PS21.10 (319)

Introduction of a dynamic monitoring system for persons with a tick bite in accordance with the incubation period of a possible Congo-Crimean hemorrhagic fever

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Purpose: Development and implementation of a dynamic monitoring system for persons with a tick bites for the timely detection identification of high-risk groups among the population, determination of the period of the epidemic season and the boundaries of natural foci of CCHF.

Methods & Materials: The authors have developed and introduced into practical health care an electronic program for dynamic monitoring of persons with a tick bites in accordance with the incubation period of possible Crimean-Congo hemorrhagic fever, including the results of 14-day medical observation of them with daily double thermometry, assessment of clinical data, in order to early detection of symptoms of CCHF.

Results: Turkestan region is one of the disadvantaged regions in terms of natural focus of Crimean-Congo hemorrhagic fever (CCHF). Since 2009, in the southern regions of Kazakhstan, there has been an acute deterioration in the epidemiological situation for CCHF. Tick bites is one of the main epidemiological factors of CCHF infection. The number of people with a tick bites who sought medical help in the region was 4997 in 2013, 4072 in 2015, 4434 in 2017, 3360 in 2018, 2979 in 2019. With the help of the electronic system we developed, during 2020, 1,450 people bitten by a tick were monitored and the first symptoms of CCHF were detected in 3 patients within an hour after the onset of the disease, which made it possible to timely isolate the patient and prescribe treatment. This automated dynamic monitoring system allows you to optimize and facilitate the work of a doctor, an epidemiologist, and makes it possible early treatment of a patient in case of CCHF development.

Conclusion: The introduction of this electronic system into the work of primary health care organizations, infectious diseases hospitals is an effective measure for improving the 14-day monitoring of victims of tick bites, which will identify patients in the early stages of the disease, as well as determine the areas subject to preventive disinsection, designate places where ticks are collected by anti-plague stations and, in the aggregate of the measures taken, will lead to a decrease in the incidence of CCHF.

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PS21.11 (754)

NTBP: A Geo-Genomic Repository of TB Data in Nigeria

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Purpose: Tuberculosis (TB) is one of the world's major infectious diseases, with an estimated 1.4 million case fatality rate in 2020. The increase in the incidence of resistant strains of Mycobacterium tuberculosis (Mtb) to first line drugs has dealt a major blow to TB control. Inadequate and untimely detection of TB infection is a major contributor to the high incidence in low-income countries like Nigeria which shares 50% of the global prevalence with seven other high-burden countries. Genomic technologies combined with computational tools such as machine learning (ML) and artificial intelligence (AI) are promising emerging machineries towards achieving real-time surveillance, prompt and accurate diagnosis of TB.

Methods & Materials: We developed a geo-genomic portal of data on TB cases in three pilot states (Oyo, Lagos and Ondo) of south-west Nigeria for real time surveillance and as a data repository for ML and AI research to guide TB management in Nigeria. The portal features patient demographics and geolocation for real-time surveillance of transmission trends, baseline chest X-ray for ML and AI diagnostics algorithms as well as the genome sequence of the Mtb isolates obtained from patients for phylogenetic and ancillary genomic analyses.

Results: The portal currently hosts 512 records with 28% (146) positive drug-resistant TB (DR-TB) cases and 72% (366) drug-susceptible TB (DS-TB) cases. There are 101 chest X-ray images from 21 DS-TB and 80 DR-TB cases. Mtb isolates have been obtained for genomic sequencing from 406 patients. The portal is actively maintained, and its size grows as more data becomes available.

Conclusion: The web interface of the portal reveals at a glance the location with the highest burden (Alafara with geocode 7.382775, 3.90489) while the dynamics of transmission can be further elucidated using the genomic data. This resource can be a critical aid in national policy formulation for the control of TB.

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Topic 22: New Pathogen Discovery

PS22.01 (439)

The discovery of novel coronaviruses in bat guano, Sarawak, Malaysian Borneo

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Purpose: Virological surveillance was conducted in to determine the presence of bat CoVs in the bat population in Wind Cave Nature Reserve, Sarawak, Malaysian Borneo.

Methods & Materials: Partial RNA dependent RNA polymerase (RdRp) gene sequences of 11 bat-CoV positive guano collected in Wind Cave Nature Reserve was analysed. Five pellets of fresh guano from insectivorous bats were collected on plastic tarp and pooled in 500uL of ice-cold viral transport medium. The 440-bp gene was amplified using family-wide hemi-nested RT-PCR for phylogenetic analysis. Amplicon sequences were analysed using Basic Local Alignment Search Tool software (BLAST) to determine their corresponding species. Sequence alignment was carried out without primer sequence and phylogenetic tree with Maximum Likelihood bootstrap-Bayesian inference value (ML_b/PP_v) support.

