak season, there was no significant difference between the number of *Anopheles gambiae* mosquitoes collected indoors and outdoors (806 vs 825) and a similar observation was made in the peak seasons (798 vs 788). No Kdr east resistance genes were identified. All the Anopheles gambiae had Kdr west mutation with 73.42% and 61.31% being homozygous in the first off-peak and peak seasons respectively. Anopheles gambiae mosquitoes were equally present in the peak and off-peak seasons had no preference for indoor or outdoor biting and all had the Kdr west resistance mutation.

Keywords: Mosquito, *Anopheles*, resistance, transmission, season

MA 021: Detection of Babesia Species in Humans: A Public Health Concern in Ghana

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Abstract:

The transmission of Babesiosis, a disease is entirely dependent on the susceptibility of both the vector and host. GHS report in 2011, estimated about 72% of all out-patients presenting with febrile illnesses but diagnosed with malaria only account for 28% – 32%. The origin of the other fevers is yet to be identified and babesiosis could be one as infection in dogs has been established in Ghana. The close similarity in phenotype and clinical manifestation of malaria and babesiosis makes the diagnosis with standard methods difficult and leads to misdiagnosis, especially, in malaria-endemic countries. Thus, this study aimed at detecting Babesia spp. and Plasmodium spp. infections in women and immunocompromised individuals in two selected hospitals in Ghana. A total of 156 archived clinical samples, 61/156 (39.1%) from mothers attending Manhyia Hospital, and 95/156 (60.9%) from HIV-infected individuals attending Korle-bu Teaching hospital were screened using specific primers targeting the 18SrRNA gene. Babesia spp. only infections were recorded in 3/156 (1.9%) of the women at the Manhyia hospital whilst 17/156 (10.9%) P. falciparum only infections were detected in samples from both Manhyia and Korle-bu Teaching hospitals in both mothers and immunocompromised individuals. There was 1/156 (0.6%) co-infection of Babesia spp. and Plasmodium spp detected in a mother at the Manhyia Hospital. This study is the first to report the detection of Babesia spp. in humans attending Manhyia Hospital. Attention must be given to fever-causing zoonotic infections among humans in Ghana.

Keywords: Babesiosis, Malaria, women, FUOs, PCR

MA 022: Plasmodium falciparum population structure and genetic variations in malaria infections among children in selected communities.

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Abstract:

Genetic variation in the Plasmodium parasite is a major deterrent to the elimination of malaria. Even with the approval of a vaccine for use by the WHO, the continuous monitoring of diversity cannot be overlooked. Here, we seek to compare the genetic diversity and population structure of P. falciparum infections in selected communities. A total of 977 children aged 0.5-12 years were enrolled at the start of the malaria season and followed up for 50 weeks. Dried blood spots (DBS) and glass slides were taken at baseline to estimate parasite carriage. Samples were taken monthly estimated asymptomatic parasitemia whereas samples from clinical participants within the follow-up period estimated symptomatic parasitemia. PCR estimated parasite carriage and Next Generation Sequencing (NGS), determined genetic diversity and population structure. Baseline parasitemia prevalence was estimated as 11.4% with cumulative malaria incidence being 4.4% (CI 3.85-5.09). Within sample F statistic (Fws) an estimator of within-sample diversity was observed as <0.95 an indicator of low inbreeding rates, high within-sample diversity and multi-genomic infections. Low nucleotide diversity was observed in both populations with average values of 0.0023 and 0.0026 among the sub-populations. A test for evidence of natural selection showed Tajima D mean values >0, a presumption the population evolved under balancing selection or after a sudden population contraction. The study provides baseline data for malaria parasite populations within two sub-populations having similar values and trends. Our results show no significant difference in population structure or genetic diversity in the 2 populations.

Keywords: Genetic Variation, Population Structure

MA 023: Low-avidity antibodies correlate with the expansion of atypical memory b cells in malaria-immune adults living in high-transmission areas

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Abstract:

Antibody avidity, a measure of affinity maturation significantly affects antibody responses during infections. High avidity antibodies are usually acquired after infrequent P. falciparum infections, especially in low transmission regions. However, it is unclear if the expansion of atypical memory B cells which usually occurs after repeated exposure is responsible for the production of low-avidity antibodies. This study sought to determine the correlation between low avidity antibodies and the expansion of atypical memory B cells in the high transmission regions in Ghana. The breadth of antibody responses and relative avidity to a

panel of P. falciparum merozoite antigens (AMA1, MSP3, MSRP5, RAMA, SERA 9 and GLURP-RO) was determined by Indirect ELISA in individuals living in a high malaria transmission area compared to individuals from a transmission area. The median plasma antigen-specific IgG levels were significantly higher for all 6 antigens in individuals from the Central Region compared to Accra. The relative avidity indices were higher in Accra compared to Efutu and Moree for RAMA, MSRP5 and CyRPA. There were elevated levels of atypical and activated memory B cells among residents of Efutu and Moree with no significant difference in the frequency of classical memory B cells across the two sites. However, there was a positive correlation between the breadth of reactivity to antigens and the measured percentage inhibition. The findings from this study suggest that the increase in the low avidity antibodies may be driven by the expansion of atypical memory B cells after repeated exposure to P. falciparum antigens.

Keywords: Atypical cells, avidity, affinity, antibody, breadth

MA 024: Breeding Water Effect on Anopheles gambiae sensu lato Insecticide Susceptibility During Laboratory Colonization

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Abstract:

The continuous success of insecticide-based control of malaria is challenged by widespread resistance in vector populations. Development of novel insecticide formulations requires tests using laboratory-maintained Anopheles gambiae sensu lato. which are initially profiled as insecticide-resistant from field collections. However, very little is known about the changes in the insecticide resistance profile of such mosquitoes after several generations of laboratory breeding, especially since the potential selection pressures from chemicals in their natural larval breeding sites are no more present. This study investigated the effect of larval water sources in maintaining the insecticide resistance status of wild Anopheles gambiae s.l. Eggs from a known insecticide-resistant field-caught Anopheles mosquito population were bred in field, tap or distilled water. They were bred under standard laboratory conditions and exposed to a WHO-discriminating insecticide dosage. A synergistic assay with piperonyl butoxide (PBO) and pyrethroids was also conducted to assess the expression of detoxification activity within the population. The WHO susceptibility results revealed high resistance to all insecticides (mortality ≤ 90%). However, when the mosquitoes were exposed to PBO before pyrethroids, resistance was reduced in mosquitoes bred in field water (mortality ≤98.7%), indicating relatively high metabolic enzymatic activity associated with field water exposure. Analyses of target site mutations and enzymatic activities in each filial generation are ongoing to understand the association of these insecticide resistance genetic and metabolic traits. This study is expected to improve insectary protocols for maintaining desired traits in mosquitoes for testing insecticide-based vector control tools.

Keywords: *Anopheles* mosquito, insecticide susceptibility, pyrethroid,

MA 025: Analysis of var genes transcription switching during pregnancy

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Abstract:

Over the past two decades, several interventions have been adopted to prevent pregnancy-associated malaria and its negative effect but there is still a window; in the first trimester of pregnancy when pregnant women are unprotected and malaria infections are prevalent and harmful. A majority of these infections during pregnancy have been suggested to be carried out asymptomatically before conception. In pregnant women, P. falciparum parasites sequester in the placenta to evade immune attack mainly by splenic clearance. This sequestration is mediated by var2csa, a member of the P. falciparum erythrocyte membrane protein 1 (PfEMP-1) family that binds to chondroitin sulfate A (CSA) on the syncytiotrophoblast of the placenta. We analyzed the expression pattern of var genes before and during pregnancy from isolates of 115 women of reproductive age (WRA) from Benin using real-time qPCR. The least transcribed genes before conception were those of var2 (22%). During pregnancy, less than 50% of transcripts of the various var genes were detected in the isolates collected from the WRA except for group C (C2), var1, var2 and var3 genes recorded more than 50 %, especially in the first trimester. Switch towards the preferred var2csa occurs right from month one due to the significant upregulation of the transcripts in the first trimester. Anti-var2csa antibodies against the ID1-ID2a region of var2csa measured by an indirect ELISA showed no significant association with var2csa expression. The data presented here further strengthens the argument for var2csa as a good candidate for vaccine development.

Keywords: *P. falciparum*, Var2csa, Sequestration, Syncytiotrophoblast, Var

MA 026: Anti-CSP antibodies as an ideal alternative measure for malaria transmission monitoring

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Abstract:

Effective transmission monitoring and control is key to sustaining and augmenting global efforts towards malaria elimination. Antibodies to the *Plasmodium* antigen circumsporozoite protein (CSP) have shown promise as efficient alternative markers for malaria transmission intensity estimation. This work aimed to determine if anti-CSP antibodies will remain relevant alternatives despite the antigen being highly polymorphic. The study adopted a prospective cohort design with a total of 180 participants (60 children, 120 adults), sampled monthly for a year. To determine malaria infection status and parasite densities, genomic deoxyribonucleic acid was extracted, and photo-induced electron transfer polymerase chain reactions were performed for each participant at the 12 different time points. Indirect enzyme-linked

immunosorbent assays were carried out to determine anti-CSP antibody seroprevalence against the recombinant PfCSP (3D7 strain) and two conserved 24-mer PfCSP peptides. About 64% of child samples were positive for Pf whiles only about 2% of adult samples were positive for Pf. The prevalence and density of Pf parasites varied significantly with age group ($p<0.0001$ and $p=0.002$ respectively). Although anti-CSP seroprevalence was high in both groups, in children, anti-CSP seroprevalence correlated with Pf prevalence whereas in adults there was no correlation. We will compare this data to CSP gene sequence information to determine the effect of polymorphisms on antibody responses. These findings demonstrate the utility of anti-CSP antibodies as ideal markers for malaria transmission monitoring.

Keywords: Circumsporozoite protein, Transmission intensity, Polymorphic, Seroprevalence

MA 027: The Circumsporozoite Protein of three Plasmodium species Profiled in terms of Sequence, Structure, and Naturally Acquired Antibodies.

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Abstract:

The need for an effective malaria vaccine is imperative. The RTS, S circumsporozoite protein (CSP) vaccine has moderate efficacy and is the only licensed malaria vaccine for use in children. . The R21 CSP vaccine candidate had >70% efficacy in a phase 1/2b trial. This contributes to the evidence that a potent vaccine can be engineered based on the CSP. The design of R21 and RTS, S is based on *Plasmodium falciparum* CSP. Recent work suggests that *Plasmodium malariae* and *Plasmodium ovale* have clinical relevance and have a higher prevalence than previously estimated. This study investigates the CSP from P. falciparum, P. malariae, and P. ovale in terms of sequence, structure, and naturally acquired antibodies. We have shown that CSPs from the three species have less than 35% sequence similarity. Also, there is significant structural discordance at the whole protein level ($TM<0.25$). However, significant structural concordance was observed at the C-terminal ($TM>0.48$) in agreement with significant sequence similarity of that domain (identity>38%). After expression of the three proteins and mass spec (TOF) confirmation, we measured total immunoglobulin G by ELISA against the CSPs in malaria asymptomatic and symptomatic (three follow-ups) populations. Higher antibody titers were associated with PfCSP compared to PmCSP and PoCSP. This was confirmed by western blot. IgG characteristics were described by sub-class and NaSCN avidity. This work suggests that the RTS, S vaccine and the R21 vaccine candidate may have less than moderate efficacy against non-falciparum malaria. There is a need to consciously design broad-coverage vaccines against human malaria parasites.

Keywords: *falciparum* malaria, non-*falciparum* malaria, CSP, ELISA

MA 028: Assessing the Behaviour of Mosquitoes During Exposure to Different Long-Lasting Insecticidal Nets (LLINs) Using the Video Cone Test (VCT)

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Abstract:

The use of pyrethroid-based Long Lasting Insecticidal Nets (LLINs) is a significant malaria control strategy in sub-Saharan Africa. Insecticide resistance mechanisms such as knockdown resistance and metabolic resistance are usually tested but much is not known about the association of mosquito behaviour with insecticide resistance. Mosquito behaviour, when properly understood will help in robust LLIN formulations and evaluations that will help decrease mosquito-human contact. This study seeks to capture and assess the behavioural characteristics in mosquitoes following contact with PermaNet® 2.0 (PN2.0), PermaNet® 3.0 (PN3.0) and Olyset® using the Video Cone Test (VCT). The VCT was conducted for 7 replicates of each LLIN treatment using 2-5 days old susceptible and resistant *Anopheles gambiae* mosquitoes. 4 replicates of the untreated net were set up as control for each treated LLIN tested. The mosquitoes were exposed to the LLINs for 1, 2, 3, 4, 5, and 6-minutes while their behaviour was being recorded. The mortality of the mosquitoes was recorded 24 hours after the test and videos were analyzed using the Boris® and ViCTA® software. Mosquitoes were observed to stay longer on untreated control nets as compared to LLINs. There was 100% mortality in PN3.0 as compared to 28.33% for PN2.0 and 12.14% for OLY. Knockdown was similar across the strains and treatments for 1-3 minutes of exposure. This study is still in progress and data for OLY is yet to be analyzed. The study is expected to provide information that will be useful for novel formulations and future evaluations of LLINs.

Keywords: malaria; insecticide resistance; vector control; mosquito

MA 030: High RON4, opsonic phagocytosis activity and invasion inhibition of merozoites are associated with protection from febrile malaria in Ghanaian children

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Abstract:

Naturally acquired immunity to malaria may involve different immune mechanisms working in concert, however, their respective contributions and potential antigenic targets have not been established. Here, we assessed the roles of opsonic phagocytosis and antibody-

mediated merozoite growth inhibition in Plasmodium falciparum infection outcomes in Ghanaian children. The levels of merozoite opsonic phagocytosis, growth inhibition activities and six P. falciparum antigen-specific IgG of plasma samples from children (N=238, aged 0.5 to 13 years) were measured at baseline before the malaria seasons in southern Ghana. The children were then actively and passively followed up for febrile malaria and asymptomatic P. falciparum infection detection in a 50-week longitudinal cohort. P. falciparum infection outcome was modelled as a function of the measured immune parameters while accounting for important demographic factors. High plasma activity of opsonic phagocytosis [adjusted odds ratio (aOR)= 0.16; 95%CI= 0.05 - 0.50, P = 0.002], and growth inhibition (aOR=0.15; 95% CI = 0.04-0.47; P = 0.001) were individually associated with protection against febrile malaria. IgG antibodies against MSPDBL1 and PfRh2a correlated with opsonic phagocytosis (OP) and growth inhibition respectively while antibodies to RON4 correlated with both assays. There was no evidence of a correlation between opsonic phagocytosis and growth inhibition (β= 0.13; 95% CI= -0.04-0.30; P=0.14). Opsonic phagocytosis and growth inhibition are protective immune mechanisms against malaria that may be acting independently to confer overall protection. Vaccines incorporating RON4 may benefit from both immune mechanisms.

Keywords: Malaria, opsonic phagocytosis, growth inhibition, merozoite

MA 031: Measuring antibody responses to crude malaria antigens in individuals of different haemoglobin genotypes.

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Abstract:

Malaria is a devastating disease and is responsible for high mortality in endemic areas. Hemoglobinopathies have been found to provide significant protection against malaria and in assessing the relationship between antibody levels to crude malaria antigens in haemoglobin genotypes, Hb AA, Hb AC, Hb AS and Hb SC, this study used plasma samples from 90 Ghanaian children from the northern and eastern regions between the ages of 1 and 15 years. There was a trend of higher median antibody levels in HbAA individuals compared to that HbAS, HbAC, and Hb SC individuals. The impact of age on antibody responses was also investigated and results showed that antiplasmodial antigen-specific antibody production increased with increasing age of individuals although this was not statistically significant. Antibody production corresponds with the prevalence of parasitemia, and this is evident in the low antibody expression in samples with the HbAS, HbAC, and Hb SC genotypes as their cellular architecture does not favour parasite growth leading to low parasitemia. This is in contrast with the antibody production in the HbAA samples which was high, suggesting high parasitemia as this particular genotype does not confer any added protection apart from the immune response.

Keywords: Malaria, Hemoglobinopathies, Antigens, Antibodies, Protection

MA 033: Measuring the Effect of Mosquito Bite on Afebrile Individuals in Malaria Endemic Communities and its Influence on immunity against Malaria

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Abstract:

Immunity is acquired after repeated exposure to malaria, and this varies widely depending on the intensity of transmission and geographical settings. This study aimed at investigating mosquito bite exposure in afebrile individuals and its influence on immunity against malaria. Participants aged between 3 and 70 years were recruited from two communities, Simiw and Obom. Whole blood (1 ml) was collected from participants in Simiw (December 2019) and Obom (January 2020). Aliquots of blood were used to prepare dried blood spots for *P falciparum* confirmation by PCR. IgG antibody against gSG6-P1 and P falciparum was quantified from plasma using indirect ELISA. The IgG against gSG6-P1 for individuals with the age groups 10-15 years for both Simiw and Obom indicated a significant difference (p=0.0001) with participants in Simiw recording higher median (95%CI) antibody concentration (2.980 (3.077-3.662) ng/ml) than those in Obom (2.088 (2.176-2.602) ng/ml). Individuals from Obom with age groups 10-15 years had higher anti-Pfs230 antibody levels (6591 (1210551-4984924) ng/ml) compared to individuals from Simiw with age group 0-9 years (4707 (5874-10446) ng/ml) (p=0.0008). Regardless of the higher exposure of participants from Simiw to mosquito bites, the majority of the bites were obtained from uninfected mosquitoes and the reason is that total anti-PfCSP IgG antibody titres were found to be relatively lower in Simiw compared to Obom.

Keywords: Immunity, Exposure, Immunoglobulin, Infectious, Malaria

MA 034: Effects of a malaria control intervention on antibody responses to a blood stage antigen (EBA-175) in an endemic area.

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Abstract:

One key factor influencing the manifestation of malaria is naturally acquired immunity (NAI) against the parasite, which is developed after repeated exposure by people living in endemic areas. Efforts to reduce malaria incidence have resulted in the implementation of a wide variety of malaria control and elimination measures, each with the potential to alter the development of NAI. We monitored IgG against EBA 175 quarterly over a year in individuals living in a high malaria transmission setting (Obom) where a mass test, treat and track (MTTT) exercise was ongoing.1500 individuals without any symptoms of malaria aged between 7months-80yrs were enrolled on the study and donated finger-pricked blood that was used to prepare dried blood spots (DBS). Genomic DNA was extracted from the DBS for PCR estimate of *P. falciparum*. Antibodies were also eluted from the DBS and used for PFEBA 175 specific ELISA. The results were stratified by age into 0-4yrs, 5-9yrs, 10-15yrs and 16+yrs groups. Across visits, there was a gradual rise in antibody levels at each time point, however, this was statistically significant. Individuals aged 16 and above had higher

antibody titres than individuals aged 15 and below. Also, antibody levels among all age groups were statistically lower at the first visit relative to the last visit (p <0.0001). Generally, higher antibody levels were associated with those infected compared to the uninfected. In this study, we have established that antibodies response to EBA-175 was not affected negatively by the MTTT intervention.

