

minutes. The developed stabilized ELISA was found to be suitable for all the three sample matrices (serum, citrate plasma and EDTA plasma) tested. The overall positivity rate in the developed ELISA was 97.92% (95%CI: 88.93%-99.95%) and 100.00% (95%CI: 75.29%-100%) for febrile adult and pediatric population respectively when cross-referenced with Bio-Rad ELISA. Additionally, four samples from pediatric and 21 samples from the adult sera panel scored positive in the developed NS1 ELISA but were negative in Bio-Rad ELISA. These discrepant samples were suggestive of DENV infection based on DENV IgM/ DENV IgG capture positivity and clinical findings. The developed immunoassay was found to be 100% (95% CI: 96.38%-100.00%) specific.

Conclusion: The large mAb repertoire, generated against DENV NS1, and extensive characterization studies, allowed us to generate a stabilized ELISA to detect DENV NS1 antigen with sensitivity higher than well-established commercial ELISA.

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OP31.08 (1186)

Successful Reversal of the 2020 Covid-19 Response Induced Collateral Damage on Malaria Control in Saudi Arabia

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Purpose: Saudi Arabia is committed to malaria elimination by 2025 and its National Malaria Program (NMP) has made enormous progress so far. However, in 2020, the COVID-19 pandemic response induced a collateral damage on the NMP: an unprecedented outbreak in Jazan, where malaria importation/transmission remains a challenge. Can a multisectoral, multidisciplinary response to this outbreak rapidly reverse the damage?

Methods & Materials: This observational study, nested within the NMP surveillance system, analyzed indicators recorded in Jazan (Indoor Residual Spraying [IRS] coverage; confirmed patients and larval source management [LSM]) temporally for the period between 2019 to 2021.

Results: By September 2021, only January to June 2021 data was available. In 2020, the COVID-19 movement restrictions and reassignment of NMP staff to pandemic response precipitated an unprecedented epidemic in Jazan with 3022 confirmed cases: comparing with 2019 figures (818), this represented a 27-fold increase. Limiting comparison to between January and June for the 3 years, patients treated were 543, 2212 and 1261, respectively. The obvious effect of the lockdown and reassigned officers is also reflected in the IRS coverage for 2019, 2020 and 2021 (till June), being 90%, 77% and 89%, respectively. The low 2020 IRS coverage (WHO minimum recommended level: 80%) supports the observed increased transmission. The 1261 cases in 2021, a 43% reduction from 2020, correlated with the 89% IRS coverage indicative of post intervention reversal. All patients were treated according to WHO protocol. Additionally, the poor indices of *Anopheles arabiensis* LSM (7040 for 2020, more than 2-fold increase from the 2019 figure of 3257) indicated pandemic disruption of larviciding activities. The 2021 midyear figure of 8471 suggests intensified LSM is needed to achieve further reductions in transmission. The Ministries of Health and Environment, Water and Agriculture coordinated IRS and LSM interventions.

Conclusion: The pandemic response engendered an unprecedented malaria epidemic and threatened years of malaria con-

trol progress. However, the improved, post-intervention and post-lockdown data provided suggests that positive rebounds can be achieved when responses are coordinated using a multi-sectoral, One Health platform.

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PS31.01 (557)

A Preliminary Survey for Filarial Parasites among Dogs and Cats in Mahawewa, Puttalam and their Vector Identification

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Purpose: This study investigated the prevalence of zoonotic filarial parasites within the canine and feline population in Mahawewa, Puttalam, and their vectors based on a brugian filariasis positive human case reported to the Anti-filariasis Campaign in January 2021.

Methods & Materials: All reachable dogs and cats, both stray and domestic, within a 500m radius of the index human case of brugian filariasis were screened for microfilaria using Giemsa stained thick blood smears prepared from capillary blood, obtained from an ear-lobe prick. Mosquito collection was done using a dog-baited trap, two window traps and a B.G. Sentinel trap from the same study site and identified using morphological keys. The head and the thorax regions of randomly selected mosquito specimens were dissected for morphological identification of larval filaria parasites via microscopy.

Results: A total of nine dogs and three cats were surveyed, of which seven dogs and one cat had filarial infections. All the infected animals harbored *B.malayi* microfilariae, while four dogs and one cat were co-infected with *Dirofilaria repens* and two dogs with an unidentified species. A total of 119 mosquitoes were caught and identified by taxonomic keys using a dog-baited trap, two window traps and a B.G. Sentinel trap from the study site. Dissection of heads and thoraces of randomly selected 12 *Mansonia annulifera*, 18 *Mansonia indiana* 20 *Mansonia uniformis* and 8 *Culex* spp. revealed filarial larvae in *M.annulifera* (n=4, 33.33%), *M. indiana* (n=14, 77.78%), *M. uniformis* (n=10, 50.00%) and *Culex* spp.(n=5, 62.5%) via microscopy.