Results: The positive rate was 47.6% (10/21) with the distribution of 60% (n=6/10) and 40% (n=4/10) Alpha and Beta-coronaviruses respectively. BatCoVs identified in this study formed four novel monophyletic clades referred to as Borneo Alpha-1 and -2, and Borneo Beta-1 and -2. Borneo Alpha-1 and -2 viruses diverged to form a monophyletic clade with Decacovirus-1 and Decacovirus-2 respectively (83.0-85.1% and 80.7-81.0% nucleotide identity) with batCoV found in Sabah (NCBI Accession# KX284940). Borneo Beta-1 viruses are also closely related to BatCoV found in Sabah (KX284939) (86.5-87.5% nt identity), forming a monophyletic group with Sarbecovirus. Meanwhile, Borneo Beta-2 are closer to BatCoVs in Loas (MN312609) (89.7-90.4% nt identity), forming a monophyletic clade with Hibecovirus. It is worthy to note that viruses found in the Sarbecovirus subgenus such as SARS-CoV-1 and SARS-CoV-2 attributed to two zooneses with Public Health Emergency of International Concern (PHEIC) over the past two decades. However, Borneo Beta-1 viruses are distant to the RaTG13 (MN996532) (69.1-697% nt identity), the proposed progenitor of the pandemic SARS-CoV-2.

Conclusion: The study has discovered both novel alpha and beta bat-coronaviruses in 40% of the guano sampled in Wind Cave Nature Reserve, Sarawak, East Malaysia based on the phylogeny of the partial RdRp gene sequence. The batCoVs are phylogenetically grouped into four clades via phylogeny confirms the presence of Borneo Beta-1 clade being monophyletic to the epidemic Sarbecoviruses.

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PS22.02 (72)

A Novel Clade of Bat-associated Bartonellae Detected in Leptocyclopodia Bat Flies (Diptera: Nycteribiidae)

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Purpose: Bartonellosis is a vector-borne disease with worldwide prevalence. Several *Bartonella* associated with companion animals such as *Bartonella henselae* and *Bartonella quintana* are the species with zoonotic implications and have become a global concern. Other bartonellae associated with wild animals, however, remain underappreciated particularly in the developing regions of the world.

Methods & Materials: To explore further on this neglected bacterial agent, *Leptocyclopodia* (Nycteribiidae) bat flies collected from *Cynopterus brachyotis* (Pteropodidae), an endemic fruit bat species in Southeast Asia, were molecularly examined for the presence of *Bartonella* based on 16S-23S ribosomal RNA and citrate synthase genetic markers.

Results: Both 16S-23S ribosomal RNA and citrate synthase sequences exhibited less than 95% similarity to all previously reported *Bartonella* spp. Further phylogenetic analysis revealed a novel clade of *Bartonella*, designated 'clade VII', providing insight into the six known clades of bartonellae associated with bats worldwide

Conclusion: Considering the zoonotic emergence from bat reservoirs, zoonotic potential of bat-associated bartonellae should not be disregarded, including the newly detected clade of Bartonella in this study. Thus, further studies of this novel clade, especially on its taxonomy, prevalence, pathogenicity as well as the vectorial capacity in bat flies should be carried out.

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PS22.03 (459)

Investigating the Emergence of Candida auris in a Resource Limited setting in West Africa

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Purpose: Candida auris is an emerging pan resistant pathogen, which is of particular importance in resource limited settings such as ours, with poor availability of drugs needed to treat its infections. It was identified in 4 blood culture samples from 4 hospitals in Nigeria. Three patients were in the ICU and one was critically ill, in a Gynaecological ward. The objective of this work was to investigate the potential reservoirs of the organism in the patients' environment.

Methods & Materials: Two hospitals gave consent for environmental investigation which was carried out using the environmental surveillance toolkit adapted from CDC's website. Swabs were collected from relevant environmental sources according to the toolkit's guidance. The samples were cultured on Saboraud Dextrose Agar slants at 37°C for 24 to 72 hours. Identification of yeast isolates was done using the Biomerieux Vitek® 2 Compact, data analysis was done using Microsoft Excel.

Results: 141 swab samples were collected from both sites, 60(42.5%) of them yielded growth. There were 9 yeast isolates: *Candida rugosa* 3(33.3%) from a bedside locker, mattress and a pulse monitor; *Cryptococcus laurentii* 2(22.2%) from an axilla and groin composite skin swab and a sink. *Candida albicans* 1(11.1%) was from a bed railing, *Candida lusitaniae* 1(11.1%) from a bedside locker, *Candida parapsilosis* 1(11.1%) and *Candida tropicalis* 1(11.1%) was from drug carts. There were 20 mold isolates from bed railings (14;70%), drug carts (3; 15%), bedside lockers (1;5%), mattress (1;5%) and a sphygmomanometer (1;5%). There were 31(22%) bacteria isolates. No *Candida auris* was isolated in this study. Three patients died and one was discharged without any antifungal therapy.

Conclusion: *Candida auris* was not isolated from the patients' environment and this is not surprising, we lacked resources to do this, like the environmental sponge sticks, circulating stomacher and the *C.auris* Chromagar. Interestingly, a significant number of molds were isolated from bed rails, but not surprising because we have a tropical climate and the ward windows are open. It is im-