Keywords: Erythrocyte Binding Antigen (EBA)-175, MTTT,

MA 035: Humoral antimalarial immune response in children exposed to helminth and malaria parasites

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Abstract:

The geographical distribution of human malaria parasites and helminths greatly overlap with each other. Dual infections of people in regions where these parasites, which elicit different types of immune responses, are endemic have commonly been reported. In a community-based cross-sectional study, the effect of Hookworm, Hymenolepis nana and Schistosoma haematobium-infections could have on the levels of immunoglobulin (Ig) directed to GMZ2, a malaria vaccine candidate, was evaluated. Methods: Blood, stool, and urine samples were collected from 5-15-year-old children with no clinical symptoms to diagnose P. falciparum (Pf), intestinal helminths (Hookworm, *Hymenolepis nana*), and *Schistosoma haematobium*-infections, respectively. Identification and quantification of intestinal helminths and S. haematobium burden were achieved by light microscopy. A molecular technique was employed to detect sub-microscopic infections of P. falciparum. Plasma levels of GMZ2-specific IgG and its subclasses were quantified by ELISA. Results: The median level of total IgG in children with Pf/H. nana-dual infections were significantly lower in the mono-infected group with Pf (p = 0.0121) or study participants without infection (p=0.0217). Similarly, the median level of IgG1 was significantly lower in *P.f/H. nana*-infected children compared to Pf-group (p=0.0137). Equally, the Pf/*H. nana*-infected individuals posted a lower level of IgG1 compared to Pf-group (p=0.0137). Conclusions: *H. nana* infection was associated with reduced GMZ2-specific IgG levels, which may have serious consequences for anti-malarial vaccine development and deployment in helminth-endemic regions.

Keywords: Malaria, helminths, antibodies, IgG,

MA 036: Detecting asymptomatic carriage of Plasmodium falciparum in southern Ghana: utility of molecular and serological diagnostic tools

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Abstract:

Background. Asymptomatic malaria infections can serve as potential reservoirs for malaria transmission. These infections range from microscopic to submicroscopic densities, making the accurate detection of asymptomatic parasite carriage highly dependent on the sensitivity of the tools used for the diagnosis. This study sought to evaluate the utility of a variety of diagnostic tools for detecting asymptomatic Plasmodium falciparum carriage in two communities with varying malaria parasite prevalence. Methods. Samples from 194 participants living in a high (Obom) and a low (Asutsuare) malaria transmission setting in Ghana. Blood smears, HRP2-based rapid diagnostic test (RDT) and dried blood spots (DBS) were prepared from each sample. Genomic DNA was extracted, and used in *Plasmodium*-specific photo-induced electron transfer polymerase chain reaction (PET-PCR) and Nested PCR, whilst the HRP2 antigen content of the DBS was estimated using a bead immunoassay. A comparison of malaria parasite prevalence as determined by each method was performed. Results. Asymptomatic parasite carriage in Obom was estimated at 71.4%, 61.9%, 60%, 37.8%, and 19.1%, whereas in Asutsuare it was estimated at 50.1%, 11.2%, 5.6%, 0% and 2.2% by Nested PCR, the HRP2 bead assay, PET-PCR, RDT and microscopy respectively. The diagnostic performance of Nested PCR, PET-PCR and the HRP2 bead assay was similar in Obom but not in Asutsuare.

Conclusions: The HRP2 bead assay and PET-PCR produced results with the highest level of inter-rater agreement relative to all the other tools tested and have the advantage of producing quantitative results and requiring fewer processing steps relative to Nested PCR.

Keywords: Bead-based, HRP2, PET-PCR, RDT, Microscope

MA 037: Genetic determinants of Plasmodium falciparum parasite carriage in afebrile school-going children in southern Ghana.

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Abstract:

The natural history of malaria is modulated by environmental factors, host genetics, host immune responses, parasite genetics and parasite virulence. It is estimated that 25% of the total phenotypic variation of malaria can be explained by variations in host genetics, of which Haemoglobin S contributed only 2%, suggesting the existence of many unknown genetic factors. This study aims to determine the association between various Single Nucleotide Polymorphisms (SNPs) and asymptomatic Plasmodium falciparum parasite

carriage in asymptomatic school-going children in Simiw, Ghana. Two hundred and thirty (230) archived samples from the "Gametocytogenesis" longitudinal study were genotyped for the following SNPs: TLR 4 Asp299Gly (A>G), IL-10 592 C/A, NOS 954 G>C and MBL G230A. Multiplex-PET PCR was used to qualitatively and quantitatively determine P. falciparum parasite infection. Two-step RT-PCR was used to qualitatively and quantitatively determine P. falciparum gametocyte infection. Statistical analysis was performed with GraphPad Prism. For NOS 954 G>C, allele frequencies constituted 0.8% (2/229) for mutants, 40.2% (92/229) for carriers and 59% (135/229) for wild-types. For TLR 4 Asp299Gly (A>G), allele frequencies constituted 1% (2/207) for mutants, 12.1% (25/207) for carriers and 87.0% (180/207) for wild-types. For IL-10 592 C/A, allele frequencies constituted 13.3% (28/210) for mutants, 49.0% (103/210) for carriers and 37.6% (79/210) for wild-types of the IL-10 592 C/A SNP. All participants (226/226) were wild types for MBL G230A. IL-10 592 C/A mutant was in high frequency.

Keywords: Malaria, Asymptomatic, Genetics, Single nucleotide polymorphisms

MA 038: Identification of Immunodominant T-cell epitopes within Plasmodium falciparum Merozoite Surface Protein- 11 (PFMSP-11).

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Abstract:

Malaria remains a major menace to developing countries. A lot of preventive and treatment strategies are hampered by the emergence of *Plasmodium falciparum*-resistant strains, even the new anti-malarial drugs. An effective malaria vaccine is needed as an additional intervention to drive malaria elimination. One characteristic of a successful malaria vaccine is its ability to elicit immune responses against different variants of the parasite in a genetically heterogeneous population, hence the need for a multi-epitope malaria vaccine which can incorporate conserved HLA-restricted peptides from multiple antigens. This study, therefore, sought to identify immunodominant T-cell epitopes within *Plasmodium falciparum* Merozoite Surface Protein -11 (PfMSP-11), a new malaria vaccine candidate antigen. The HLA A and B type binding specificity of MSP-11 synthetic peptides were predicted using the in-silico algorithm NetMHC and cryopreserved PBMCs from 5 HLA-typed subjects were stimulated with 22 synthetic PfMSP-11 peptides in Fluorospot Assays. The data were expressed as spot-forming cells per million (sfc/million) PBMCs and a set of criteria was used to determine the positivity of the peptides. Out of the 22 peptides tested against the five participants' PBMCs, four responded positively to four peptides that bound to HLA A02, A03, B07, B27, B44 and B58 supertypes. In conclusion, this study has identified immunodominant regions within PfMSP-11 antigen in this limited number of HLA-typed subjects, with the potential to identify more MSP-11 epitopes within a larger population.

Keywords: T cell, Epitope, IFN- γ, PfMSP-11

MA 039: Prevalence of Plasmodium falciparum dhfr and dhps mutations among pregnant women in the forest-savannah area of Ghana

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Abstract:

Intermittent preventive treatment during pregnancy (IPTp-SP) is used to prevent malaria. *Plasmodium falciparum* dihydrofolate reductase (dhfr) and dihydropteroate synthase (dhps) genes confer resistance to pyrimethamine and sulfadoxine, respectively. This study determined the prevalence of SP resistance markers among pregnant women in the forest-savannah area of Ghana. DNA was extracted from 255 *P. falciparum*-positive dried blood spots obtained from pregnant women aged ≥18 years at the first Antenatal Care clinic visit from 2017-2019, amplified and sequenced to detect mutations in dhfr and dhps genes. In the dhfr gene, single nucleotide polymorphisms were detected in 83.1% (157/189), 92.0% (173/188) and 91.0% (171/188) at codons 51, 59, and 108 respectively. The dhfr triple mutant C51I, N59R and S108N (IRN) was carried by 80.5% (128/159) of isolates. In the dhps gene, SNPs were detected in 76.2% (138/181), 33.2% 60/181), 1.2% (2/174), 0% (0/183), and 15.6% (27/173) at codons 436, 437, 540, 581 and 613 respectively. Quadruple mutant (IRN-GK) was present in 25.8% (33/128) of isolates. Quintuple mutant alleles (IRN-GE) were detected in 0.8% (1/128) of samples. No mutations were identified at dhfr codons 16 or 164 or dhps 581. There is a high prevalence of dhfr triple mutant infections among pregnant women in the area. Prevalence of the IRN-GK and IRN-GE was low, and no dhps A581G mutant was detected, indicating that SP is still likely to be efficacious for IPTp-SP in the forest-savannah area.

Keywords: SP, Resistance, Pregnant women, Ghana

MA 040: Iron Fortification Improves IgG Response to Malaria-Specific Antigens and Offers Immunity against Malaria in Pre-school Children in Ghana

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Abstract:

Iron fortification and micronutrient initiatives are cost-effective developmental strategies against malnutrition and health emergencies in preschool children. This was a retrospective community-based, placebo-controlled, double-blinded, cluster-randomized trial study conducted in Wenchi Municipal and Tain District of Bono Region. One thousand nine hundred and fifty-eight (1958) children aged 6-35 months were enrolled, from which 967 children were randomized to receive micronutrient powder with iron and 991 without iron. Semi-liquid homemade meals mixed with either iron-free micronutrient powder (placebo group) or with iron (intervention group; 12.5 mg of iron daily), given daily for 5 months. Standardized clinical and epidemiological questionnaires were administered. Blood samples were also taken to measure IgG responses to GLURP R0, GLURP R2 and MSP3 FVO recombinant antigens using the Afro Immunoassay (AIA) protocol. Out of the 1958 children enrolled, 871 were evaluated, of which 435 received prophylactic micronutrient powder with iron and 436 received a placebo. The iron-fortified children had a significantly higher IgG response to GLURP R0 and GLURP R2 compared to healthy children in the iron group after the intervention. The response to MSP3 FVO antigen in malarious children was significantly higher compared to the healthy children after the iron intervention. After the intervention, the female iron group participants had considerably higher antibody responses to malaria-specific antigens than their male counterparts. Iron fortification offered protection against malaria for children with adequate iron status.

Keywords: Iron Fortification, Malaria immunity, preschool children

MA 041: In-silico and Molecular Characterization of the Plasmodium malariae Reticulocyte Binding Protein 2b

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Abstract:

P. malariae is widely spread in tropical and sub-tropical areas and has an overlapping presence with *P. falciparum* (Pf) especially, in sub-Saharan countries. Due to its low parasitaemia, P. malariae infections usually go undetected during diagnosis. This enables it to live within an individual for a long period and tends to cause several rare complications such as nephrotic syndrome, acute cholecystitis, severe anaemia, and convulsions. Thus, emphasizing the need to study this species and as well, identify molecular targets to aid in the development of an efficacious malaria vaccine. PmRBP2b is a secretory protein from P. malariae merozoites that might be involved in the invasion of human RBCs. Fragments of PmRBP2b were assessed for sequence and structural conservation, then recombinantly expressed before they were purified to assess their seroprevalence among individuals living in Ghana. Computationally, PmRBP2b was found to be highly conserved and has both erythrocyte and nucleotide binding regions. ELISA assay showed that people living in malaria-endemic areas have antibodies elicited against PmRBP2b with an increasing titre against increasing age

Keywords: Vaccine candidate, Antibody response, *Plasmodium malariae*

MA 042: IgG3 hinge region length polymorphism is associated with cerebral malaria in Ghanaian children

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Abstract:

Cerebral malaria may cause mortality or long-term neurological damage in children and several host genetic risk factors have been reported. Malarial-specific IgG3 antibodies are crucial to the human immune response against malaria. The hinge region of IgG3 exhibits length polymorphism (L-long, M-medium, S-short alleles) which may influence its functionality. Here, we studied IgG3 hinge region length polymorphisms in 136 Ghanaian children with malaria. Using logistic regression models, we found children with the recessive MM allotype encoding medium IgG3 hinge region length had an increased risk (aOR=6.67; 95%CI=1.30-34.32, p=0.004) of cerebral malaria. This has implications for future epidemiological studies on cerebral malaria.

Keywords: IgG3 hinge, cerebral malaria, polymorphism, IGHG3

MA 043: Wider antibody breadth against multiple Plasmodium falciparum antigens is associated with a reduced risk of malaria in southern Ghana

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Abstract:

Naturally acquired immunity to malaria results from repeated infection with Plasmodium parasites. However, measuring immune correlates of immunity against febrile malaria in a low transmission setting is quite challenging due to few malaria cases. We sampled 973 children, aged 6 months to 12 years, in southern Ghana out of which 227 were exposed to *Plasmodium falciparum*. Total IgG levels were determined using indirect ELISA. We found the cumulative incidence of malaria to be high in children under 5 years, and a significant association between higher IgG levels to MSPDBL1 (adjusted P-value (aP)=0.030), MSPDBL2 (aP=0.013), MSP3 (aP<0.0001), Glurp-R2 (aP=0.006), and N-MSP3 (aP=0.003), and reduced number of malaria episodes was observed. Also, antibody co-acquisition was

high in children under five years. Wider antibody breadth was associated with protection, parasitaemia and single malaria episode. The data from this supports the use of multivalent vaccines containing these proteins in low-transmission settings.

Keywords: Malaria, immunity, antibody co-acquisition ELISA

MA 044: Plasmodium falciparum-specific cytokine expression in chronic HBV and HBV-negative individuals

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Abstract:

Chronic hepatitis B virus (CHBV) infection remains a major public health problem. Exhaustion of T cells usually contributes to the progression of the chronic state of HBV infection, and this can affect the induction of immune responses to other pathogens such as *Plasmodium falciparum*. This may also consequently affect the efficacy of malaria vaccines when administered. This study compared the cytokine expression profiles between chronic HBV treatment-naive and HBV-negative persons. Non-cytolytic T cell function was determined by measuring cytokine expression levels using a 13-plex Luminex assay by stimulating their blood cells with three *Plasmodium falciparum* (3D7) antigens (CSP, AMA-1 and TRAP) in whole blood assays. There was no significant difference in the ability to produce cytokines between the CHBV and HBV-negative individuals. Also, T-regulatory function was comparable between the two groups as there was a corresponding production of IL-10 in response to pro-inflammatory cytokines such as IL-6 and IL-1β. This may be because chronic HBV patients are not on medication since they have not reached that point of needing treatment. Chronic HBV-infected individuals exhibited similar non-cytolytic T-cell functionality as that of HBV-negative individuals. Cytokine responses to the vaccine candidates from both groups are similar, hence, there is no impairment to an effective immune response to malaria parasites in this category of chronic HBV patients

Keywords: Cytokine, chronic HBV, whole blood assay

MA 046: Immunodominant T-cell peptides from four candidate malarial antigens for multi-epitope malaria vaccine design

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Abstract:

A malaria vaccine with high efficacy and the capability of protecting against clinical malaria within genetically diverse populations is urgently needed to complement ongoing disease control and elimination efforts. This study extends our previous work which used peripheral blood mononuclear cells (PBMCs) from adults with life-long exposure to malaria parasites to identify immunodominant antigen-specific 15mer overlapping peptide pools from four malaria antigens that elicited T cell interferon-gamma (IFN-γ) and granzyme B (GrzB) responses. Our current study aimed to identify CD8+ T cell epitopes within these previously identified positive peptide pools. Cryopreserved PBMCs from 109 HLA-typed subjects were stimulated with predicted 9-11mer CD8+ T cell epitopes from *P. falciparum* circumsporozoite protein (CSP), apical membrane antigen 1 (AMA1), thrombospondin related anonymous protein (TRAP) and cell traversal for ookinetes and sporozoites (CelTOS) in FluoroSpot assays. A total of 135 epitopes out of 297 tested peptides from the four antigens were experimentally identified as positive for IFN-γ and/or granzyme B production in 65 of the 109 subjects. Forty-three of 135 epitopes (32%) were promiscuous for HLA binding, with 31 of these promiscuous epitopes (72%) being presented by HLA alleles that fall within at least two different HLA supertypes. Furthermore, about 52% of identified epitopes were conserved when the respective sequences were aligned with those from 16 highly diverse *P. falciparum* parasite strains. In summary, our data support the possibility of developing multi-antigen, multi-epitope vaccines based on conserved epitopes that could be effective against multiple *P. falciparum* parasite strains in genetically diverse populations.

Keywords: Epitope, Malaria, T cell, peptide, FluoroSpot

MA 047: Investigating the effect of natural malaria infection on the induction of cross-strain antibodies in adults

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Abstract:

The expression of several polymorphic forms of antigens such as Apical Membrane Antigen 1(AMA1) by *Plasmodium falciparum* is an immune evasion mechanism. Antibodies against one variant form of such polymorphic antigens target both variant-specific and cross-strain epitopes and are therefore not fully effective at recognizing other forms since only the cross-strain fraction is effective. This study aimed to assess the levels of cross-strain anti-AMA1 antibodies in adults living in a malaria-endemic area. Polyclonal antibodies from naturally exposed persons aged 18 years and above were purified with allelic forms of AMA1 from the HB3 or CAMP malaria parasite variants and shown to recognize and bind at varying degrees

to other allelic forms of AMA1 (in competitive enzyme-linked immunosorbent assays). We then performed an inhibitory ELISA with the cross-strain rat 4G2 monoclonal antibody which showed very minimal recognition of its conformational AMA1 epitope by the HB3 (4.03%) and CAMP (5.02%) AMA1-specific antibodies. Antibody avidities as measured by a NaSCN ELISA were comparable irrespective of which of the antigen variants were used to capture antibodies. These results collectively show that there is an induction of cross-strain antibodies in naturally acquired malarial infections in adults with the least cross-reactivity between the various AMA1 alleles in this study is 69.13% however, strain-specific responses were still present. Also, the epitope recognized by the conserved 4G2 conformational epitope makes up a very small fraction of epitopes present on the AMA1 antigen.

Keywords: Antibodies, Malaria, Polymorphism.

MA 049: Global Analysis of Plasmodium falciparum Dihydropteroate Synthase Variants Associated with Sulfadoxine Resistance Reveals Variant Distribution and Mechanisms of Resistance

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Abstract:

The therapeutic efficacy of sulfadoxine-pyrimethamine chemotherapy is continuously impacted by sulfadoxine (SDX) resistance which necessitates ongoing research to guide its continued use. This study examined SNPs associated with SDX resistance, highlighting distributions and the potential effect of mutations on *Plasmodium falciparum* dihydropteroate synthase (Pfdhps) protein structure. Based on computational approaches, 6336 genomic sequences from 13 countries were analysed. The prevalence of SNPs and their corresponding haplotypes were estimated. The impact of mutation and haplotypes was unveiled via homology modelling, energy-based techniques, and molecular dynamics (MD) simulations. A437G was nearing fixation in all countries studied with a peak in Malawi. K540N allele was seen in isolates from Southeast Asia (Thailand; 6.88 %, Cambodia; 3.37 % and Vietnam; 4.35 %). Mutation A613S displayed variable prevalence across most of the sites except for isolates from DR Congo and Malawi. Molecular interactions between SDX and Pfdhps showed a general loss of interactions in mutant proteins compared to the wild type (WT). SDX made unfavourable interaction with residue Tyr663 in mutant K540E and haplotype A581G/A613S. During MD analysis, SDX was released from the active site in mutants A581G, and A613S before the MD simulation run time. Protein RMSD showed multiple conformational changes and unfolding behaviour in mutants relative to the WT. Overall, continuous analysis of SNPs and their effects on the structure is encouraged to track the mutations and their effect. This will help inform the use of SDX in malaria prevention in pregnant women and children.