Conclusion: *M.indiana* was incriminated as a potential vector of filarial parasites for the first time in Sri Lanka. Preliminary evidence generated indicate a high prevalence of *B.malayi* and *D.repens* among dogs and cats in Mahawewa, Puttalam with an abundance of mosquito vectors mostly of *Mansonia* and *Culex* spp. This warrants further studies with a larger sample size and molecular identification of the filarial larvae within mosquito and animal samples, especially as re-emergence of brugian filariasis in humans is being reported after four decades of quiescence, and a zoonotic

brugian parasite has been detected over the recent past, raising a concern from a one health perspective.

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PS31.02 (746)

Molecular identification of sibling species of the members of the *Anopheles punctulatus* group in the Jayapura regency, Papua province, Indonesia

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Purpose: Precise mosquito species identification is an essential step for proper management and control of malaria vectors. Misidentification of members in the *Anopheles punctulatus* group, some which are primary malaria vectors in Papua (Indonesia), Papua New Guinea (PNG), Solomon Islands, Vanuatu and northern Australia, remains problematic because of indistinguishable or overlapping morphological characters between sibling species. Distinguishing these species from each other requires molecular diagnostic methods.

Methods & Materials: Mosquitoes obtained from seven districts of Jayapura regency, Papua province, Indonesia representing a variety of habitats were analyzed by using polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) of the ribosomal DNA (rDNA) internal transcribed spacer 2 (ITS2).

Results: Results of the identification based on morphological characteristics of the members of the *An. punctulatus* group found in Jayapura Regency are: *An. farauti*, *An. koliensis* and *An. punctulatus*. Further species identification using PCR-RFLP for sibling species of the *An. punctulatus* group was found four species in Jayapura Regency: *An. farauti* s.s., *An. farauti* 2, *An. farauti* 4 and *An. koliensis*. Morphological species *An. farauti* identified using PCR-RFLP were shown to be three sibling species: *An. farauti* s.s., *An. farauti* 4 and *An. koliensis*, the morphological species of *An. koliensis* were shown to be two sibling species: *An. farauti* 2 and *An. koliensis* while the morphological species of *An. punctulatus* to be one sibling species: *An. koliensis*

Conclusion: This PCR assay is simpler, quicker, cheaper and readily interpreted. This study is the first effort to make malaria vector mapping in Indonesia base on molecular approach.

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PS31.03 (101)

West Nile Virus in Africa: Current Epidemiological Situation and Knowledge Gaps

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Purpose: West Nile virus (WNV) is an arthropod-borne zoonotic pathogen which represents a continuous source of concern for public health worldwide due to its expansion and invasion into new regions. Its distribution and circulation intensity in African countries is only partially known. The aim of the present study is to provide an updated overview on the current knowledge of WNV epidemiology in Africa, providing available data on incidence

in humans and animals, the circulating lineages and clades, other than an updated list of the principal arthropod vectors identified and the availability of vector competence studies.

Methods & Materials: We searched pertinent articles to be included in the Scoping Review according to PRISMA and QUORUM criteria. We searched PubMed and Google Scholar electronic databases on January 21, 2020, using selected keywords. From the references of each article, we explored further references as appropriate. Additional references have been later identified and added accordingly to expert opinion.

Results: This review, based on the analysis of 150 scientific papers published between 1940 and 2020, highlights: (i) the co-circulation of WNV-lineages 1, 2, and 8 in the African continent; (ii) the circulation of Koutango virus in Senegal, Gabon, Somalia, and Niger (iii) the presence of diverse WNV competent vectors in Africa, mainly belonging to the *Culex* genus; (iv) the lack of vector competence studies for several other mosquito species found naturally infected with WNV in Africa; (v) evidence of circulation of WNV among humans, animals and vectors in at least 28 Countries; and (vi) the lack of knowledge on the epidemiological situation of WNV for 19 Countries.

Conclusion: This study provides the state of art on WNV investigation carried out in Africa, highlighting several knowledge gaps regarding i) the partial knowledge on the current WNV distribution and genetic diversity, ii) its ecology and transmission chains including the role of different arthropods and vertebrate species as competent reservoirs, and iii) the real disease burden for humans and animals, therefore highlighting the needs for further research and surveillance studies to be addressed with high priority in this Continent.

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PS31.04 (510)

A Qualitative Risk Assessment for the Introduction of Crimean-Congo Haemorrhagic Fever (CCHF) in Bhutan

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Purpose: Crimean-Congo Haemorrhagic Fever (CCHF) has been widely reported in India but no cases have been reported in humans in Bhutan. However, a serological study conducted in 2015, detected CCHF virus specific IgG antibodies in imported goats from the southern parts of Bhutan. The disease is often non-clinical in animals but can cause severe haemorrhagic fever in humans. CCHF is transmitted through the bites of an infected tick, crushing infected ticks, and direct contact with infected blood and tissues of viraemic livestock and humans. The porous border with the neighboring states of India facilitates free and unregulated movement of animals, posing continuous risk of disease incursion into the country. Furthermore, due to anthropogenic factors, such as increasing human travel, increased import of animal and meat from India, there is a risk of CCHF introduction into Bhutan.

Methods & Materials: In this study we estimated the risk of CCHF introduction into Bhutan by performing a qualitative risk assessment based on an import risk assessment method developed by World Organization for Animal Health (OIE). Our assessment