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providers that often hampers a correct diagnosis and management of both diseases. Therefore, during the COVID-19 pandemic, health-care providers in areas where dengue is endemic or who treat patients with recent travel history to these areas, need to consider dengue and COVID-19 in the differential diagnosis of acute febrile illnesses.

Global Implications and Opportunities and COVID-19 have mild illness and do not require hospitalization, both diseases can cause severe illness that may result in death. Indeed, clinical management for people with severe illness due to either of these two diseases is quite different, often requiring hospital-based care.

High index of suspicion is necessary in handling COVID-19 cases in tropical setting where dengue is endemic. Acute febrile cases with leucopenia and thrombocytopenia should be screened for dengue. Since false positive dengue serology or cross-reactivity with SARS-Cov-2 infections are known to occur, and have a potential impact on clinical outcome, or else, result in delay in COVID-19 or dengue appropriate treatment, the risk of occurrence of complications and death is increased.

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S10: Hepatitis C Elimination – Global Opportunities

Date: Saturday, Nov 19, 2022 Time: 10:30-12:00

Venue: Conference Hall 3, Level 3

EGYPT'S EXPERIENCE IN THE ELIMINATION OF HEPATITIS C

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Over 70 million individuals are chronically infected with hepatitis C virus (HCV), and more than a million people die each year from illnesses associated with the HCV. For a long time, Egypt was at the top of the list of nations with the highest HCV prevalence. While several issues continue to hinder virus eradication, certain nations are making headway in the eradication of HCV. These constraints include a lack of international financing for medical care, delayed diagnosis, scanty data, and insufficient screening. Since 2007, the treatment of HCV has risen to the top of the national priority list in Egypt. Egypt launched a countrywide treatment program with the goal of eradicating HCV from the country. Pegylated interferon and ribavirin were first used in a mass HCV treatment program between 2007 and 2014. Yet, with the development of highly-effective direct acting antivirals (DAAs) for HCV, elimination of the disease has become a real possibility. In its fight against HCV, Egypt devised a strategy that serves as an example of care for other countries with high HCV prevalence rates. With this, Egypt was able to treat more than 4 million people with DAAs. Additionally, Egypt launched an extensive screening program for HCV infection that was able to screen more than 60 million citizens over 7 months. The model of HCV management in real-life Egyptian settings and the results of various treatment strategies are covered in this presentation. Obstacles associated with HCV eradication and the potential for future eradication will be also discussed. It also covers existing and future initiatives for HCV prevention and screening.

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S10: Hepatitis C Elimination – Global Opportunities

Date: Saturday, Nov 19, 2022 Time: 10:30-12:00

Venue: Conference Hall 3, Level 3

MALAYSIA'S HEPATITIS C ELIMINATION JOURNEY – GLOBAL IMPLICATIONS AND OPPORTUNITIES

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In line with the global goal to eliminate hepatitis C as a public health threat by the year 2030, Malaysia has adopted a few strategies to expand the screening and treatment coverage in people living with the disease over the last few years. The application of compulsory licensing in the year 2017 on sofosbuvir allowed the import of its lower-priced, generic version, successfully enhancing the accessibility of direct-acting antivirals (DAAs) in Malaysia. Such an initiative also enabled the launch of a WHO-recommended DAA combination (sofosbuvir/ daclatasvir) as the standard treatment for hepatitis C and catalyzed the decentralization of hepatitis C care through primary healthcare centers in Malaysia. Despite the constant growth of treatment coverage over the years, Malaysia realizes the need to go beyond the people who seek care from public health institutions, so-called the “low-hanging fruit”, in case-finding for hepatitis C. Our focus going forward is to find the missing millions via inter-organizational collaborations and outreach programs, targeting unreached populations ranging from prisoners, people who inject drugs to refugees. In partnership with international civil society organizations, Malaysia will also continue to explore options for hepatitis C treatment and screening through R&D.

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S11: AMR Challenges in the Post COVID-19 Era

Date: Saturday, Nov 19, 2022 Time: 10:30-12:00

Venue: Conference Hall 1, Level 3

PATIENT-CENTERED SURVEILLANCE OF DRUG-RESISTANT INFECTIONS

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Drug resistance or multidrug resistance is multidimensional and complex. Over the past decade and especially during the covid-19 pandemic, the incidence of drug resistant infections increased despite the implementation of infection control precautions. This was most commonly seen in low- and middle-income countries, due to the higher burden of infectious diseases, lack of proper infrastructure, unregulated antimicrobial prescriptions over the counter, limited surveillance of antimicrobial use and resistance patterns. This was further compounded by the dearth of healthcare personnel trained in appropriate infectious disease management. Strategies in high income countries to prevent and manage drug resistant infections are unfortunately, not implementable in LMICs due to differences in antimicrobial resistance (AMR) burden, access to newer antibiotics, limited infrastructure and human resources with requisite expertise with lack of economic investment by regulatory authorities to tackle AMR.

During the covid-19 pandemic, the lack of therapeutic options and the similar clinical picture initially led to rampant antimicrobial use which in turn contributed to rise in multi-drug resistant infections (MDR). Along with inappropriate antimicrobial use, redistribution of staff assigned to enforce infection control practices,

shortage of personnel protective equipment, overcrowded health-care settings, use of prolonged broad-spectrum antimicrobials in patients requiring during intensive care and mechanical ventilation contributed to the rise in hospital transmission of multidrug resistant infections during the pandemic.