Keywords: Pfhps, sulfadoxine, malaria, haplotype, mutations

MA 050: GMZ2 Vaccine-Induced Antibody Responses, Naturally Acquired Immunity and the Incidence of Malaria in Burkinabe Children

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Abstract:

GMZ2 is a malaria vaccine candidate evaluated in phase 2b multi-centre trials. Here we assessed antibody responses and the association of naturally acquired immunity with an incidence of malaria in one of the trial sites, Banfora in Burkina Faso. The analysis included 453 (GMZ2 = 230, rabies = 223) children aged 12-60 months old. Children were followed up for clinical malaria episodes for 12 months after the final vaccine administration. Antibody levels against GMZ2 and eleven non-GMZ2 antigens were measured on days 0 and 84 (one month after the final vaccine dose). Vaccine efficacy (VE) differed by age group (interaction, (12-35 months compared to 36-60 months), p = 0.0615). During the twelve months of follow-up, VE was 1% (95% confidence interval [CI] -17%, 17%) and 23% ([CI] 3%, 40%) in the 12 - 35 and 36 – 60 months old children, respectively. In the GMZ2 group, day 84 anti-GMZ2 IgG levels were associated with reduced incidence of febrile malaria during the follow-up periods of 1-6 months (hazard ratio (HR) = 0.87, 95% CI = (0.77, 0.98)) and 7-12 months (HR = 0.84, 95%CI = (0.71, 0.98)) in the 36-60 months old but not in 12-35 months old children. Multivariate analysis involving day 84 IgG levels to eleven non-vaccine antigens, identified MSP3-K1 and GLURP-R2 to be associated with reduced incidence of malaria during the 12 months of follow-up. The inclusion of these antigens might improve GMZ2 vaccine efficacy.

Keywords: GMZ2, MSP3-K1, GLURP-R2, naturally acquired immunity

MA 051: Extended follow-up of children in a phase2b trial of the GMZ2 malaria vaccine

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Abstract:

The GMZ2/alum candidate malaria vaccine had an efficacy of 14% against clinical malaria over 6 months of follow-up in a phase 2b multicentre trial in children 1–5 years of age. Here we report the extended follow-up of safety and efficacy over 2 years. A total of 1849 (GMZ2 = 926, rabies = 923) children aged 12–60 months were randomized to receive intramuscularly, 3 doses of either GMZ2/alum or rabies vaccine as control 28 days apart. The children were followed up for 24 months for clinical malaria episodes and adverse events. There were 2,062 malaria episodes in the GMZ2/alum group and 2,115 in the rabies vaccine group. Vaccine efficacy (VE) was 6.5% (95% CI: -1.6%, 14.0%). In children aged 1–2 years at enrolment, VE was 3.6% (95 %CI: -9.1%, 14.8%) in the first year and -4.1% (95 %CI: -18.7%, 8.7%) in the second year. In children aged 3–5 years at enrolment VE was 19.9% (95 %CI: 7.7%, 30.4%) in the first year and 6.3% (95 %CI: -10.2%, 20.3%) in the second year. A total of 187 (GMZ2= 91, rabies= 96) serious adverse events were recorded in 167 individuals. There were no GMZ2 vaccine-related serious adverse events. GMZ2/alum was well tolerated. Follow-up over 2 years confirmed a low level of vaccine efficacy with slightly higher efficacy in older children, which suggests GMZ2 may act in concert with naturally acquired immunity.

Keywords: GMZ2, Malaria Vaccine, Plasmodium falciparum, Efficacy

MA 052: Therapeutic Efficacy of Dihydroartemisinin-piperaquine combination in the treatment of uncomplicated malaria in three malaria sentinel sites in Ghana

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Abstract:

In 2020, Dihydroartemisinin-Piperaquine (DHAP) was adopted as a second-line antimalarial for uncomplicated malaria in Ghana following a review of the country's antimalaria medicines policy. Available data obtained in 2007 had shown DHAP therapeutic efficacy of 93.3% using a day-28 follow-up schedule. In 2020, the standard 42-day follow-up schedule for DHAP was used to estimate current efficacy levels in three malaria sentinel sites representing the three main ecological zones of the country- savannah, forest, and coastal. PCR genotyping distinguished between recrudescence and re-infection using merozoite surface protein 2 (MSP2)-specific primers: FC27 and 3D7. Per protocol, the analysis showed day-28 efficacy of 100% in all three sentinel sites. Day-42 PCR-corrected efficacy ranged between 90.3% (95% CI: 80.1 – 96.4%) in the savannah zone to 100% in the forest and coastal zones, yielding a national average of 97.0% (95% CI: 93.4 – 98.8). We conclude that DHAP is highly efficacious in the treatment of uncomplicated malaria in Ghana. This data will serve as a baseline for subsequent DHAP efficacy studies in the country.

Keywords: Therapeutic Efficacy, Dihydroartemisinin-piperaquine, Uncomplicated malaria, Ghana

MA 053: Tracking malaria slide positivity rates in 30 sentinel sites across Ghana

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Abstract:

In Ghana, effective case management remains one of the main interventions for the achievement of the primary goal of malaria control, which is to reduce malaria-related morbidity and mortality. Key to the provision of effective malaria case management is an adequate diagnosis, which is vital for assessing the impact of preventive strategies such as deployment and use of long-lasting insecticide-treated Nets (LLINs), indoor residual spraying (IRS), intermittent preventive treatment in pregnancy (IPTp), and seasonal malaria chemoprevention (SMC). Over the years malaria diagnosis has largely been presumptive leading to poor case management and poor data on malaria parasite positivity rates, which is necessary for the assessment of the country's progress along the control-elimination continuum. It is in this light that the National Malaria Control Programme (NMCP), in collaboration with the Noguchi Memorial Institute for Medical Research (NMIMR), established sentinel sites across the country to generate data for monitoring malaria slide positivity rates (mSPRs). The surveillance activity aims at tracking mSPRs in 30 sentinel sites across Ghana with 2014 as the baseline. Data generated over the past 7 years show a significant decline in the overall mSPR from 23.7% (95% CI: 23.3-24.1) in 2014 to 11.1% (95% CI: 10.8-11.4) in 2021 with regional variations. *Plasmodium falciparum* mono-infection remains the most prevalent infection type in the country: 97.3% (95% CI: 97.2-97.4). We conclude that malaria interventions over the years have had a significant positive impact on mSPR in Ghana.

Keywords: Tracking, Malaria, Slide positivity, Sentinel, Ghana

MA 054: Identification of avian malaria parasite species causing disease in Ghanaian birds

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Abstract:

Malaria is a major public health concern around the globe affecting mammals as well as other vertebrate hosts including birds and reptiles. Malaria and related parasites in birds have been extensively studied in the temperate regions but there seems to be some sampling deficit in the Afrotropical causing a lack of resolution of the haemosporidian phylogeny. In contributing to solving this research gap, this study sought to identify parasites in poultry communities where poultry farms usually share boundaries with wild bird habitats. This is based on the hypothesis that boundary sharing increases the possibility of parasite sharing among birds in the same ecological zone. Blood samples were collected from birds and published Polymerase Chain Reaction protocols coupled with traditional microscopy were used to screen for parasites, and sequencing of a partial region of the cytochrome b

gene was used for genus-specific and lineage identification. A total of 1082 domestic and free-range birds and 28 wild birds were sampled. The overall prevalence of avian malaria parasites was 21.5% for all species, 8.9% for *Plasmodium*, 2.1% for *Haemoproteus*, 0.5% for *Leucocytozoon* and 9.8% for *Plasmodium* and *Leucocytozoon* co-infections. Comparing the three groups of birds, parasite prevalence was 37.6%, 15.1% and 39.3% in free-range, farmed and wild birds respectively.

Keywords: Avian malaria, *Leucocytozoon*, *Haemoproteus*, *Plasmodium*, Prevalence

MA 055: Circulating endothelial cells and endothelial progenitor cells are altered in preeclampsia and placental malaria

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Abstract:

Preeclampsia (PE) and placental malaria (PM) are pregnancy complications associated with endothelial dysfunction. Circulating endothelial cells (cECs) and circulating endothelial progenitor cells (cEPCs) are surrogate markers of endothelial damage and repair respectively. Based on this knowledge, we assessed the profile of endothelial cell phenotypes in PE and non-PE pregnancies and how these cells discriminate against the PM. Endothelial cell phenotypes were quantified from peripheral, placental and cord blood in 69 non-PE and 71 PE-diagnosed women using flow cytometry. The presence of PM was assessed by histological analysis. Cord blood cEPCs were higher in PE compared to non-PE pregnancies ($P = 0.009$). The matured phenotype of cEPCs showed a strong correlation with fibroblast growth factor ($r = 0.69$, $P < 0.0001$) and a moderate one with CD146 ($r = 0.46$, $P < 0.01$) in the peripheral blood of the non-PE pregnancies. In the placenta, cECs were lower in PE-diagnosed women compared to non-PE women with active PM ($P = 0.03$). The expression pattern of all endothelial cell phenotypes was generally high in the placenta compared to peripheral blood in either PE or non-PE women with active or past placental infections. This observation was also seen in the placentas of non-PE women with no placental infections but not that of the PE group. Endothelial cell phenotypes and the angiogenic factors that stimulate their release are altered in both healthy and PE pregnancies. Also, PM further altered the levels of cECs and cEPCs in both PE and non-PE pregnancies.

Keywords: Endothelial cells, Preeclampsia, placental malaria

MA 056: Identification of the equilibrative nucleoside transporter 1 (PfENT1) gene in Plasmodium falciparum laboratory strains and Ghanaian clinical isolates.

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Abstract:

The emergence of parasite resistance to effective antimalarial drugs necessitates the identification of new targets for drug development. One such potential drug target is the malarial purine metabolic pathway. *Plasmodium falciparum* is a purine auxotroph, relying on the host erythrocyte for purine nucleosides and nucleobases for growth. The PfENT1 gene is presumably the major route of purine transport across the parasite plasma membrane. This study, therefore, investigated the presence of the PfENT1 in *P. falciparum* culture-adapted laboratory strains 3D7, NF54 and DD2 as well as Ghanaian clinical isolates collected in 2016. The laboratory strains were cultured using complete RPMI and the parasitemia was determined after every 48 hours. A plot of parasitemia against time (hours) showed the highest parasitemia on the 10th day. DNA was extracted from 30 archived dried blood spots from Begoro, Navrongo and Cape Coast and cultured lab strains. Conventional polymerase chain reaction (PCR) was used to amplify the gene followed by agarose gel electrophoresis to determine successful amplification. 80% (24/30) of lab strains run were positive for the PfENT1 gene with 20% (6/30) being PCR negative. 73% (22 /30) of clinical isolates were PCR positive while 27% (8/30) yielded no amplification. The study presented findings that support a previous study that identified PfENT1 in culture-adapted laboratory strains and for the first time, PfENT1 has been identified in clinical samples from three ecological zones in Ghana. However, further studies are ongoing as part of efforts in demonstrating PfENT1 as a potential target for novel antimalarial drugs.

Keywords: Purine, *Plasmodium falciparum*, Parasitemia

MA 057: Development of local powdered beans, maize, and dried herring formula as feed in laboratory maintenance of Anopheles mosquito larvae

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Abstract:

Laboratory maintenance of mosquitoes is important in studying vector biology, the transmission of diseases and testing vector control tools. Standard operating procedures require feeding larvae with commercial fish meals. However, there are procurement challenges in importing these products. There are also inconsistencies in the adaptation

of larvae to different brands of fish meals which affect the production of mosquitoes for research purposes. We investigated locally acquired beans, maize, and dried herrings on the development of mosquito larvae reared under laboratory conditions. 100 Anopheles gambiae 1st instar larvae were introduced into 500mL of dechlorinated tap water for 4 replicates per treatment and kept under standard insectary conditions. 40mg of powdered beans, maize, and herrings as single and combined treatment was introduced into each replicate for each treatment with the Tetra Goldfish meal as control. Larval mortality and the number of pupae were recorded daily. 25 adults from each treatment were blood fed and allowed to lay eggs to assess fertility. Mosquitoes were sampled for wing measurement and weighing. Maize treatment recorded high larval mortality but there was no significance in mortality for all treatments compared to the control. There was no significant difference in the emergence rate (p, 0.5122), blood feeding rates (p, 0.3351), or fecundity (p, 0.0663). Morphologically there was no significant difference in mosquito weight and wing measured across all the treatments with p values 0.5272 and 0.6014 respectively when compared to the control. The local feed has proven to be a good source of nutrients for larval development for raising mosquitoes in the laboratory.

Keywords: Feeding, *Anopheles gambiae*, malaria, mosquito weight

MA 058: In-silico design of vaccine candidates against Plasmodium falciparum targeting the circumsporozoite protein

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Abstract:

The malaria burden in endemic regions especially in sub-Saharan Africa remains relatively high. One main tool lacking in the arsenal is a broadly effective vaccine against the most lethal causative parasite of malaria, Plasmodium falciparum. The circumsporozoite protein (CSP) has been one of the most promising targets for vaccine design as the currently most advanced malaria vaccine, RTS, S/AS01 was designed from the CSP antigen. The efficacy of the RTS, S/AS01 vaccine was about 39%, which falls short of the World Health Organisation (WHO) target of at least 75% vaccine efficacy. Using the same CSP as the target, 308 9mer immunogenic epitopes were predicted and docked molecularly to nine human leukocyte antigens (HLA). The hits from the molecular docking were complexed with the nine HLAs and subjected to molecular dynamic simulations to ascertain how stable their interactions could be. These have identified ten immunogenic leads as vaccine candidates that had more than 85% population coverage for three populations in Ghana; Cape Coast, Kintampo and Navrongo. These ten epitopes had docked well with all nine HLAs and produced stable root means square deviation (RMSD) from the molecular simulations. Six of these lead epitopes were predicted as non-allergens and none of the leads was within the RTS, S/AS01 vaccine region. These lead immunogenic epitopes could further be explored in wet lab experimental designs for the development of broadly efficacious vaccines against malaria.

Keywords: in-silico, vaccine, Plasmodium falciparum, epitopes, circumsporozoite-protein

MA 060: In vitro Antiplasmodial Activity and LC-MS Analysis of Extracts and Fractions from Two Ghanaian Medicinal Plants

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Abstract:

Medicinal plants are used worldwide for the treatment of several human ailments including Malaria. This study assessed the activity of extracts and fractions of different parts of *Alchornea cordifolia* and *Carapa procera*, against the NF54 strain of *P. falciparum* parasite using the SYBR Green I assay. Phytoconstituents and the LC-MS profiles of the most active extracts and fractions were also determined. A. cordifolia extracts were more potent than C. procera extracts with all the leaf extracts of A. cordifolia having IC50 of 0.83-4.58 µg/ml. The most active of all the extracts was the 100% ethanolic extract of A. cordifolia leaves (ACLE1) with IC50 0.83 µg/ml. Moderate inhibitory activities were recorded for the 100% ethanol stem (CPSE1) and leaf (CPLE1) extracts of C. procera, with IC50 of 37.94 and 14.79 µg/ml respectively. Fractionation of two extracts each of A. cordifolia (ACSE1, ACLE2) and C. procera (CPLE1, CPSE1), indicated five fractions recording IC50 values below 10 µg/ml with the chloroform fraction, CPSE1C, being the most active (IC50 0.20 µg/ml). Fractionations improved activity for most of the selected crude extracts. LC-MS analysis indicated eight or more components in each fraction. These findings affirm previous studies and support the traditional use of the plants and have provided a basis for further in vivo studies as potential antimalarials.

Keywords: cordifolia, procera, antiplasmodial, phytochemicals, LC-MS

MA 061: In vitro Antiplasmodial Activity and LC-MS Analysis of Extracts and Fractions from Two Ghanaian Medicinal Plants

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Abstract:

Medicinal plants are used worldwide for the treatment of several human ailments including Malaria. This study assessed the activity of extracts and fractions of different parts of *Alchornea cordifolia* and *Carapa procera*, against the NF54 strain of *P. falciparum* parasite using the SYBR Green I assay. Phytoconstituents and the LC-MS profiles of the most active extracts and fractions were also determined. *A. cordifolia* extracts were more potent than *C. procera* extracts with all the leaf extracts of A. cordifolia having IC50 of 0.83-4.58 µg/ml. The most active of all the extracts was the 100% ethanolic extract of *A. cordifolia* leaves (ACLE1) with IC50 0.83 µg/ml. Moderate inhibitory activities were recorded for the 100% ethanol stem (CPSE1) and leaf (CPLE1) extracts of *C. procera*, with IC50 of 37.94 and 14.79 µg/ml respectively. Fractionation of two extracts each of *A. cordifolia* (ACSE1, ACLE2) and C. procera (CPLE1, CPSE1), indicated five fractions recording IC50 values below 10 µg/ml with the chloroform fraction, CPSE1C, being the most active (IC50 0.20 µg/ml). Fractionations improved activity for most of the selected crude extracts. LC-MS analysis indicated eight or more components in each fraction. These findings affirm previous studies and support the traditional use of the plants and have provided a basis for further in vivo studies as potential antimalarials.

Keywords: In vitro; antiplasmodial; phytochemicals; LC-MS

MA 062: Kinetics of anti-GMZ2, anti-GLURP R0 and anti-MSP3 vaccine-induced antibody responses in Ghanaian children aged 12 – 60 months

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Abstract:

The GMZ2/Alum phase IIb clinical trial conducted recently in children in Africa suggests that the vaccine efficacy was delayed. Here, we assessed the dynamics of antibody responses to the GMZ2 vaccine and its constituent antigens in the trial cohort. Plasma specimens from 198 children aged 12 – 60 months from Navrongo, Ghana; one of the GMZ2/Alum phase IIb clinical trial sites were analysed. IgG, IgG1and IgG3 subclass antibody levels against GMZ2, GLURP R0, and MSP3 were measured using enzyme-linked immunosorbent assay. Antibody response was very rapid, following the vaccination. GLURP R0 was the most immunogenic (mean fold increase; MFI = 77.6 [95%CI: 25.5; 129.8]) vaccine constituent whiles MSP3 (MFI: 6.2 [95%CI: 4.7; 7.7]) was the least. The magnitude of antibody response was highest in young children 12 – 35 months. There was an inverse relationship between baseline parasitaemia status and vaccine-induced antibody levels although it was not statistically significant. Pre-existing anti-GMZ2 ($p < 0.001$), anti-GLURP R0 ($p = 0.0029$) and anti-MSP3 ($p = 0.001$) IgG antibody levels were associated with higher antibody levels post-vaccination. IgG1 levels were higher after the vaccination compared to IgG3 levels which were higher than IgG1 before vaccination. Antibody decay showed a two-phase decay pattern. GMZ2 vaccination induced a rapid antibody response, however, the cytophilic IgG3 to IgG1 ratio was imbalanced. This has implications for the antimalarial activities of the vaccine-induced antibodies and efficacy. Future antibody subclass analysis is recommended for the development of vaccines such as GMZ2.

MA 063: In-silico design of vaccine candidates against Plasmodium falciparum targeting the circumsporozoite protein.

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Abstract

The malaria burden in endemic regions especially in sub-Saharan Africa remains relatively high. One main tool lacking in the arsenal is a broadly effective vaccine against the most lethal causative parasite of malaria, *Plasmodium falciparum*. The circumsporozoite protein (CSP) has been one of the most promising targets for vaccine design as the currently most advanced malaria vaccine, RTS, S/AS01 was designed from the CSP antigen. The efficacy of the RTS, S/AS01 vaccine was about 39%, which falls short of the World Health Organisation (WHO) target of at least 75% vaccine efficacy. Using the same CSP as the target, 308 9mer immunogenic epitopes were predicted and docked molecularly to nine human leukocyte antigens (HLA). The hits from the molecular docking were complexed with the nine HLAs and subjected to molecular dynamic simulations to ascertain how stable their interactions could be. These have identified ten immunogenic leads as vaccine candidates that had more than 85% population coverage for three populations in Ghana; Cape Coast, Kintampo and Navrongo. These ten epitopes had docked well with all nine HLAs and produced stable root means square deviation (RMSD) from the molecular simulations. Six of these lead epitopes were predicted as non-allergens and none of the leads was within the RTS, S/AS01 vaccine region. These lead immunogenic epitopes could further be explored in wet lab experimental designs for the development of broadly efficacious vaccines against malaria.

Keywords**:** *in-silico*, vaccine candidate, *Plasmodium falciparum*, epitopes, circumsporozoite protein.

MA 064: Computational Drug Discovery of Natural Product Compounds Against the Activities of the Mutant Plasmodium falciparum kelch 13 Protein.

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Abstract

Artemisinin resistance is spreading in Southeast Asia. If resistance spreads in Africa, it will be catastrophic for the global efforts to eradicate malaria. Presently, however, there is no substitute antimalarial therapy for the treatment of uncomplicated malaria apart from the Artemisinin combination therapies (ACTs). Recent research indicates that artemisinin resistance is conferred by mutations in the *Plasmodium falciparum* kelch13 (Pfk13) by inhibiting haemoglobin endocytosis. We identified potential bioactive compounds by targeting the Pfk13. We hypothesize that inhibition of the activities of the mutant K13 will inadvertently prolong the lifespan of the ACTs. Lipinski's rule of five was used to reduce an integrated library of 450044 African-derived compounds from the ZINC database to 26356 before the compounds were molecularly docked against K13 (PDB ID: 4YYE) using Qvina. Using Discovery Studio, LigPlot+, and molecular dynamics simulations, structural insights into the mechanisms of binding of the top 7 compounds in both the wild type and mutant K13 were characterized. In both the wild type and mutant K13, seven zinc database compounds demonstrated good binding affinities, with one exhibiting the highest binding

affinity of -14.1 kcal/mol. These molecules interacted with C580Y and A675V, in hydrogen and hydrophobic bonds. Molecular dynamics (MD) showed that only one compound departed the binding site before the MD run-time. Thus, six compounds plausibly disrupt the activities of the mutant K13 by promoting haemoglobin metabolism for the activation of artemisinin. These compounds have the potential to be novel scaffolding that could be used in ACTs and require experimental validation.

Keywords: Artemisinin resistance, Kelch-13, Molecular Docking, Molecular Dynamic Simulations

MA 065: Association of antimalarial drug resistance markers with resistance phenotypes in Ghana

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Abstract

Monitoring resistance markers, and the efficacy of drugs in patients using *in vivo* studies, and *in vitro* studies to evaluate parasite sensitivity to drugs, complement each other to inform the emergence and spread of anti-malarial drug resistance. Our study assessed the association between known drug resistance markers (*pfcrt*, *pfmdr1*, *pfdhps*, *pfdhfr*, and *pfk13*) and phenotypic outcomes (increased IC50 and late parasitological failure) of antimalarial drugs in two ecological zones in Ghana. Drug resistance phenotypes were determined in efficacy trials and in vitro assays conducted between 2014 and 2017 to assess artesunate-amodiaquine's efficacy and to determine the parasites' sensitivity to selected drugs respectively. Drug resistance markers were genotyped using the Illumina MiSeq sequencing platform after molecular inversion probe capture. The prevalence of markers was compared with late parasitological failure (parasitemia between day 4 and day 28) and drug sensitivity using the chi-square test/Fisher exact test. There was no surge in the prevalence of the modulating *pfmdr1* mutant haplotype *pfmdr1* YYY (86Y, Y184, and 1246Y, which is linked to amodiaquine resistance was less than 2%) in circulating Ghanaian *P. falciparum* isolates. The prevalence of drug resistance markers in Ghana showed varying associations with parasite susceptibility to the drugs used in Ghana. There was no association between *pfmdr1* markers and late parasitological failure (p value>0.05). However, *pfmdr1* Y184 was significantly associated with reinfection on day 28 (OR=0.33, CI=0.12,0.95, p-value=0.04). Monitoring the emergence and spread of drug resistance are critical tools for preserving the efficacy of current antimalarial therapies.

Keywords**:** *Plasmodium falciparum*, Malaria Drug resistance, Amodiaquine, ACT, *pfcrt*, *pfmdr1*, Ghana

MA 066: Relative abundance of a promising candidate for paratransgenesis is increased in both sexes of Anopheles gambiae s.l mosquitoes after feeding.

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Abstract

The discovery of a high prevalence of anti-Plasmodial fungus, *Microsporidia* MB, in both sexes of Anopheles mosquitoes has informed the need to include males in the study of the mosquito-associated microbiome for new disease control strategies. In this study, the bacterial composition of male and female *Anopheles gambiae* s.l was compared considering their feeding status.20 males and 20 females each of 1-day-old, 4-5 day-old sugar-fed, and 20 24-hr post-blood-fed females were randomly selected for genomic DNA extraction and bacterial 16SrRNA amplicon sequencing. Bacterial diversity, taxa abundance and differential compositional analyses were performed using established pipelines. Without considering the feeding status of mosquitoes, males and females were observed to share similar microbiota (p= 0.73). Feeding status increased dissimilarity among males (p=0.007) and females (p=0.001). The amount of variation was greater in females (48% p=0.002) than in males (29% p=0.02), likely driven by the absence of blood feeding in males. *Elizabethkingia meningoseptica* was the only common differentially abundant bacteria between unfed and sugar-fed mosquitoes of either sex ($p < 0.01$). The relative abundance of this bacterium is higher in blood-fed compared to non-blood-fed females (Linear Discriminant Analysis (LDA) scores >5.0; $p<0.01$). A promising candidate bacterium for Paratransgenesis, Asaia, and Chryseobacterium which is known to support egg production were also differentially more abundant in sugar-fed and blood-fed females, respectively (LDA scores >3.5). Presence of *E. meningoseptica*, a bacterium known to have anti-Plasmodial effects in females, warrants further functional investigation in males to better understand opportunities for developing novel transmission-blocking strategies.

Keywords: Microbiota, *Anopheles gambiae*, *Elizabethkingia meningoseptica*

NEGLECTED TROPICAL DISEASES

NT 002: Single dose albendazole treatment outcomes of hookworm infections linked to human gut microbiome alterations

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Abstract:

Microbes play key roles in human gut homeostasis, metabolic, immunologic and physiopathology. Our longitudinal study on hookworm transmission conducted from 2018-2021 in the Kintampo North Municipality in Ghana recorded low cure rates with single-dose 400mg albendazole therapy (SDAT). To investigate the involvement of the gut microbiome, we obtained faecal samples from consenting hookworm-positive participants who were either cured or non-responsive after SDAT. At each sampling event, samples were collected pre-treatment and 10-14 days following albendazole administration. We used 16S rRNA amplicon sequencing of genomic DNA extracted from stool to investigate the composition and biodiversity of the gut microbiota and to identify potential microbial biomarkers associated with treatment outcomes. Analyses revealed a significant increase in microbial diversity among cured individuals after successful therapy. However, microbiota composition did not revert to a non-infected state. We noticed a 30% variation in microbiota diversity between cured and non-responsive individuals after SDAT (p= 0.0007) which was mainly driven by a compositional increase in species from the Prevotellaceae family (LDA score > 4) in cured individuals and a corresponding increase in members of Clostridia family such as Blautia and Ruminococcus (LDA score > 4) within non-responsive individuals. This study suggests a relationship between human gut microbiota and albendazole therapy outcomes of hookworm infection. Further studies will be conducted to explore these microbial biomarkers to establish their potential for the assessment of pharmacological responses to anthelminthic therapies.

Keywords: Hookworm, albendazole, treatment outcomes, gut microbiome

NT 003: Environmental determinants of soil-transmitted helminths transmission using geospatial technology

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Abstract:

Soil-Transmitted Helminthiasis (STH) is targeted for elimination by 2030 and there are concerns about achieving this target in Ghana due to reports of persistent low albendazole cure rates following treatment. Kawampe a rural community in the Bono Region, recorded a 23% prevalence of hookworm in 2015 and has consistently remained high despite interventions in cohort studies. To investigate the persisting high prevalence in this community, this study aimed to identify pathways for transmission. A cross-sectional study was carried out involving 59 consenting participants. They were screened for hookworm infection to enable grouping into positive and negative cases. Each participant wore a GPS tracking device for 10 consecutive days and the movement data was captured in real-time, recorded, plotted and put in clusters. Soil samples were also collected from these clusters where participants spent most of their time as well as places of interest. Soil physical and chemical properties were measured using standard methods. Determinants of larvae counts were estimated with Multivariate Negative Binomial Regression (MNBR). Soil pH was positively associated with the number of larvae as well as Carbon and sandy-loamy textures ($P<0.001$) whilst high nitrogen and clay contents were significantly associated with low larvae counts ($P<0.001$). The larvae count of infected (n=93) and non-infected (n=173) were not significantly different (P=0.59). Our metagenomics analysis of larval DNA has identified *Parastrongyloides trichosuri*, *Ancylostoma caninum* and *Panagrolaimus superbus* as dominant larvae in soil samples around rubbish dumps, markets and toilet areas, which was expected.

Keywords: Soil-transmitted helminths, transmission, GPS tracking/technology.

NT 004: Insights into transmission dynamics of soil-transmitted helminths (STH) using metagenomics

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Abstract:

Soil-transmitted helminths (STH) infections including *Ascaris lumbricoides* (roundworm), *Necator americanus* (hookworm) and *Trichuris trichiura* (whipworm) are neglected tropical diseases exacting a huge health toll on deprived communities worldwide. The control/elimination strategy is regular mass administration of at-risk populations with benzimidazoles e.g., albendazole. However, MDA alone does not interrupt transmission and there is a need to interrogate the determinants of their transmission dynamics. The study was aimed at using metagenomics analysis to gain insights into where infections are picked up by inhabitants by identifying areas in a hookworm-endemic Ghanaian community. Soil samples were collected at various sites including rubbish dumps, marketplace, etc. and helminth eggs in soil were reared to larvae and counted and whole DNA was extracted and sequenced. The soil types were loamy sand, sandy-clay loam, sandy loam and silt loam with a mean pH of 5.589. To aid in the metagenomics analysis, a Kraken2 database named Nematode Viral was created using the genome sequences of 160 flatworm and nematode species and their taxonomic information obtained from the NCBI Taxonomy database. The DNA sequence reads from each soil sample were quality checked and trimmed. The trimmed reads were

run against NematodeViral and the classified reads with their taxonomy assignments were visualized using Pavian. The four abundant species found were *Parastrongyloides trichosuri* (a nematode parasite of possum and native to Australasia), *Panagrolaimus superbus* (an anhydrobiotic nematode), *Trichuris trichiura* (human parasite), and *Ancylostoma caninum* (dog hookworm). There were no hits for *N. americanus* in all 54 soil samples. High larvae counts were significantly associated with high pH and sandy loam soil while low counts were associated with carbon, nitrogen and clay content. The policy implications of our findings are discussed as well as the unexpected discovery of *P. trichosuri* in Ghana.

Keywords: Soil-transmitted helminths, metagenomics, transmission, taxonomy classification

NT 005: First report of novel SNPs of Cryptosporidium virulent isolates in Ghana

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Abstract:

Cryptosporidium transmission in Africa contributes significantly to juvenile morbidity and mortality. Genomic studies have provided a glimpse of markers or putative molecules that could influence *Cryptosporidium* pathogenicity and virulence. These studies have suggested major gene loci important in parasite pathogenicity (parasite invasion and establishment) and host tropism. However, such studies are limited in Africa where disease and virulent isolates are most prevalent. With evidence of cryptosporidiosis incidence in both symptomatic and asymptomatic children in Ghana, the focus of this work was to decipher diversity in Cryptosporidium putative virulent genes specifically by assessing the prevalence of the *Cryptosporidium spp*. infection, expression and variations in these pathogenic genes. *Cryptosporidium spp*. infection prevalence was assessed at the 18SrRNA gene locus by nested PCR in 122 community surveillance samples from Ada-West and 50 archived clinical samples from symptomatic patients. Overall, *Cryptosporidium* prevalence was 18.6% (32/172), consisting of 2.3% (8%; 4/50) symptomatic and 16.3% (23%; 28/122) asymptomatic cases. RT-qPCR revealed that Mucin, mucin-like proteins (MLP) and cysteine protease genes involved in cell attachment and invasion were over-expressed in samples suggesting high infectivity and virulence of these Ghanaian *Cryptosporidium* isolates. Sequencing of the invasive gene MLP revealed 5 new Single Nucleotide Polymorphisms (SNPs) at positions T29135C, T29155C, A29293G, A29143G and T29209G that need functional characterization with advanced techniques such as infectivity assays, CRISPR/Cas9 and in animal model studies. The gene targets and mutations reported in this study could be essential for transmission blockade, vaccine or therapeutic targets, and epidemiological markers for *Cryptosporidium species* differentiation.

NT 007: Comparison of PCR-RFLP and a Taqman qPCR for characterization and quantification of Cryptosporidium species infections in Ghana

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Abstract:

Cryptosporidiosis is a parasitic diarrheal disease which occurs in both humans and animals globally. However, diarrhoeal research in Africa is mostly focused on viral and bacterial pathogens. We adopted qPCR for improved identification of Cryptosporidium parasites from human faecal samples in Ghana. In a cross-sectional surveillance study, human stool samples obtained from five study sites across Ghana were analysed using PCR-RFLP or TaqMan quantitative PCR (qPCR), genotyping, and quantitation of cryptosporidiosis. We analysed stool samples collected from children of both sexes aged ≤ 12 years. 168 samples analysed by PCR-RFLP detected 60 (35.7%) *Cryptosporidium spp*. infections consisting of 39 (23.2%: 14.9% *C. hominis*; 7.1% *C. parvum*; 0.6% each of *C. meleagridis* and *C. baileyi*) in clinical patients and 21 (12.5%: 6.0% *C. hominis* and 6.5% *C. parvum*) non-clinical samples. In a follow-up study, 92 new faecal samples, all from children in non-clinical settings, were analysed by TaqMan qPCR. *Cryptosporidium spp* infections were detected and quantified in 26 (28.3%) children. This consisted of 7 (7.6%) *C. parvum* (103 oocysts/g faeces), 15 (16.3%) *C. hominis* (103 - 106, oocysts/g faeces), and 4 (4.4%) with *C. parvum* and *C. hominis* co-infections. From our studies, TaqMan qPCR emerged as more efficient than PCR-RFLP in detecting and successfully quantifying *C. parvum* and *C. hominis* in humans. Confirmation of other zoonotic *Cryptosporidium spp* detected by PCR-RFLP requires further sequencing. Therefore, this qPCR system can be adapted for such species as well to enhance molecular epidemiological studies on cryptosporidiosis in Africa.

Keywords: Diarrheal disease, Ghana, PCR-RFLP, qPCR, Cryptosporidiosis

NT 008: The effect of MDA on the evolution of non-responsiveness of hookworm to single-dose albendazole (400 mg) treatment

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Abstract:

The study aimed to identify host modifiable factors associated with response to single-dose albendazole by monitoring the response following treatment in the context of the longitudinal study. The rationale is that previous studies in rural communities in the Kintampo North Municipality found that after 5 years of biannual treatment with albendazole, hookworm prevalence decreased initially but remained at 20% with no

indication of a downward trend toward zero. We conducted longitudinal studies on a cohort of 496 consented participants in nine rural communities whose faecal specimens were screened for intestinal parasites at baseline, 9 months and 27 months using the Kato-Katz method. At each time point, those found positive were treated with albendazole (400 mg) and their samples were again screened 10-14 days post-treatment. The hookworm prevalence at the three-time points was 20.01%, 9.22% and 5.3% respectively and the albendazole treatment failure rates were 17.25%, 29.03% and 40.9% respectively. The intensities of hookworm infection (in eggs per gram) at the time points were 138.3, 40.5 and 135, which showed a likely association with climatic seasons because the baseline and the 27 months surveys were conducted in the wet season and the 9-month during the dry season. We surmise that the observed increased treatment failures could be due to increased albendazole tolerance among the participants who remained infected throughout the study period. Why the intensities of hookworm infections in humans should be higher in the wet than in the dry season warrants further investigations.

Keywords: Host, Albendazole, Hookworm, Prevalence, Failure

NT 009: Urogenital schistosomiasis among pregnant women: a need for routine diagnosis and treatment at antenatal care (ANC) visits in Ghana.

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Abstract:

Urogenital schistosomiasis caused by *Schistosoma haematobium* (Sh) is prevalent in Ghana. Ghana scaled-up community distribution of praziquantel during mass drug administration (MDA), but the target has primarily been school-aged children. MDA excludes treatment in pregnant women in Ghana. Our objective was to investigate urogenital schistosomiasis during pregnancy in two hospitals in the Volta Region and its consequences on maternal health. Urine samples were collected at the first antenatal care visit (ANC) (N= 672) and delivery (N = 198) and screened using microscopy to detect Sh ova. Socio-economic and clinical data were obtained from hospital records. Sh. prevalence at first ANC was 3.72% and 1.6% at delivery. Women carried low infection intensities, except for one high *Sh* intensity (≥50 eggs/10 ml). In *Sh*-infected women, haemoglobin (Hb) levels ranged from (5.4-12.5 g/dL) with a mean of 10.90 g/dL. Severe anaemia (5.4 g/dL) matched the highest egg intensity at ANC. Mean Hb was lower at ANC compared to delivery ($P<0.02$). Age, malaria, bed-net usage and SP-IPTp influenced Hb levels. High infection intensities showed a trend which needs to be investigated further. In the two hospitals, pregnant women were not subjected to routine Sh screening and treatment at ANC. This population represents an obstacle in disease control, serving as a reservoir for transmission. Sh infection during pregnancy can impair maternal and neonatal health. We suggest the implementation of a new strategy to screen and treat pregnant women in high-risk endemic areas during ANC.

Keywords: Urogenital, schistosomiasis, screening, diagnosis, Antenatal Care

NT 011: Mapping the risk of hookworm infections and intestinal schistosomiasis in Ghana for effective control programmes

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Abstract:

The global health community has set 2030 as the target for the elimination of neglected tropical diseases including hookworm and *Schistosoma* infections. The current strategy to achieve the objective is using mass drug administration. Questions have been raised about the feasibility of achieving the goal, especially with the challenges of implementation in low-resourced settings and hard-to-reach areas. To enable a focused targeting of resources to achieve elimination, we aimed at identifying high-risk endemic areas of hookworm and intestinal schistosomiasis in Ghana. From 7 administrative regions in Ghana, residents of 52 communities in 17 districts were surveyed. Approximately 87% (4753/5,467) consented individuals provided full data of bio and sociodemographic information and stool samples for the detection of intestinal parasites using the Kato-Katz method. All the community prevalence of hookworm (1-37%) and intestinal schistosomiasis (1-49%) were georeferenced within the spatial polygon of Ghana. The inverse distance weighting (IDW) mathematical interpolation model was used to estimate unknown values by specifying search distance, barriers and closest points to produce the risk maps. The predictive modelling revealed a high risk (21%) of hookworm infections in the middle belt while intestinal schistosomiasis was high up to 33% in the north and south of Ghana mostly associated with water bodies. Our findings provide information to aid the national NTD Elimination Programme to utilize its limited resources efficiently by reinforcing measures in areas of high risk.

Keywords: Mapping, Hookworm, Schistosomiasis, Control, Modelling

NT 012: Assessment of Schistosoma spp mixed infections among school-aged children in a peri-urban community along the Weija Lake.

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Abstract:

Schistosoma haematobium and *S. mansoni* are two major schistosome species widely distributed in Ghana. Mixed infections with the two species have recently been reported in an area where they overlap. Our study sought to assess the level of mixed infection with *S. mansoni* and *S. haematobium* in a peri-urban community where there is an overlap of the two species. We collected stool and urine samples and used parasitological methods to determine the level of single and mixed *S. mansoni* and *S. haematobium* infections in school children in Tomefa. The overall prevalence rates for urogenital and intestinal schistosomiasis were 16.3% (31/190) and 90.4% (169/187), respectively. All those

with urogenital schistosomiasis also had intestinal schistosomiasis. Of the 31 urogenital schistosomiasis cases, 15 had *S. haematobium* eggs only and 16 had *S. mansoni* and/or *S. haematobium* eggs. Of the 169 individuals with intestinal schistosomiasis, only 1 had both *S. mansoni* and *S. haematobium* eggs. Furthermore, 57% of individuals presenting *S. mansoni* eggs in urine, also had high *S. mansoni* infection intensities from their stools. Also, 3 individuals presenting high *S. haematobium* egg infection intensities had ectopic *S. mansoni* infections in addition. The overwhelmingly high prevalence of intestinal infections and ectopic *S. mansoni* eggs in urine indicates a bias towards *S. mansoni* infections in areas with schistosome species overlap. This could have implications for morbidity, as well, as hybridization with a possible challenge to drug treatment effectiveness.