To mitigate the effects of drug resistance, healthcare systems must ensure effective implementation of surveillance of antimicrobials, AMR patterns especially in MDR HAIs and antimicrobial stewardship interventions to promote optimal antimicrobial use. National level investment to improve diagnostics must be given priority as it can limit drug resistance and promote the role of biomarkers in streamlining antimicrobial use. These need to be planned to facilitate future integration with any future pandemic surveillance.

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S11: AMR Challenges in the Post COVID-19 Era

Date: Saturday, Nov 19, 2022 Time: 10:30-12:00

Venue: Conference Hall 1, Level 3

PLACING ANTIMICROBIAL RESISTANCE IN THE CONTEXT OF COMPETING PUBLIC HEALTH PRIORITIES IN SUB-SAHARAN AFRICA, A PERSPECTIVE FROM MALAWI

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Antimicrobial resistance is a major threat to human health that is predicted to impact most heavily on sub-Saharan Africa, however there is a lack of clinical outcome data from drug-resistant infections in this setting. There are reasons to expect the COVID-19 pandemic to have both positive and negative impacts on AMR in Africa. We have recruited a series of prospective longitudinal cohorts from Queen Elizabeth Central Hospital (QECH), Blantyre, Malawi and the surrounding communities in the Southern Region of Malawi. The data from these cohorts has been used to describe the aetiology of febrile illness, the burden of antimicrobial resistance in this setting and the distribution of extended spectrum beta-lactamase producing bacteria in humans, animals and the environment. Amongst a cohort of patients presenting to QECH unwell with febrile illness, 67% were living with human immunodeficiency virus (HIV). We identified a diagnosis in 145 of 225 (64%) participants, most commonly tuberculosis (TB; 34%) followed by invasive bacterial infections (17%), arboviral infections (13%), and malaria (9%). In a second cohort with drug resistant infection, resistance to third-generation cephalosporins was associated with an increased probability of in-hospital mortality (hazard ratio [HR] 1.44, 95% CI 1.02–2.04), longer hospital stays (1.5 days, 1.0–2.0) and decreased probability of discharge alive (HR 0.31, 0.22–0.45). In the community cohorts, a paucity of environmental health infrastructure and materials for safe sanitation was identified across all sites and ESBL-Enterobacterales were isolated from 41.8% of human stool, 29.8% of animal stool and 66.2% of river water samples and was associated with the wet season, living in urban areas, advanced age and in household-animal interactions. Life threatening febrile illness is common in Blantyre however, diagnostics are few, however the COVID-19 pandemic has led to rapid expansion of diagnostic capacity. We are, however frequently treating the wrong bugs with ceftriaxone, further there was significant expansion of azithromycin demand and usage during the pandemic. Cur-

rent management of sepsis has not been optimised and ceftriaxone use is promoting carriage of ESBL bacteria out of the hospital and ESBL *E. coli* and *K. pneumoniae* are ubiquitous in the community, where environmental hygiene infrastructure and community antimicrobial stewardship are critically lacking.

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S12: Global Genomic Infectious Disease Surveillance and Response

Date: Saturday, Nov 19, 2022 Time: 10:30-12:00

Venue: Banquet Hall, Level 3

SPOTTING UNSEEN OUTBREAKS USING WG

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While classical infection prevention and control (IPC) methods successfully control most obvious outbreaks, there is a possibility of hidden transmission of pathogens in the hospital environment without a significant surge in case numbers.

Whole Genome Sequencing (WGS) has a role in identifying such transmissions. Additionally, WGS can also be used to test hypotheses in the IPC field. In this talk, the speaker will touch on the role of WGS in uncovering hidden transmissions and hypothesis testing.

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S12: Global Genomic Infectious Disease Surveillance and Response

Date: Saturday, Nov 19, 2022 Time: 10:30-12:00

Venue: Banquet Hall, Level 3

TB GENOMICS FOR PUBLIC HEALTH

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Mycobacterium tuberculosis complex (MTBC), the causative organisms of tuberculosis (TB), has afflicted man for millennia. TB was declared a global health emergency by the World Health Organization in 1993. Before the 2020 Covid pandemic, it was responsible for 10 million new cases annually and was the leading infectious disease killer worldwide. MTBC strain typing represents an important complementary tool to guide TB control measures. TB programmes can use genotyping results in combination with epidemiological information to determine if recent transmission has likely occurred, and hence identify outbreaks that require targeted public health action. MTBC genotyping also can differentiate between relapse or re-infection, detect false-positive cases, and identify and monitor the circulating TB strains in the population over time. Restriction Fragment Length Phenotyping (RFLP), introduced in the 1990s, was labour intensive, required large amounts of DNA and was not easily comparable between laboratories. These disadvantages are overcome by the PCR-based MIRU-VNTR and spoligotyping methods. More recently, whole genome sequencing (WGS) of MTBC has been shown to provide high resolution identification of recent transmission chains and their direction, as well as drug resistance prediction. Its increasing reliability and affordability has enabled this technology to transition from the research arena to clinical care and public health functions. Its application in high TB