Keywords: schistosomiasis, urogenital, intestinal, ectopic

NT 013: Epidemiological study of two human schistosome species infections in two communities along the Weija Lake.

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Abstract:

Schistosoma haematobium and *Schistosoma mansoni*, are two important schistosome parasite species in Ghana, causing debility to the urogenital, intestinal and related organs, which persist despite countless interventions in endemic areas. Schistosomiasis has been a major health issue in areas along the Weija Lake. It persists due to the unavailability of clean water, and poor sanitation conditions. This study, therefore, sought to profile and compare the prevalence of the various species in two communities along the Weija Lake. A total of 298 children between the ages of 7 and 14 years from Tomefa and Torgahkope communities in the Ga South Municipal District of the Greater Accra Region were involved in the study. Urine and stool samples obtained were examined using microscopy after filtration and Kato Katz techniques were applied respectively. Of the samples collected, 65% were from Tomefa, while the remaining 35% were from Torgahkope. In Tomefa, a high prevalence (90%) of *S.mansoni* was observed in stool samples of study participants, with one case of ectopic *S. haematobium* ova recorded. Similarly, in urine samples, a 30% prevalence of *S. haematobium* was recorded, with a prevalence of mixed *Schistosoma spp* infection at 9%. Also in Torgahkope, *S. mansoni* prevalence was higher (27%) than *S. haematobium* (15%), with a 2% prevalence of mixed infection. Conclusively, the prevalence of *Schistosoma* infection was higher in Tomefa than in Torgahkope, with *S. mansoni* yielding higher prevalence in both communities.

Keywords: Schistosomiasis; *S.mansoni*; Prevalence; *S. haematobium*

NT 014: A comparative study of LF-related perceptions among MDA-compliant and non-compliant groups in the Ahanta West Municipality of Ghana

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Abstract:

The Global Programme to Eliminate Lymphatic Filariasis (GPELF) was established in 2000 to eliminate the disease as a public health problem through: i) treatment of entire endemic populations for at least five years, to break transmission and ii) morbidity management to alleviate the suffering of individuals affected by the disease. Many countries including Ghana have implemented mass drug administration (MDA) to endemic populations and have recorded significant reductions in the population at risk of requiring treatment. There are however challenges, the major ones being the presence of hotspots despite several years of treatment, and non-treated individuals to MDA who may serve as reservoirs re-infecting their communities. Strategies are therefore needed to identify and treat these individuals. This study was conducted to generate baseline data to inform the development and implementation of an "Engage and Treat (E&T)" or "Test and Treat (T&T)" strategy following an MDA round to address the challenges of non-compliance.

Keywords: Lymphatic Filariasis, Perception, MDA, Compliant, Ghana

NT 017: Antileishmanial effects and mode of action of phenolic compounds and Glucantime combinations on Leishmania donovani

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Abstract:

The search for alternative treatments for leishmaniasis remains a priority. Combination therapy is an existing strategy that is making progress in the treatment of other infectious diseases. This strategy could provide an effective means for treating leishmaniasis. Phenolic compounds are important molecules in drug development because of their safety and abundance in nature. In this study, combinations of phenolic compounds (PCs) and the first-line drug (Glucantime) were found to be effective against *Leishmania donovani* promastigotes. The PCs-PCs and PCs-Glucantime combination effects revealed five synergistic combinations with a combination index of less than 1.0. (0.32-0.6). None of the treatments was toxic to THP-1 macrophages. Only the most intriguing associations were studied in terms of the mechanism of action.

Keywords: combination therapy, phenolic compounds, Glucantime

NT 018: Art-based interventions and behaviour change in strategies for NTDs control among rural populations

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Abstract:

The present project is the continuation of the ATPC2 project (2014-2017) funded by UBS Optimus Foundation in which I was involved for my PhD studies. The mid and long-term evaluation of the project on the behaviour of targeted communities was not planned. We request additional funds to achieve this gap and to validate our assumption that participatory art-based interventions are likely to contribute to the change of behaviour within the community. The aim was to capture various avenues of knowledge production and dissemination. This study was based on a qualitative approach. Disposable cameras were entrusted to 4 people in each of the four villages (respecting the criteria of age and sex), and pictures generated from people's environment were discussed during Focus Group Discussions (FGDs). The activities were completed with one-on-one interviews with 18 key informants. Findings defined the importance of the participatory approach in the design of sustainable health interventions. They highlighted how participatory art-based tools can contribute to sustaining health interventions through a deep behavioural change.

Conclusion: Health education can help the rural population to improve their knowledge regarding Neglected tropical diseases and reduce their contamination among the population.

Keywords: Art-based, behaviour change, NTDs, control

NT 019: Impact of a community-wide treatment program on the transmission of Schistosoma species Infections.

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Abstract:

Schistosomiasis remains a public health burden in Africa, contributing to 93% of the 250 million cases worldwide. Just like many neglected tropical diseases, developing and adopting improved mass drug administration has the potential to significantly reduce disease burden. A 1-year longitudinal study comprising parasitological and malacological surveys was carried out to assess the impact of a community-wide treatment program on the transmission and control of *Schistosoma sp.* in communities around Weija Lake. A single dose of praziquantel

treatment was administered to all persons in the communities, resulting in 88.5% coverage of residents after baseline parasitological assessment. Post-treatment assessments were done at 2, 6, and 12 months to check the cure rate and egg reduction rates. *Bulinus* and *Biomphalaria spp*. snails were collected at water contact points bordering the communities to assess transmission of schistosomiasis. A significant ($p<0.05$) reduction in infection was observed at 2 months post-treatment in all study communities. Snail species were found shedding schistosome cercariae at all survey time points, indicating environmental contamination with viable *Schistosoma sp*. eggs. Our findings show that expanded access to praziquantel has the potential to significantly reduce schistosomiasis infections, confirming the efficacy of anti-schistosomiasis drug treatment. However, reinfection occurred over a few months, approaching pre-control levels due to the continuous presence of transmission factors. A multi-sectoral approach including snail control, health education, and improved access to clean water should be integrated into control programs to achieve the holistic goal of schistosomiasis elimination in such areas.

Keywords: Impact, community, treatment, control, schistosomes

NT 020: Helminths infection and sickle cell crisis among children in selected communities in Accra.

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Abstract:

In Sub-Saharan Africa, the overlap of Sickle cell disease (SCD) and Neglected Tropical Diseases (NTDs), mostly schistosomiasis and soil-transmitted helminths infections are common. NTDs can exacerbate the SCD crisis, as they have been shown to cause severe complications or chronic organ dysfunction leading to crisis conditions in SCD patients. This study assessed the current prevalence of selected helminth infections and their association with sickle cell crisis development in children (2-12 years old) in two communities in the Greater Accra Region. Blood and stool samples were obtained from the children. Sickle cell status and the presence of helminths were determined from the blood and stool samples, respectively. Out of the 330 participants recruited, 1% had sickle cell (SS) with the traits (AS) being (14%). Normal (AA) haemoglobin genotype constituted 67.6% and other genotypes SC (1%), CC (1%), SF (0.3%), AC (13.3%), ACF (0.3%) and AF (1.8%). The current overall prevalence of helminth infections in the two communities was 39% (*Ascaris*, hookworm, *Strongyloides*, *Trichuris* and *Schistosoma*). IL-6 and IL8 levels which is a measure of sickle cell crises were found to be elevated in the Hb SS group followed by the Hb AS group as compared to the other groups. Also, the Hb AS group had higher parasite prevalence (4.5%) and their IL-6 and IL8 levels were also higher as compared to the other groups (SC, CC, SF, AC, ACF and AF). The study suggests that higher IL-6 and IL8 levels may clear parasites as seen in the Hb SS group.

Keywords: Sickle cell, NTDs, haemoglobin, cytokines, helminths

NT 022: Assessment of zoonotic enteric parasites in wild animals in Ghana

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Abstract:

Anthropogenic activities such as hunting wild animals increase the risk of zoonotic transmission as human encroachment of wildlife habitats expose them to infective stages of various parasites including helminths. This coupled with the handling, processing, and consumption of bushmeat poses a greater risk to human health. This study sought to identify and determine the parasitic helminth burden in wild animals and their zoonotic potential. Parasitological analysis of faecal samples collected from a total of fifty-two (52) wild animal carcasses at the Atwemonom bushmeat market in Kumasi showed 10 genera of parasites with an overall prevalence of 71.0% enteric parasites. Individual parasites species prevalence observed were: *Ascaris sp.* (25.0%), *Strongyloides sp.* (19.2%), *Ancylostoma sp.* (17.30%), *Fasciola sp.* (9.60%), *Dicrocoelium sp.* (7.7%), *Trichuris sp.* (5.8%), *Taenia sp.* (3.8%), *Enterobius sp.* (1.9%), *Hymenolepis sp.* (1.9%) and *Eimeria sp.* (1.9%). Thirty-three per cent (33%) and 39% of wild animals had single and multiple parasite species infections, respectively. Molecular analysis showed, at least, one parasite in all samples analyzed. Species-specific analysis indicated the presence of *Strongyloides stercoralis* and *Trichuris trichiura* in 12.5% and 77.5%, respectively. These two parasites are known to cause human illnesses that are considered among the neglected tropical diseases. The study showed a high prevalence of enteric parasites in wild animals with *S. stercoralis* and *T. trichiura* indicating the need to intensify one health approach in disease control as these parasites have high zoonotic potential.

Keywords: Enteric, zoonotic, neglected tropical diseases, Wildlife

NT 023: Detection of exposure to Leishmania infection and confirmation of cutaneous leishmaniasis in the Oti Region of Ghana

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Abstract:

Cutaneous leishmaniasis (CL) is the most common leishmaniasis, a neglected vector-borne disease of the skin caused by parasites of the genus *Leishmania*. Annually, an estimated 0.7 to 1.3 million new cases of CL are reported globally. We conducted an epidemiological assessment in the Oti Region, encouraged by recent reports of potential cases of CL. Using

a cross-sectional study design, exposure to Leishmania infection was investigated in three communities of the Oti Region based on the leishmanin skin test (LST). Suspected active cutaneous lesions (ACL) were sampled using non-invasive sequential tape strips for DNA extraction and polymerase chain reaction (PCR) for the detection of *Leishmania* parasites. LST results for 3,071 participants indicated an overall prevalence of 41.8% exposure to Leishmania infection. There was a higher odd of exposure to *Leishmania* infection which was associated with being male [AOR = 1.27; CI: 1.09, 1.49], living in the study community Keri [AOR = 1.83; CI: 1.43, 2.34] and adults aged 41–65 years old [AOR = 5.08; CI: 2.98, 8.68]. A total of 595 skin ulcers were sampled from 426 participants, out of which 150 (25.2%) ulcers from 136 individuals tested positive for Leishmania infection. This accounted for an overall CL prevalence of 31.9% among persons with skin ulcers. Detection of exposure to Leishmania infection and confirmation of CL in the study area suggests an active cycle of transmission of *Leishmania* infection. There is also a need to investigate potential causes of *Leishmania* test-negative skin ulcers.

Keywords: Cutaneous leishmaniasis, *Leishmania*, Leishmanin skin test

NT 024: Assessing the knowledge, attitudes and practices of school-age children in Tomefa on schistosomiasis and their infection prevalence

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Abstract:

Schistosomiasis remains a major public health concern globally. WHO envisages control by 2025 following their proposal for an integrated control approach. Coordinated control programmes require local epidemiological data, for well-informed decisions to be taken. This study sought to assess the knowledge, practices and attitudes (KAP) of school-age children in Tomefa concerning schistosomiasis and their infection levels. One hundred and sixty-nine schoolchildren from Tomefa Basic School aged 7 to 19 years were involved in the study. A questionnaire focusing on KAP that enhances the risk of contracting schistosomiasis was administered to each child, and the responses obtained were analyzed. Stool and urine samples from each child were collected for laboratory analysis as well. Out of a total of 169 study participants, 52.7% admitted they have heard and knew about schistosomiasis. The majority (81.7%) claimed they had been dewormed even though most could not remember the last time they did. 131 (77.5%) children indicated daily contact with the water, either through fetching, swimming, or fishing. Microscopy from 10 ml urine filtration and Kato-Katz for stool revealed 7.1% and 54.9% *Schistosoma haematobium* and *Schistosoma mansoni* infected participants, respectively. Although 57% of those with urogenital schistosomiasis also had *S. mansoni* eggs, none of those with intestinal schistosomiasis presented *S. haematobium* egg. The prevalence of infection was consistent with the knowledge, attitudes and practices on the disease. More education should be done as an integral, and deworming should continue while WASH should be made a priority for inhabitants around the Weija lake.

Keywords: WASH, *Schistosoma haematobium*, *Schistosoma mansoni*

NT 025: Epidemiological study of two human schistosome species infections in two communities along the Weija Lake

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Abstract:

Schistosoma haematobium and *S. mansoni*, are two important schistosome parasite species in Ghana causing debility to the urogenital, intestinal and related organs. Despite countless interventions in endemic areas, it is still very prevalent. This study, therefore, sought to profile and compare the prevalence of the various species in two communities along the Weija Lake. A total of 295 children between the ages of 7 and 14 years from Tomefa and Torgahkope, communities in the Ga South Municipal District of the Greater Accra Region were involved in the study. Urine and stool samples obtained were examined using microscopy, after filtration and Kato Katz technique applied respectively. Of the samples collected, 65% were from Tomefa while the remaining 35% were from Torgahkope. In Tomefa, a very high prevalence (89.5%) for *S. mansoni* was observed in stool samples with one participant showing ectopic ova (*S. haematobium*) compared to 15.7% of *S. haematobium* only, and a 9% mixed infection in urine samples. In Torgahkope, *S. mansoni* prevalence was higher (28.2%) than *S. haematobium* (14.5%) infections and there was a 2% mixed infection. Conclusively, the prevalence of Schistosoma infection is higher in Tomefa than in Torgahkope, with *S. mansoni* yielding a higher prevalence.

Keywords: Schistosomiasis; *Schistosoma mansoni*; Prevalence; *Schistosoma haematobium*

NT 026: Relationship between haematuria and intensity of Schistosoma haematobium infection

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Abstract:

Urogenital schistosomiasis, caused by the trematode *Schistosoma haematobium*, is a chronic disease of the poor in over 74 countries, with more than 750 million people at risk. Haematuria among infected children has long been recognized as a sign of infection, and the degree of haematuria in children may be related to the intensity of *S. haematobium* infection. The prevalence, intensity, and related morbidity of urogenital schistosomiasis vary according to the epidemiology, transmission patterns, and ecology of each endemic area. The aim was to detect the presence of haematuria and the total parasite egg count in *S. haematobium*-infected children. The study was conducted in two endemic communities along the Weija Lake and involved 295 school-age children. Each child was provided between 15 – 50 ml of urine and a reagent strip was placed in it to record haematuria with other parameters. Subsequently, 10 ml of urine was filtered through a filter membrane and the parasite eggs were counted by microscopy. Out of 295 children, 46 were haematuric, consisting of 17 non-hemolyzed traces (NHT), 7 were hemolyzed trace (HT), 13 had moderate (M) amounts of blood, six (6) had large (L) amounts of blood and 1 person each had small,

trace and trace (200). Twenty-three (23) out of those that showed signs of haematuria were positive for *S. haematobium* with either low or high intensities. In conclusion, Haematuria detected by strips identified a high proportion of infected children compared with those diagnosed by microscopic examination using a filtration technique

Keywords: Hemolyzed trace, Non-hemolyzed trace, Haematuria

NT 027: Exploring the intracellular phase of Mycobacterium ulcerans using macrophages and amoeba as possible hosts

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Abstract:

Mycobacterium ulcerans (MU) is the causative agent of Buruli ulcer; a necrotizing skin disease. It is an environmental pathogen that has undergone genome reduction and acquisition of insertion sequences responsible for the production of the macrolide toxin called mycolactone. The mode of transmission of Buruli ulcer remains an enigma, however, endemicity has been associated among people living close to slow-moving water bodies. Linking the MU environment to Buruli ulcer, the amoeba has been reported as a possible reservoir against the background of close sympatric association within a common environmental niche. The discovery of the intracellular stage of MU within phagocytes may owe credence to environmental adaptation within amoeba in the environment. The study aimed to explore intracellular survival and escape mechanisms as well as the genes implicated in these interactions. Murine macrophages and *Acanthamoeba polyphaga* were co-cultured with MU at different time points and MOI of 3. Intracellular presence and viability were assessed by AFB staining and LIVE/DEAD Bactlight fluorescent assay. The expression levels of 9 genes comprising 3 mycolactone-producing and 6 others previously described in phagolysosome interference, described in mycobacterium tuberculosis were assessed using RT qPCR. Microscopic analyses showed that at 24hr time points, the *M. ulcerans* initiates phagocytic escape through apoptosis. Using a genomic-based comparative approach, three genes involved in mycolactone synthesis were upregulated over time. *M. ulcerans* exhibits resistance to macrophage and Amoeba phagocytosis through a carefully regulated gene profile. Functional analysis of the transcriptome would provide information on possible gene exchange in the course of the interactions.

Keywords: *Mycobacterium ulcerans*, Amoeba, Macrophage, transcriptome

CLIMATE CHANGE AND DISEASE/HEALTH SYSTEMS: EQUALITY, EQUITY AND ACCESS

HS 002: Simulation studies on phantoms with an optical Fourier domain imaging system

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Abstract:

Microwave imaging is proposed for imaging soft tissues or organs of the human body like the human breast. The Optics group of the Department of Physics, University of Ghana, has for the past six years working on implementing an Optical Fourier Domain Imaging (OFDI) system that uses microwave signals as a source. This has gained recognition in Africa and beyond as the group present their research findings to the research community on setting up the Optical Fourier Domain imaging device, how the detection of the sample is attained and characterization of the sample by way of extracting thickness and dielectric property information of the sample. With the information gathered so far, simulation studies are ongoing with breast-like Phantoms that mimic their biological counterpart (tissue or organ) not just in shape, size and texture but in composition as well. The successful complexion of the simulation stages would pave way for Clinical trials and an ultimate system for Clinical applications such as breast cancer detection.

Keywords: Optical, Fourier, Domain, Imaging system, (OFDI)

HS 004: Emergency obstetric care; knowledge and practices among practising midwifery students in Northern region

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Abstract:

Maternal and newborn mortality is a major public health concern globally. Adequate knowledge and skilled health care professionals providing timely and quality emergency obstetrics care have been identified as means of reducing maternal and newborn deaths. This study assessed the knowledge and practices of emergency obstetrics care among practising midwifery students on emergency obstetrics care. Using a facility-based cross-

sectional study design, we randomly sampled 207 participants from all four levels in Midwifery undergraduate classes at the University for Development Studies. Data were analyzed using SPSS and results were presented in the form of Tables, frequency, percentages and Charts. Chi-square test, Logistics regression, and correlation analysis were used to conduct Inferential analysis. P-values of 0.05 at a 95% confidence level were considered statistically significant. Our results show that 63% of participants had good knowledge of emergency obstetric care, with age and education being factors that influenced participants' knowledge. More than half of the participants (56%) were skilful in the practice of emergency obstetric care and 61% were very confident in the practice of emergency obstetric care. Age and years of experience were positive influencers for skills and confidence in emergency obstetric care among participants. Knowledge and practices of emergency obstetric care among the participants were significant. Age, educational level and years of experience are positive factors influencing knowledge and practice. The study, therefore, recommends the provision of quality education and training on emergency obstetric care to increase competency levels among midwives in the study area and Ghana at large.

Keywords: Emergency obstetric care, Obstetric complications

HS 006: Climate change and respiratory diseases.

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Abstract:

The impact of global climate change on diseases is speculative until we learn more about the degree of change in temperature and humidity caused by anthropogenic activities. There has been an increase in respiratory diseases such as chronic obstructive pulmonary disease, asthma, and lung cancer among others. Adverse weather conditions, such as high temperatures, can directly affect the respiratory tract, causing allergic respiratory illness. Although there have been reported increases in the prevalence of respiratory diseases, the link between climate change and the enhanced prevalence of diseases remains elusive when taking into consideration the human population that can adapt. This study seeks to investigate the relationship between climate change and respiratory diseases. We investigated anthropogenic activities and how they gradually influence climate change, which is linked to respiratory diseases and then assessed the impact of high prolonged temperatures on patients suffering from respiratory diseases. The study found some factors that linked climate change to respiratory diseases.

Keywords: Climate change, respiratory diseases, Anthropogenic activities.

HS 007: Risks Perceived by HIV Healthcare Providers in Ghana on HIV Cure-Related Research and Clinical Trials

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Abstract:

Although antiretroviral therapy has reduced mortality and improved life expectancy among HIV patients, it does not provide a cure. Patients must remain on lifelong daily medications, and deal with drug resistance and side effects. This underscores the need for HIV cure research. However, participation in HIV cure research and clinical trials has risks that healthcare providers must understand, accept and encourage their patients to consider participation in cure trials. We determined what HIV healthcare providers know about potential HIV cure trials, the risks involved in cure research and what they are likely to recommend for their patients. In-depth qualitative interviews were performed with 39 HIV healthcare providers; consisting of 12 clinicians, 8 counsellors, 14 nurses, 2 pharmacists, 2 laboratory scientists and 1 'Model of Hope', from three hospitals in the Greater Accra region of Ghana. Interviews were transcribed and coded and thematic analysis was done independently by two investigators. Study participants were hopeful for a cure and most described a cure as "unable to transmit the virus", or "total eradication of viral particles from the body". The majority of the respondents had a low-risk tolerance level and would only accept risks such as transient fevers, stomach aches, or mild self-limited symptoms, which are some of the symptoms patients on ART experience. These healthcare providers categorically rejected the risk of death or permanent disability as an acceptable risk. Their main motivation to recommend patients for HIV cure trials would be scientific evidence that the test strategy or product had previously worked, with high success.

Keywords: HIV Cure, Clinical trials, Healthcare providers

HS 008: The contribution of community health workers to primary health care delivery in the Jirapa district of Ghana.

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Abstract:

Very few trained health personnel are available to provide healthcare services to everyone in sub-Saharan African countries, including Ghana. Thus, Community Health Workers have often been used to provide these services in rural and hard-to-reach communities. Despite the immense help that Community Health Workers provide to public health, very few studies have been conducted on their contribution to primary healthcare at the community level. Hence, this particular study fills the identified knowledge gap by using qualitative research methodology to assess the contribution that Community Health Workers make to the delivery of primary healthcare services in the Jirapa District of Ghana. In-depth interviews and focused group discussions were used to allow the researcher to obtain in-depth responses from participants. More specifically, the study explored the types of services provided by Community Health Workers and the contribution of such services to primary healthcare delivery. Also, the study examined the influence of gender, the significance of indigenous knowledge and the influence of policy on the work of Community Health Workers. Findings from the study suggest that Community Health Workers make a huge contribution to primary healthcare delivery in Ghana by improving access to services and preventing the spread of contagious diseases at the community level. In addition, research findings suggest that low literacy levels and restrictive gender norms limit the number and effective delivery of services by female Community Health Workers. The study recommends the extension of the services delivered by Community Health Workers and the formulation of a comprehensive national policy in Ghana.

Keywords: Community Health Workers, Primary Healthcare, Ghana

HS 016: Variation in PM2.5, PM10 and atmospheric conditions in the three (3) ecological zones in Ghana

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Abstract:

While clean air is a basic human requirement, air pollution continues to be a major global health problem. This is largely due to its impact on climate change and its significant association with morbidity and mortality. This study focused on the particulate matter with an aerodynamic diameter of fewer than 2.5 micrograms (PM2.5) and 10 micrograms (PM10), which are part of the pollutants listed in the Ghana air quality standards. We examined the pollution levels and atmospheric conditions in the three ecological zones (Savannah Belt, Forest Belt, and Coastal Belt) of Ghana, which exhibit different climatic characteristics. Data for the study was collected from June 1st, 2020, to February 28th, 2022. Link analysis of the overall pollution concentrations and weather data revealed a negative correlation between humidity and PM2.5 and PM10 but a positive correlation with temperature. In terms of ecological variations, the savannah zone had the best air quality levels with median PM2.5 and PM10 values of 16.07µg/m3 and 19.47µg/m3 respectively. The three ecological zones studied had average PM2.5 and PM10 levels higher than recommended by the Air Quality Guidelines of the World Health Organization (WHO). The Savannah zone, which recorded the least, had levels about two or three times higher than recommended by WHO.

Keywords: Particulate Matter, Ecological, weather

HS 009: Towards healthier culinary practices among Ghanaian women: cooking practices among Ghanaian women, a photovoice study

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Abstract:

The role of dietary factors, including overconsumption of energy-dense and nutrient-poor diets such as foods rich in fats and oils, sugars and high in salt in the obesity 'epidemic' and its prevention is well established in the literature. Several studies have shown associations between obesity and diet-related non-communicable diseases such as diabetes mellitus, cancers and hypertension. The literature on the relationship between culinary practices and the risk of overweight/obesity among Ghanaian women is, however, scanty. The present study, therefore, seeks to examine the culinary practices of Ghanaian women. The study will adopt a photovoice approach to provide an accessible way to describe realities, and perspectives and raise awareness. Informed by data saturation, the study aims to recruit an estimated 30 consented women aged 18 years and above, using a purposive snowballing method. With the aid of their smartphones, participants will be tasked to take pictures depicting their cooking practices, and environmental, social and other factors that inform their cooking. Following the pictures taken, in-depth interviews will be held with them to tell the "stories" of the pictures. Additionally, participants' nutritional status will be

assessed through anthropometry. Data will be analyzed thematically using both inductive and deductive approaches. The expected outcomes of this study include understanding the cooking behaviours and factors that influence cooking practices among participants. Findings will inform the design of interventions aimed at improving the Ghanaian diet

Keywords: Photovoice, Ghanaian, women, culinary, obesity

HS 010: Ethnographic observations of wound management at traditional therapeutic setting in Atwima Mponua District of the Ashanti Region of Ghana

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Abstract:

Skin NTDs such as leprosy and Buruli ulcer are perceived as diseases of the poor and treatment seeking at the traditional therapeutic settings most often precedes the health facility. The objective of the study was to understand how wounds are managed in traditional therapeutic settings as well as the interactions between the care provider and patients on one hand and among patients on the other. Direct observations were made at wound dressing scenes to better understand interactions during wound management in the traditional healer's setting. Observations showed that wounds were dressed using some biomedical dressing materials such as gauze, cotton, bandages and hydrogen peroxide in addition to local preparations. The traditional healer was observed dressing wounds with unsterilized pair of scissors and most of the time, the same pair of gloves was used on all the patients throughout the day. However, no traces of stigma were observed as the traditional healer was seen on several occasions sympathizing and empathizing with patients during treatment. Our finding implies that using unsterilized pairs of scissors to treat patients could aid the transmission of other infections from patient to patient. It is recommended that the district health directorate and other relevant stakeholders establish a network of traditional healers in the district and introduce them to proper wound management practices for them to improve upon treatment-seeking outcomes for patients with skin NTDs.

Keywords: wound, leprosy, Buruli ulcer

HS 011: Mobile Phone Use Among Adolescents and Its Implications on Routine Health Check-ups in Cape Coast Metropolis of Ghana

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Abstract:

The proliferation of mobile phone use among adolescents has necessitated a study that will inform intervention on routine health check-ups for adolescents in Cape Coast

Metro. The main objective of the study was to examine the usage of mobile phones (MP) among adolescents and their implications on routine health check-ups in the Cape Coast Metropolis. The convergent mixed method design was used to collect data from four selected communities in Cape Coast Metropolis. Conclusions from the quantitative strand of the study were based on 336 adolescents while the qualitative strand was based on 4 health workers, and 23 adolescents. The majority of adolescents have access to mobile phones which were self-owned. Chatting, playing games, and watching videos dominated activities adolescents use their mobile phones for. Adolescents have some level of awareness and knowledge on the use of MPs for a health check-ups. Also, the study discovered that malaria was the most prevalent health condition adolescents check with the use of mobile phones, others were candidiasis, gonorrhoea, HIV/AIDS, Covid-19 and menstrual pains within the last 6 months. The method of health check was via mobile apps and the internet. Lastly, the majority of the adolescents have a higher interest in joining the adolescent well-being club that will improve health check-ups in Cape Coast Metro. Some adolescents are already using MPs for a health checks. Hence, the incorporation of MP use for a health check-up as an intervention will improve health check-ups among adolescents.

HS 012: Gender-Related Factors and Treatment Seeking Behaviour of BU/LP/LF Patients in some selected districts in the Central Region, Ghana

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Abstract:

Many skin NTD programmes over-looked how gender-related factors such as decision-making power, access to and control of resources, gender norms, and gender roles, affect the treatment-seeking behaviour of Buruli Ulcer (BU), Leprosy (LP), and Lymphatic filariasis (LF) patients in endemic areas. The main objective of this study was to explore the gender-related factors and their influence on treatment seeking behaviour of BU, LF, and LP patients in Upper Denkyira East, Upper Denkyira West, and Gomoah East districts in the Central Region. The mixed method approach was used for this study by employing surveys, FGD and In-dept interviews for data collection. The study revealed that, gender roles such as bathing the children, providing for the family, going to the farm etc., influenced treatment-seeking behaviour. Also, the study identified that decision-making power was high among men and it had an effect on themselves and their spouses in terms of seeking care. It was again discovered that females were more likely than men to associate sociocultural beliefs such as witchcraft with the causes of their conditions. It is therefore recommended that skin NTD programmes consider gender-sensitive policies and interventions that will help improve health-seeking among BU, LP, and LF patients.

Keywords: Gender, Buruli Ulcer, Lymphatic filariasis, Leprosy

HS 014: Implementation of a protein-to-creatinine dipstick test for proteinuria detection in Ghana: user perspectives, challenges, and opportunities

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Abstract

Measurement of blood pressure and proteinuria is recommended to screen for preeclampsia during pregnancy. Protein-only dipsticks are the most common proteinuria screening tests particularly in low-income settings as they are low-cost and easy to use. However, they have significant limitations because they do not account for fluctuations in hydration. Dipsticks measuring the protein-to-creatinine (PrCr) ratio have shown performance benefits over those measuring protein alone. This study assessed the appropriateness, acceptability, and feasibility of implementing the Test-it™ PrCr Urinalysis Dipstick Test (LifeAssay Diagnostics, South Africa) at three referral hospitals in Ghana. One hundred healthcare professionals were trained on the PrCr test, which was integrated into protocols alongside standard-of-care tests between November 2021 - April 2022. Test users completed questionnaires post-training, three focus group discussions and seven key informant interviews were conducted to evaluate test procedure comprehension, insights into training effectiveness, usability/user confidence, perceptions, attitudes toward the test, and barriers and facilitators of the PrCr test use. High product usability, user confidence, and satisfaction were reported. Staff perceived the test as easy to use (19/20) and its use as similar to current products in use. On a Systems Usability Scale (SUS), the test's score was 75/100. Facilitators of use included effective training, sensitization about the product, and key stakeholder endorsement. Challenges impacting implementation feasibility identified included the short shelf life (3 months) of test strips after opening canisters and the added complexity of the ratio metric result interpretation. Although the Test-It PrCr test is easy-to-use and well-accepted, key product attributes limit its implementation feasibility.

Keywords: Preeclampsia, proteinuria, point-of-care diagnostic, implementation research, LifeAssay Test-it™ PrCr Urinalysis Dipstick

HS 015: Improving Skin NTD surveillance and management: Piloting the use of a mobile phone-based surveillance and management system.

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Abstract:

Health reporting and management systems of most developing countries are designed for diseases with high prevalence and occurrence. These have not been very effective for the management of Neglected Tropical Diseases (NTDs), therefore innovative interventions are needed to support the usually low prevalent but very economically impactful effect of such infections on affected communities. Interventions for the management of Skin NTDs must address the challenges of delay in diagnosis and treatment. This study aims at designing and evaluating a software program that bridges the reporting gap between patients, doctors, disease control officers and researchers in the management of Skin NTDs. This software, which is Android based and compatible with mobile phones (Mobile Health) will serve the entire Skin NTD information management value chain to improve care at peripheral health facilities. The program called sKINs captures all required information and photographs of the affected patient's lesion, generates a unique identification number, and relays the information in real-time to a disease control officer, who subsequently takes a medical/ management decision on the patient. Treatment outcomes, confirmatory diagnosis and management supplies distribution would also be monitored on this deferential access-controlled platform. Using Figma, a cloud-based design tool for design, prototyping, design systems, and UI/UX design, we have created the application software prototype. The software's front end was created by Bravo Studios and AppGyver, while its back end was created using Google Firebase. The software is currently being piloted in the Akuapim South and Amansie Central Districts of the Ashanti Region of Ghana.

Keywords: Mobile Health, Skin NTDs, Software Programme, Disease Surveillance

NON-COMMUNICABLE DISEASES

NC 001: The Effect of Inhibiting Il-8/Cxcr2 Axis on Epithelial-Mesenchymal Transition in Breast Cancer Vasculogenic Mimicry.

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Abstract:

IL-8 secretion and induction of the EMT are both effective for VM formation in triple-negative breast cancer. Evidence suggests that VM formation in TNBC leads to the rapid growth of these tumours. The association between the IL-8/CXCR2 axis and EMT is less studied. We investigated the promotion of VM formation by the IL-8 secretion by tumour cells through the induction of EMT. Tissue samples of 80 mastectomy tumour cases were retrieved at the University of Ghana Medical School, and a comparison was made of the expression of IL-8/CXCR2 and vimentin among the cases. Tube formation assay and RT-qPCR were carried out on MDA-MB-231 cell lines to study the impact of targeting IL-8/CXCR2 signalling on the EMT using CXCR2 inhibitor and CXCR2 gene knockdown. IL-8 was expressed in 13 out of 37 cases of TNBC and 27 out of 34 non-TNBC cases. CXCR2 was also expressed in 13 TNBC and 31 non-TNBC cases. Of the 8 cases that expressed positive stain for VM (PAS+/CD34-), 3 were TNBC while 5 were non-TNBC cases. The tendency of MDA-MB-231 cells to form VM was confirmed using a tube formation assay. Inhibition of CXCR2 by its inhibitor suppressed cell proliferation and tube formation. RT-qPCR analyses revealed that the inhibition of IL-8/CXCR2 signalling also resulted in the downregulation of the mesenchymal markers and upregulation of the epithelial marker. These findings showed that the IL-8/CXCR2 axis acts in consonance with the EMT to promote tumour growth, proliferation and the formation of VM in the TNBC cell lines.

Keywords: Epithelial-mesenchymal transition, vasculogenic mimicry, cancer

NC 002: Randomized Versus Real-World Evidence on the Efficacy and Toxicity of Checkpoint Inhibitors in Lung Cancer or Melanoma: A Meta-analysis

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Abstract:

Both randomized controlled trials (RCTs) and real-world evidence (RWE) studies provide results regarding the efficacy and toxicity of checkpoint inhibitors in cancer patients. The results from these two sources are considered complementary but may not be comparable. This study aimed to compare the efficacy and toxicity of checkpoint inhibitors between RCTs and RWE studies in advanced non-small cell lung cancer or melanoma. Two electronic

databases were searched for either RCTs or RWE studies, investigating the efficacy or toxicity of checkpoint inhibitors given for indications that were approved by the European Medicines Agency at the date of the last search. A meta-analysis was performed and the pooled estimates of objective response rates (ORR), progression-free survival (PFS), overall survival (OS), and toxicity and treatment discontinuation between RCTs and RWE studies were compared. In total, 43 RWE studies and 15 RCTs were eligible, with adequate data regarding non-small cell lung cancer and melanoma. No statistically significant or clinically meaningful differences in terms of pooled PFS, OS, or rates of treatment discontinuation due to toxicity between RCTs and RWE studies were observed. In some indications, a higher response rate and a lower rate of toxicity in favour of RWE were observed. In patients with melanoma or non-small cell lung cancer, the clinical value of checkpoint inhibitors is evident in both RCTs and real-world settings.

Keywords: checkpoint inhibitors, melanoma, lung cancer

NC 003: Synedrella nodiflora Extract Depresses Excitatory Synaptic Transmission and Chemically-Induced In Vitro Seizures in the Rat Hippocampus

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Abstract:

Extracts of the tropical Cinderella plant Synedrella nodiflora are used traditionally to manage convulsive conditions in the West African sub-region. This study sought to determine the neuronal basis of the effectiveness of these plant extracts to suppress seizure activity. Using the hippocampal slice preparation from rats, the ability of the extract to depress excitatory synaptic transmission and in vitro seizure activity were investigated. Bath perfusion of the hydro-ethanolic extract of Synedrella nodiflora (SNE) caused a concentration-dependent depression of evoked field excitatory postsynaptic potentials (fEPSPs) recorded extracellularly in the CA1 region of the hippocampus with maximal depression of about 80% and an estimated IC50 of 0.06 mg/ml. The SNE-induced fEPSP depression was accompanied by an increase in paired-pulse facilitation. The fEPSP depression only recovered partially after 20 min washing out. The effect of SNE was not stimulus-dependent as it was present even in the absence of synaptic stimulation. Furthermore, it did not show desensitization as repeat application after 10 min washout produced the same level of fEPSP depression as the first application. The SNE effect on fEPSPs was not via adenosine release as it was neither blocked nor reversed by 8-CPT, an adenosine A1 receptor antagonist. In addition, SNE depressed in vitro seizures induced by zero Mg2+ and high K+ -containing artificial cerebrospinal fluid (aCSF) in a concentration-

dependent manner. The results show that SNE depresses fEPSPs and spontaneous bursting activity in hippocampal neurons that may underlie its ability to abort convulsive activity in persons with epilepsy.

Keywords: hippocampus, fEPSP, adenosine, seizure

NC 004: Hematological, biochemical and growth rate evaluation of laboratory rats fed with proGARI (Micronutrient fortified soybean gari blend)

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Abstract:

The prevalence of malnutrition in Sub-Saharan Africa seems to be on the ascendancy though many effects have been put in place to curtail it. The United Nations Sustainable Development Goal 2 seeks to end all forms of hunger and malnutrition by 2030. This agenda can be greatly achieved through nutritional food-based intervention for target groups. As part of efforts to meet SDG 2 through food-based intervention, proGARI (micronutrient-fortified soybean gari blend) was developed. proGARI has the same cooking and eating qualities as conventional gari. Most in vitro analyses showed that proGARI can provide the needed nutrition to support healthy human growth. The objective of this study was to determine the effect of the consumption of proGARI on haematological, biochemical and growth parameters in a rat model. Micronutrient premix, soybean and cassava mash were processed into proGARI and raw (unfortified and blended) gari which was used as a control. Laboratory rats were fed with raw gari, proGARI and normal laboratory animal feed for 28 days. Feed consumption, weight gain, and haematological and biochemical analyses were performed to determine the effect of proGARI on the rats. Results showed that rats fed with raw gari had poor growth performance compared to those fed with proGARI and normal laboratory animal feed. The addition of soybean and micronutrients to gari can support healthy growth and can be an excellent medium for food-based nutritional intervention in West Africa because it is economical, have a positive effect on the environment and is widely consumed by a large population

Keywords: proGARI, food intervention, micronutrient, SDG 2

NC 008: Evaluating the effect of oncogenic HIV proteins on the proliferation of HPV-infected cervical cancer cells

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Abstract:

Cervical Cancer (CC) remains a major health burden, especially in Human-immunodeficiency virus (HIV)-endemic parts of Africa. Women co-infected with HIV and Human papillomavirus (HPV) have a 6-times higher risk of developing invasive CC compared to HPV-only infected individuals. Unlike other HIV/AIDs-defining cancers, such as Kaposi Sarcoma, the incidence of CC has remained stable in the antiretroviral therapy era. This suggests that immune suppression may not be a key driver of CC progression. Thus, how HIV contributes to faster CC progression remains unclear. Considering the close association between HIV-infected leukocytes and cervical cells via ICAM-1, we hypothesized that HIV proteins from T cells infiltrate HPV-infected cervical cells and enhance cancer phenotypes. Here, we evaluated the effect of four HIV proteins, TAT, GP120, NEF and RT on the proliferation of HeLa cells, which are constitutively infected with HPV. Each of these has previously demonstrated oncogenic potential in other cancers. We transfected each of these proteins into Hela cells. Seventy-two hours post-transfection, a proliferation assay was performed using Cell Titer-Glo. Simultaneously, we extracted total RNA for expression analysis of the Ki-67 gene proliferation marker using RT-qPCR. Our analysis revealed that NEF, GP120 and TAT significantly increased proliferation and Ki-67 expression compared to mock transfections. These findings suggest that these HIV proteins may play a role in cancer phenotypes among HIV/HPV co-infected women. These findings, part of a larger study, may eventually explain the elevated progression of CC even with antiretroviral therapy. This and related work may eventually lead to insights into treating and managing HIV/HPV coinfections.

Keywords: Cervical cancer, HIV-HPV co-infection, Proliferation

NC 009: Antipsychotic activity of Piper guineense root extract in experimental animal models of psychosis

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Abstract:

Piper guineense, popularly known as Ashanti pepper (soro-wisa), is a slender climber that is mostly distributed in high forest areas. Traditionally, it is used in the management of neurological disorders. The effects of the hydroethanolic root extract of P. guineense (PGE) on the positive, negative, and cognitive symptoms of psychosis were tested in this study using ketamine-induced experimental models of psychosis. PGE was tested for its effects on ketamine-induced hyperlocomotion, heightened immobility, poor social interaction, and difficulty recognising novel objects at doses of 100, 300, and 1000 mg/kg, p.o. Both the impact of PGE on catalepsy brought on by haloperidol and its capacity to cause it in naive mice were evaluated. Phytochemical screening revealed the presence of the following phytoconstituents: tannins, flavonoids, alkaloids, glycosides, and terpenoids. Preliminary studies revealed the extract had motor, autonomic, and sedative effects at doses of 300 mg–3000 mg. The extract also significantly reduced hyperlocomotion induced by ketamine at 1000 mg/kg. Additionally, the extract showed beneficial effects on the negative symptoms of psychosis as it significantly reduced the duration of immobility in the forced swim test. In the social interaction test, PGE at 100 and 300 mg/kg counteracted asociality induced by ketamine. Memory deficits induced by ketamine were reversed by PGE in the novel object

recognition test. PGE caused catalepsy at high doses and potentiated catalepsy when given with haloperidol. The root extract of Piper guineense has antipsychotic potential with minimal risk for extrapyramidal symptoms.

Keywords: Piper guineense, haloperidol, ketamine, antipsychotic, catalepsy

NC 010: Effect of Polymorphisms in BCL11A, APOL1 genes and Expression of Fetal Hemoglobin on Sickle Cell Disease Phenotypes

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Abstract:

Renal complications are a leading cause of early mortality in sickle cell disease (SCD). Fetal haemoglobin (HbF), a major genetic modulator in SCD, ameliorates related complications. Mutations in the BCL11A gene also induce increased expression of HbF transcription. However, APOL1 genetic variants (G1 and G2) are linked with the development of chronic kidney disease (CKD). This study sought to understand the interplay of APOL1 and BCL11A mutations in SCD-associated CKD. Cross-sectional random sampling was used to recruit 384 SCD patients visiting Komfo Anokye and Korle Bu Teaching Hospitals. Haematological and biochemical tests were conducted to determine SCD phenotypes followed by haemoglobin fractionation. Genomic DNA was isolated from whole blood followed by TaqMan SNP assays and PCR-Ligase detection reaction to genotype BCL11A and APOL1 SNPs. Age was inversely correlated with HbF levels in all participants(p=0.014). In phenotypes with high HbF levels compared to normal, APOL1 risk alleles G0, G1, G1/G1, G1/G2 and G2 were significantly associated with CKD (p=0.043,0.047,0.027, and 0.018 respectively). Only APOL1 risk variant G1/G1 was inversely associated with CKD. Also, age was significantly associated(p=0.014) with CKD. Non-CKD groups showed a significantly weak negative correlation with age and HbF (r2=0.005). The most association was observed for the homozygous G2 risk alleles with CKD. HbF may modulate SCD complications for an extended life expectancy. APOL1 may be used as a genetic modulator for SCD clinical management. More research is required to confirm these novel findings.

Keywords: SCD, APOL1, Haemoglobin F, BCL11A

NC 011: Antioxidant and anticancer properties of Vernonia amygdalina

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Abstract:

The medicinal properties of plants are investigated globally due to their pharmacological activities. *Vernonia amygdalina* possesses phytochemicals that exhibit anticancer properties. Thus, the prevalence of use, antioxidant and anticancer properties of *V. amygdalina* was investigated in this study. Data was collected from three Hospitals using a systematic random sampling method. Antioxidant activity of VA and Cytotoxic effect of VA extracts against Jurkat, MCF-7, HepG2 and Chang liver cells were determined using 2,2, diphenyl-1-picrylhydrazyl (DPPH) and 3,4,5-(dimethylthiazol-2-yl)-2, 5-diphenyltetrazolium bromide (MTT) assay respectively. A total of 359 Patients and Health workers participated in the study with a mean age of 39±1.33 years, made up of 73.4% females. Seventy-six per cent of the study participants indicated the usefulness of traditional medicine and the prevalence of the use of VA was 53.1%. The use of VA was significantly associated with ethnicity (p=0.008) and educational level (0.004). The mixture of the leaves and the lime juice extract exhibited the best free radical scavenging activity with an EC50=2.14±0.06mg/ml. The mixture of the leaves and lime extract was active against all the cell lines with the strongest inhibition against Jurkat (IC50 value = 96.341µg/mL). The study population has good knowledge about VA with a high prevalence of use. A combination of the VA and lime juice extract exhibited a good antioxidant property and was effective in inhibiting Jurkat cell lines. Ethnicity and educational level were significantly associated with the use of VA.

Keywords: Vernonia amygdalina, phytochemical, prevalence, anticancer, antioxidant

NC 012: Assessing trends of sickle cell disease among newborns at Kumasi Metropolis: A decade retrospective study

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Abstract:

Sickle cell disease (SCD) is the most prevalent hemoglobinopathy worldwide in terms of frequency and social impact. It is an inherited blood disorder marked by defective haemoglobin. A retrospective study was conducted to assess the trends and prevalence of SCD among newborns in 48 health facilities in the Kumasi metropolis. A total of 188,203 babies were screened for SCD in the Kumasi metropolis between 2012 and 2021 using the Iso-electric Focusing method. From the study, 2013 recorded height births accounting for 16% of total births within the period, whiles 2018 recorded the least birth at 2%. Babies born with SCD were highest in 2019 with a proportion of 3% while it was 2% in the other years. Over the last decade, 2% of babies born had SCD. Babies with sickle cell trait accounted for 23% of total births, 4% of babies had Hb S- beta-thalassemia disease, while 75% had HbA only. The proportion of male-to-female births was approximately the same (92,876: and 92,657, respectively). There was no statistical difference between sex and sickle cell disease and the analysis was not statistically significant, hence there was no association between

sex and sickle cell disease. There was an association between low birth weight and sickle cell disease (OR = 2.1, 95%, P-value of 0.00). The study reveals that the prevalence of SCD has not reduced over the last decade and prevalent conditions were worse in 2019. Testing for SCD and education on inheritance are imperative to reduce or eliminate the disease.

Keywords: Sickle Cell Disease, trends, prevalence

NC 013: Determination of Aflatoxin Levels in Burkina Beverage

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Abstract:

Aflatoxins are a group of highly toxic substances produced by the fungi *Aspergillus flavus* and *A. parasiticus*. Burkina is a beverage prepared from dairy milk, millet and sugar. However, the safety of this beverage on the market, with regards to aflatoxin levels had not yet been reported. This study aimed to investigate levels of total aflatoxin and aflatoxin M1 in Burkina beverages. Burkina, dairy milk and millet were purchased monthly over 7 months from Burkina producers at Ashaiman and Nima in Ghana. Total aflatoxin and aflatoxin M1 levels were measured using a fluorometric procedure and High-Performance Liquid Chromatography. Aflatoxin levels in Burkina samples ranged from 1.0 to 21.0 ppb for the Ashaiman samples and 1.0 to 23.0 ppb for the Nima samples. Out of 21 samples from each site 1 from Ashaiman and 2 from Nima had levels above the acceptable limit of 20 ppb. For the millet, levels ranged from 1.0 to 55.0 ppb, with 2 samples from Ashiaman and 6 from Nima having levels above 20ppb. The levels of Aflatoxin M1 in milk ranged from 0.09 to 12.55 ppb, with 12 from Ashaiman and 10 from Nima having levels of Aflatoxin M1 above the acceptable limit of 0.5 ppb. All Burkina samples tested were contaminated with aflatoxin. Therefore, farmers and Burkina producers must be educated on good storage practices and monitored to protect the public from aflatoxin exposure and toxicity since all doses of aflatoxin have a cumulative effect on the risk of liver cancer.

Keywords: Aflatoxin, Burkina, Contamination, Milk, Millet

NC 014: Screening for Hypertension in Adolescents Living with HIV: Protocol for a Cluster Randomized Trial to Improve Guideline Adherence

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Abstract:

Although AIDS-related deaths have reduced with increased access to antiretroviral care, cardiovascular disease-related morbidities among persons living with HIV are rising.

Contributing to this is the higher incidence of hypertension among them. The duration of exposure to the virus and antiretroviral drugs plays a vital role in the pathogenesis, putting perinatally infected children and adolescents at higher risk than behaviorally-infected ones, supporting the calls for increased surveillance of hypertension among them. Despite the availability of guidelines to support this surveillance, the blood pressure (BP) of adolescents living with HIV (ADLHIV) is not checked during clinical visits. This study aims to assess the effect of a theory-based intervention on healthcare workers' adherence to the guidelines for hypertension screening among adolescents. A multi-facility cluster-randomized study will be conducted. The clusters will be 24 antiretroviral therapy sites in the Greater Accra Region with the highest adolescent caseload. Data will be extracted from the folders of adolescents (10-17 years) who received care in these facilities six months before the study. The ART staff of intervention facilities will receive a multi-component theory of planned behaviour-based intervention, including orientation on hypertension risk among ADLHIV, provision of job aids, and pediatric sphygmomanometers. Six months after the intervention, the outcome measure will be the change from baseline in the proportion of ADLHIV whose BP was checked during clinical visits. The calculated sample size is 480 folders. This study will generate evidence on the clinical effectiveness of a multi-component theory-based intervention for improving the implementation of clinical practice guidelines.

Keywords: Hypertension, HIV, Clinical Practice Guidelines, Adolescents

NC 015: Genetic association of APOL1 variants and Pre-eclampsia (PET) in Ghana

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Abstract:

Pregnant African Americans carry more than a 2-fold higher risk of PET as compared to non-Hispanic Whites and Hispanic Americans. Studies suggest that Africans in Sub-Saharan Africa (SSA) have a similarly high predilection to PET as do African Americans which suggests that these two populations may share common genetic predispositions for such. One possible contributor to preeclampsia is variants in the apolipoprotein L1 gene found only in people of African origin, encoding for apolipoprotein L1 (APOL1) and which evolved some 10,000 years ago to protect against human trypanosomiasis. Studies from the USA have suggested that fetal but not maternal APOL1 variants are associated with PET. The present study was a case-control study involving 323 unrelated pregnant Ghanaian women obtaining antenatal care at the Korle-Bu Teaching Hospital (154 women with preeclampsia and 169 pregnant healthy controls). Isolated genomic DNA was multiplex-PCR amplified, and Ligation-Detection Reaction was assayed for single-base variants. Gel electrophoresis separation identified SNP-variant ligation products APOL1 G1 and G2. Using the chi-square test and logistic regression, the association between maternal and fetal APOL1 variants and PET was determined. Fetal APOL1 high-risk genotype increased the risk of PET (OR 2.56 95% CI 1.26-4.13, p=0.008). We conclude from our study that fetal, but not maternal APOL1 high-risk (HR) variants are associated with an increased risk of PET. Future studies should assess the effects of environmental and maternal factors that

may serve as an underlying trigger for the development of preeclampsia in those with the fetal APOL1 high-risk genotype

Keywords: Preeclampsia, APOL1, G6PD, Sickle Cell, Fetal

NC 016: Molecular analysis of down syndrome critical region genes expression in solid tumour: a bioinformatics approach

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Abstract:

The Down syndrome critical region (DSCR) is a chromosome 21 region that is hypothesized to be responsible for the majority of Down Syndrome symptoms. Epidemiological studies have shown that except for an increased risk of leukaemia, retinoblastomas and lymphomas, the risk of developing solid tumours is lower in both children and adults with Down Syndrome. Despite this, only a few molecular studies have been conducted on this conundrum. This study seeks to identify potential DSCR genes that negatively regulate solid tumour development. Data were obtained from the Gene Expression Omnibus database and processed into Trisomic Mutants and Trisomic Ts65Dn. R programme in GEO2R was used to identify differentially expressed genes and Down Syndrome Critical Region genes were selected and submitted to Strings. Gene Expression Profiling Interacting Analysis software and UALCAN were used to compare gene expression and methylation respectively. Eighteen DSCR genes were identified from the significantly upregulated genes indicating their contribution to Down Syndrome phenotypes. Interaction Analysis revealed RCAN1 is co-expressed with ETS2 and DRYK1A. Also, DOPEY2 is co-expressed with BREW1, B3GALT5, and DYRK1A whiles MORC3 does not interact with any gene. DOPEY2 was significantly expressed in breast cancer but not in lung cancer. ETS2 and RCAN1 were found to be significantly expressed in normal tissue compared to cancer tissue indicating that ETS2 and RCAN1 contribute to the suppression of solid tumour development. Methylation of RCAN1 promoter in cancer cells indicates that RCAN1 gene silencing is required for tumour development and progression.

Keywords: Down Syndrome, ETS2, RCAN1, tumour

NC 023: Investigating the Apoptotic Effects of Crytolepine on Breast Cancer

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Abstract:

Breast cancer is the leading cause of death among women worldwide. Cancer cells can resist apoptosis whilst normal cells undergo apoptosis during cellular damage. These cancerous cells express anti-apoptotic genes and suppress pro-apoptotic genes during carcinogenesis, thus resisting apoptosis. It has also been shown that high levels of Bcl2

expression are linked to drug resistance. Crytolepine has traditionally been used to treat malaria in West Africa, but little research has been conducted on its anticancer properties. Crytolepine is cytotoxic to mammalian cells. The apoptotic effects of crytolepine on MDA-MB 231 and MDA-MB 468 breast cancer cell lines were investigated in this study. The MTT assay was used to determine the IC50 values of crytolepine on MDA-MB 231 and MDA-MB 468. To investigate its effects on apoptosis, live/dead, dapi stain, and cell morphology studies were carried out. RT-qPCR was used to examine the expression of apoptotic genes. The MTT results were 0.99 µM for MDA-MB 231 and 0.700 µM for MDA-MB 468 indicating potent activity, the various assays on apoptosis revealed a high level of apoptosis, gene expression analysis showed significant downregulation of Bcl2 an apoptotic marker. In conclusion, crytolepine can induce apoptosis in MDA-MB 231 and MDA-MB 468 breast cancer cell lines and down-regulate the anti-apoptotic Bcl2. These findings suggest that crytolepine might be a potent anti-cancer drug.

Keywords: Crytolepeine, Breast cancer, Apoptosis, Apoptotic genes

NC 017: Effect of iron fortification on anaemia and risk of malaria among Ghanaian pre-school children with haemoglobinopathies and different ABO blood groups

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Abstract:

Haemoglobinopathies and glucose-6-phosphate dehydrogenase (G6PD) deficiency as well as differences in ABO blood groups have been shown to influence the risk of malaria and/or anaemia in malaria-endemic areas. This study assessed how iron fortification in addition to weaning meals affects anaemia and the risk of malaria in preschool children with haemoglobinopathies and different ABO blood groups. A community-based, double-blinded, randomly clustered trial was conducted within six months among 860 children aged 6 to 35 months in rural Ghana. Participants received daily semi-liquid home-prepared meals mixed with either micronutrient powder without iron or with iron (12.5 mg of iron daily) for 5 months. Malaria microscopy, haemoglobin (Hb) levels were measured. Reversed ABO blood grouping microtube assay and PCR-RFLP genotyping were performed. The prevalence of G6PD deficiency in hemizygous males (8.5%) was higher than that in homozygous females (2.7%) (p=0.0005). The prevalence rates of sickle cell traits (HbAS and HbSC) and sickle cell disorder (HbSS) were 19.6% and 0.5%, respectively. Blood group O was dominant (41.4%). Children on an iron supplement with HbAS had significantly moderate anaemia at the endline (EL) compared to the baseline level (BL) ($p = 0.004$). However, subjects with HbAS and HbAC and blood groups A and O in the iron group had an increased number of malaria episodes at EL than at BL ($p < 0.05$). Iron supplementation increased anaemia in children with HbAS genotypes but provided less protection against malaria in children with HbAC and AS and blood groups A and O.

Keywords: Iron Fortification, Haemoglobinopathies, ABO Blood Groups

NC 019: Contextual Awareness, Response and Evaluation (CARE): Diabetes in Ghana

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Abstract:

Type-two diabetes (T2D) affects approximately 6% of adults in Ghana and prevalence is expected to increase, following trends in the region. However, the lack of cost-effective T2D prevention programmes designed specifically for the Ghanaian population warrants urgent attention. Building on the substantial body of work on T2D in Accra, Ghana by the University of Ghana, this study aims to generate a contextual understanding of diabetes in Accra and identify opportunities for community-based intervention strategies for T2D prevention and control. This will be done by conducting an epidemiological survey alongside primary and secondary qualitative research which will include desk-based reviews, individual interviews and focus group discussions with members of the community and key stakeholders. The study will take place in urban Accra, Ghana, namely Ga Mashie (James Town and Ussher Town), communities that represent lower socioeconomic groups, areas that are densely populated and have a growing double burden of infectious and chronic disease. Evidence generated from this research will help to build a detailed understanding of contextual drivers and the consequences of diabetes in Accra and build an evidence base for participatory approaches to prevent and control diabetes and non-communicable diseases more widely. In addition, our engagement with civil society organisations and local stakeholders for the project can also provide mutual benefits to these communities.

Keywords: Type-2 Diabetes; contextual understanding, Accra; community

NC 020: Estimation of Direct Cost of Cervical Cancer Treatment in a Tertiary Hospital in Ghana

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Abstract:

Cervical cancer is the second most prevalent cancer affecting women in Ghana and the cost of treatment remains a barrier to accessing care. The study estimated the mean direct cost of treatment for the first year after initiation of therapy by surgery, radiotherapy, or concurrent chemoradiotherapy in a tertiary Hospital in Ghana. Data from 104 paper-based medical records were extracted from the National Radiotherapy Oncology and Nuclear Medicine Center, and Obstetrics and Gynecology Department of the hospital, and used to estimate the cost by micro-costing. A consecutive cohort treated from 2015 to 2018 with curative intent with cancer stages Cervical Intraepithelial Neoplasia (CIN), I, II and III, and Eastern Corporative Oncology Group (ECOG) performance status 0 to 3 were included in the study. The age range of the patients was from 30 to 78 years (median 52.80). The mean direct cost for the first year of treatment by concurrent chemoradiotherapy, radiotherapy only and surgery were Ghana Cedi (GHC) 8,742.48±4,473.45, GHC 5,150.04±2,228.50 and GHC 5,764.98±122.57 respectively. One United States dollar was equivalent to Five Ghanaian cedis in December 2018. The difference in the cost of cervical cancer treatment among the three modalities was found to be statistically significant. The cost incurred for any of the treatment modalities was high, and the entire cost is borne by the patients. This is a financial barrier to accessing health by these women and a challenge to the nation's quest to achieve Universal Health Coverage.

Keywords: Cervical cancer, treatment, cost, chemotherapy, radiotherapy, surgery.

OTHERS

OT 001: Bionomics and insecticide resistance status of Aedes mosquitoes in Ghana

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Abstract:

Despite the existence of a safe vaccine for yellow fever, arboviruses continue to cause morbidity and mortality in thousands of people in Africa. The re-emergence of these viruses in areas where the incidence had been controlled or eliminated is largely due to increased insecticide resistance in the *Aedes* vector and human-vector migration. This study investigated the bionomics and insecticide resistance status of *Aedes* mosquitoes in Ghana. Spatio-temporal distributions of immatures and adult Aedes mosquitoes were determined seasonally using BG traps, human landing catch, and prokopack aspirator 2017/2018 at all sites. The phenotypic resistance status of *Aedes* mosquitoes to insecticides was determined using WHO bioassays. A total of 16,711 Aedes immatures were sampled from car tires (73.9%), discarded containers (18.8%), air-condition saucers (4.4%), buckets (1.4%), tanks (1.3%) and drums (0.3%). There were more positive habitats during the rainy season 50 (61.73%) compared to the dry season 31 (38.27 %) ($df = 5$; $\chi 2 = 19.4435$; $p = 0.001$). A total of 1,895 adult Aedes mosquitos were collected consisting of Ae. aegypti (97.8%), Ae. africanus (2.1%) and *Ae. luteocephalus* (0.1%). *Aedes aegypti* populations were resistant to DDT at all study sites (0-88%). Vectors showed suspected resistance to bendiocarb (96-97%), permethrin (90-96%) and deltamethrin (91-96%) and were susceptible to malathion at all study sites. About 90% of vectors had taken a blood meal from humans. Resistance to pyrethroids and carbamates may limit the efficacy of current vector control tools and requires constant monitoring.

Keywords: Aedes, resistance, Arboviruses, Bionomics, Bioassay

OT 002: Insecticide resistance status of Aedes aegypti in urban and suburban areas of Ghana

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Abstract:

The study assessed the insecticide resistance status in *Aedes aegypti* populations from urban sites (Accra and Tema) and suburban sites (Navrongo and Ada) in Ghana. Phenotypic resistance was determined by the WHO susceptibility tests using *Aedes aegypti* collected as larvae and reared into adults. Knockdown resistance (kdr) genes were detected using PCR. Synergist assays were performed with piperonyl butoxide (PBO) to detect the involvement of monooxygenase enzymes in resistance. All sites showed high phenotypic resistance to

DDT (11.3% to 75.8%) and pyrethroids (62.5% to 88.8%). Moderate to high frequencies of the F1534C kdr allele and V1016I kdr allele (0.65 to 1) was detected in resistant and susceptible *Aedes* mosquitoes from all sites, suggesting that these mutations may be nearing fixation in Aedes populations from the study sites. Low frequencies of the V410L kdr allele (0.03 to 0.31) were observed. To our knowledge, this is the first report of the presence of the V410L kdr allele in Ghana. Pre-exposure to PBO restored the susceptibility of *Aedes aegypti* from sub-urban sites to deltamethrin and permethrin. This indicates that metabolic enzymes (monooxygenases) may be involved in the resistance phenotypes observed in the Aedes aegypti populations in these sites. This data will be useful in developing appropriate vector control strategies for arboviral disease control in Ghana.

Keywords: resistance, Knockdown, Aedes aegypti, PBO, Ghana

OT 004: Assessment of Dietary Habits and Iodine Status Among Pregnant Women

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Abstract:

Iodine is a micronutrient essential in the production of thyroid hormones for normal neurodevelopment. Nearly two billion (28%) of the world's population, including more than 321 million Africans (39%), are in danger of inadequate iodine intake based on iodine nutrition global data. The WHO estimates that 60% of pregnant women worldwide do not meet the required intake. Current studies have associated iodine deficiency during pregnancy with a wide range of disorders; stillbirth, spontaneous abortions, hearing defects in infants, and cretinism. This study aims to determine the iodine level and dietary habits in pregnant women. This was a cross-sectional study performed among women attending antenatal clinics at Pentecost Hospital, Madina (PHM). Dietary information related to iodine was obtained by using a food frequency questionnaire (FFQ). Urine iodine concentration (UIC) was determined using on-the-spot urine collection, using the Sandell-Kolthoff reaction method with ammonium persulfate as the digesting agent. Results obtained showed that 50.6% (80/158) of participants had urine iodine levels below the WHO optimum range. Week of gestation had a positive association with the iodine levels in pregnant women. Regarding dietary habits, oats, yoghurt, salted fish, and meat intake were significantly associated with iodine levels (r ranging from 0.1 - 0.2, $p<0.05$ in all cases). Milk showed a positive correlation with iodine but this was not statistically significant ($r=0.65$, $p=0.36$). The study showed, pregnant women visiting PHM in Ghana's Greater Accra Region have a high prevalence of iodine deficiency. Urine iodine concentration (UIC) was related to the gestational age of the pregnancy.

Keywords: Urine iodine concentration (UIC), Iodine deficiency

OT 007: Nuisance Blood Suckers

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Abstract:

Bedbugs are blood-sucking nocturnal insects of vertebrates, including humans, known to harbour more than forty (40) human pathogens, but have not been implicated in their transmission except for Chagas diseases and Rickettsia. The increase in international travel and the emergence of insecticide-resistant species have led to difficulty in their control, leading homeowners to abandon their houses and rooms. Around the globe, bed bug control has been a challenge, and in Ghana, reports have been from senior high schools, halls, hostels, hotels, hospitals and homes. The presence of bed bugs and their biting activities have led to some students developing skin diseases, stress and anxiety symptoms, which have contributed to their low academic performance. For effective control of any species, it is important first to identify the species. The study characterized bedbugs across selected educational institutions in the Greater Accra Region. The collection of bedbugs was carried out in six educational institutions; two tertiary and four senior high schools. Bed bug specimens were examined with the aid of a dissecting microscope, species were identified by their physical features using a guide (identification keys) developed by Usinger (1966). A total of 335 bedbugs were collected, of which 230 were adults and 105 were nymphs. Three species of bed bugs were identified, *Cimex lectularius* (common bed bug), *Cimex hemipterus* (tropical bed bug) and a third species suspected to be *Cimex pipistrelli* (bat bugs) which is important. This scientifically confirms the presence and species of bed bugs in Ghana, and the temperatures they could survive in. This can greatly influence their control and management.

Keywords: Bed bugs, Zoonotic diseases, insecticide resistance

OT 009: Prevalence and distribution of a Plasmodium-blocking fungus, Microsporidia MB, in Anopheles mosquitoes in Ghana

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Abstract:

Novel measures using mosquito-associated microbes are being developed for malaria vector control. The discovery of Microsporidia MB, a fungal symbiont that inhibits the transmission of *Plasmodium falciparum* in *Anopheles arabiensis* from Kenya has sparked the promise of blocking malaria transmission. This study aims to investigate the prevalence, ecological distribution, and diversity of Microsporidia MB in *An. gambiae* s.l mosquitoes in Ghana.

Late-stage larvae and pupae of *Anopheles* mosquitoes were collected from breeding-selected sites in northern and southern Ghana and maintained until they emerged as adults. Conventional PCR was used for species identification of the mosquitoes and qPCR to detect the presence of Microsporidia MB. Of the 787 female mosquitoes collected, 33% were identified as *An. gambiae s.s*, 19% *An. coluzzii* and 8% *An. arabiensis*. 625 male mosquitoes were distributed as 48% *An. gambiae s.s*, 28% *An. coluzzii* and 11%. *An. arabiensis*. Microsporidia MB infection was found only among *An. gambiae s.s* and *An. coluzzii* mosquitoes at a prevalence of 0.8% and 0.96% respectively in males and 0.1% in

females of both species. This prevalence rate did not differ significantly between the two Anopheles gambiae sibling species ($\chi 2 = 0.43$, $p = 0.51$). 62% of the MB-positive mosquitoes were from northern Ghana. Further analyses will investigate the water physicochemical parameters associated with the presence of MB and sequence variations of the fungus detected in Anopheles in Ghana.

Keywords: Microsporidia-MB, *Anopheles gambiae*, **prevalence, vector control**

OT 010: Nudging for good: Real-time AI-driven diagnostics to improve adolescent girls' diets and nutrition in Accra

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Abstract:

Micronutrient deficiencies are widespread, with an estimated prevalence of anaemia of 44% among adolescent girls. In parallel, approximately 1 in 5 children in urban areas are estimated to be overweight or obese. Shifts to unhealthy diets and reductions in physical activity contributed to the global increase in unhealthy weights. Behaviours related to food choice are mediated by individual and environmental factors including food availability, access, social influence, taste and preferences. Existing technology-assisted dietary assessment is constrained by a lack of validity testing and feasibility of use in LMICs. This project involved the development and validation of an AI-driven mobile application for dietary assessment. The first stage involved preparing a food database and associated image library. In the second stage, the annotated images were used to train semantic segmentation models for food recognition and estimation of portion sizes. Lastly, the Food Recognition Assistance and Nudging Insights (FRANI) mobile app was developed and validated as a dietary assessment tool against the gold standard; weighed records method and the 24-hour recall method. The findings suggest that AI-assisted dietary assessment can estimate intake for energy and 10 micronutrients in adolescent females within a 20% equivalence bound. The potential for FRANI is clear; however larger evaluations are needed to ensure that the technology is feasible, valid and effective.

Keywords: Dietary Assessment, adolescent, AI, behaviour change

OT 012: Assessment of the effectiveness of the Reaching Every Child Immunization Strategy among children 0-6 weeks in eight urban market centres in Accra

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Abstract:

Achieving immunization coverage and an access rate of at least 80% in all districts has remained a challenge in Ghana. Ghana and other WHO member Countries across the globe signed up to implement the Reaching Every District Immunization Strategy which Ghana recast to the Reaching Every Child immunization Strategy. This study assesses the effectiveness of the Reaching Every Child Immunization Strategy among children 0-6 weeks in eight selected urban market centres in the Accra Metropolis. A prospective cohort study design with a mixed methods sequential explanatory approach was used. The study followed children aged 0 to 6 weeks whose mothers worked or traded at eight urban market centres for nine months. Seven hundred and fifty-nine (759) eligible mother/child pairs were recruited. An innovative strategy was implemented in urban markets. The findings showed three components of the strategy to be highly implemented, while two of them were implemented moderately in the intervention market. The effect of the REC strategy on full immunization was 572 (75.4%). The access rate of immunization was 98.2% and 97.3% whereas coverage was 96.8% and 99.2%) respectively in the two market centres. The dropout rate was 1.8% and 0.3% in both markets. The REC components were poorly implemented in the intervention market centre. This could account for the low (75.0%) immunization status of the children at 36 weeks in the study falling below the WHO target of at least 80.0% coverage regionally. However, in terms of access and coverage rate, this study found high access and coverage with a significantly low dropout rate for DPT 1-3 above the 10.0% recommended rate by WHO.

Keywords: Child Immunization, access, coverage and dropout rate

OT 013: Impact of iron fortification on anaemia and iron deficiency among preschool children living in rural Ghana

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Abstract:

Anaemia in young African children may be due to the double burden of malaria and iron deficiency. The primary analysis of trial data from iron fortification in Ghanaian children

found no difference in malaria risk between intervention and placebo groups. Here, we performed a secondary analysis of the trial data to assess the impact of iron fortification on the risk of iron deficiency and anaemia in trial subjects. This population-based randomized-cluster trial involved 1958 children aged between 6 to 35 months, identified at home and able to eat semi-solid foods. The intervention group (n = 967) received a daily dose containing 12.5 mg of elemental iron (as ferrous fumarate), vitamin A (400 µg), ascorbic acid (30 mg) and zinc (5 mg) for 5 months. The placebo group (n = 991) received a similar micronutrient powder but without iron. At baseline and endline, health assessment questionnaires were administered and blood samples were collected for analysis. The two groups had similar baseline anthropometry, anaemia, iron status, demographic characteristics, and dietary intakes ($p > 0.05$). Post-trial, the intervention group had higher haemoglobin ($p = 0.0001$) and serum ferritin ($p = 0.0002$) levels than the placebo group. Soluble transferrin receptor levels were more saturated among children from the iron group compared to the non-iron group ($p = 0.012$). Anaemia status in the iron group improved compared to the placebo group ($p = 0.03$). Continued long-term routine use of micronutrient powder containing prophylactic iron reduced anaemia, iron deficiency and iron deficiency anaemia among preschool children living in malaria-endemic areas.

Keywords: Iron fortification, anaemia, malaria, preschool children

OT 015: Anemia prevalence and associated factors among school-age children in Accra and Kumasi metropolis in Ghana

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Abstract:

Anaemia, a public health issue globally affects the learning ability and physical development of children. It contributes to a quarter of Africa's nutrition-related Disability Adjusted Life Years. The objective of this study was to determine the prevalence of anaemia and its associated risk factors among school children (SAC) between ages 9 and 15 years in urban settings in Ghana. Socio-demographic, household characteristics, anthropometric and haematological data were collected and analysed. The relationship between haemoglobin and socio-demographic variables was established with Chi-square and binary logistic regression. The mean haemoglobin concentration of the study participants was 12.9±1.3 g/dL. SAC in Kumasi had higher mean haemoglobin concentration (13.1±1.2 g/dL) than SACs in Accra (12.6±1.3 g/dL; p=0.001). Mean haemoglobin concentration was significantly higher among males than females (13.0±1.4 g/dL vs 12.8±1.2 g/dL; p=0.002). The prevalence of any anaemia was 20.4%. Anaemia cases were higher in public schools (24.6%) compared to private (18.2%). Two-thirds of the anaemia cases (64.0%) were from schools in Accra. Males had a significantly higher prevalence of anaemia (26.5%) than females (15.9%; p <0.05). Thinness (OR=2.60, 95% CI: 1.11-5.75), stunting (OR=1.85, 95% CI: 1.99-3.10) and overweight (OR=0.60, 95% CI: 0.36-0.94) were significantly associated with anaemia. In this study, anaemia was significantly associated with body mass index, city of residence, and stunting status.

Keywords: Anaemia, haemoglobin, schoolchildren, Ghana, urban settings

OT 016: Triple burden of malnutrition and infections in older children, adolescents, and adults in rural communities of Kintampo-North Municipality, Ghana

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Abstract:

Malnutrition and infection often lead to anaemia of public health concerns. The objective of this study was to establish the prevalence of the triple burden of malnutrition, infection and anaemia among residents of Kintampo-North Municipality, Ghana. Haemoglobin concentration, anthropometric and infection data were collected. Student t-test and ANOVA were used to compare means. Binary logistic regression was used to establish associations between categorical variables. Mean haemoglobin concentrations of older children, teenagers, and adults were 12.18±1.45g/dl, 12.95±1.33g/dl and 13.78±1.63g/dl respectively different at p=0.001. Anaemia in older children, teenagers and adults was 32.0%, 20.3% and 17.9% respectively (p=0.006). Hookworm prevalence was highest in adults at 14.7%. The prevalence of malaria parasitaemia was 19.7%, 56.8% and 61.6% in adults, adolescents, and children. Thinness was 52.0% and 62.0% in males and females respectively. Thinness and stunting were most prevalent in children at 91.2% and 13.5% respectively. Overweight (17.2%) and obese (4.5%) were only present in adults. Anaemia was prevalent in adult males and females at 5.3% and 28.1% respectively different at p=0.001. Overweight was 6.9% and 25.6% in male and female adults respectively at p=0.001. Anaemia was associated significantly with malaria parasitaemia [OR=1.9, CI=1.116-3.066, p=0.017] and females [OR=2.516, CI=1.523-4.157, p=0.001]. Anaemia, stunting and being overweight were prevalent while hookworm and malaria co-existed among study participants.

Keywords: Malnutrition, Co-infections, children, Adolescents, Adults, Ghana

OT 017: Building Laboratory Capacity for Health Emergency Response: The Role of Noguchi Memorial Institute for Medical Research

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Abstract

The Noguchi Memorial Institute for Medical Research (NMIMR) was set up in 1979 as a semi-autonomous institute of the University of Ghana with the mandate to conduct research into diseases of public health importance, train postgraduate students in biomedical sciences, and support the public health programmes of the Ministry of Health and the Ghana Health Service. The Institute has, over the years, contributed to national and international capacity building in several ways. These include undergraduate and post-graduate teaching and theses supervision; internships and experiential learning; placement of National Service Persons (NSPs); and specific local and international training programmes. Specific international training programmes hosted by the Institute include the annual training course on "Enhancing Laboratory Skills for Infectious Diseases in West and Central African Countries". This is an eight-week course funded by NMIMR and the Japan International Cooperation Agency (JICA) and facilitated by the Parasitology, Bacteriology, and Virology

departments of the Institute. Participating countries are Ghana, Benin, Burkina Faso, Côte d'Ivoire, Gabon, Guinea, Liberia, Nigeria, Sierra Leone and The Democratic Republic of Congo. In 2020, the Institute was selected to host the H3ABioNet introductory course on bioinformatics (IBT2020). The 3-month course aims at providing an introduction to the field of bioinformatics, with a focus on important bioinformatics tools and resources. In 2022 the Institute conducted a 10-day training workshop on "Next Generation Sequencing for Genomic Surveillance". This was in collaboration with the World Health Organization (WHO) and the Africa Centre for Disease Control (Africa CDC), targeting participants from Benin, Cape Verde, Côte d'Ivoire, Guinea, Liberia, Mauritania, Sierra Leone and Togo. The training aimed at providing hands-on experience in SARS-CoV-2 sequencing using the Oxford Nanopore Technologies (ONT) MinIon platform, as well as training in bioinformatics data analysis. The Institute has also conducted training workshops on "Whole Genome Sequencing and Surveillance of Antimicrobial Resistance in Bacteria" to build capacity for genomic AMR surveillance in Ghana and other African countries including Benin, Cameroon, Eswatini, Kenya, Malawi, Nigeria, South Africa, Sudan, Zambia, and Zimbabwe. Since the outbreak of the COVID-19 pandemic, the Institute has trained over forty (40) laboratories within Ghana on SARS-CoV-2 testing in support of the National containment strategy. External institutions benefiting from NMIMR SARS-CoV-2 training include the National Public Health Laboratory in Botswana. In addition, over 20 private laboratories in Ghana have been trained in biosafety/biosecurity and sample collection. The NMIMR will continue to support capacity building for health emergency responses within Ghana and sub-Saharan Africa.

Keywords: Laboratory Capacity, Health Emergency, Response, Noguchi Memorial Institute for Medical Research

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