FIRST DETECTION OF WEST NILE VIRUS ANTIBODIES IN ANIMALS IN LIBYA

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Intro: West Nile virus (WNV) is a global important mosquito-borne flavivirus causing West Nile disease (WND) with morbidity and mortality in humans and animals. It is endemic in many North African countries, however, in Libya, WND was reported in humans by serology but never been reported in animals.

Methods: A total of 578 and 63 serum samples from horses and dogs, respectively, were collected from healthy unvaccinated animals between 2016 - 2019. A commercially available competitive ELISA (c-ELISA) kit was initially used to test samples. Positive and doubtful sera for anti-WNV IgG antibodies using the c-ELISA were confirmed and also screened for WNV and Usutu virus (USUV) antibodies using virus neutralization test (VNT).

Findings: The results of anti-WNV antibodies using c-ELISA showed that 13.1% (76 out of 578) of horses samples and 30.1% (19 out of 63) of dogs samples were positive. A confirmation of ELISA equine and canine positive and doubtful samples using VNT was done. VNT showed that 68.4% (52 out of 76) of serum horses samples were positive and had an overall titration from 1:10 to 1:80. Among the ELISA dogs positive and doubtful samples, VNT showed that 78.9% (15 out of 19) were positive and had an overall titration from 1:10 to 1:80.

Discussion: There is lack of information from many African countries and the real burden of WNV infections in Africa is not well known, however, strong evidence on the circulation of WNV in the continent. Horse remains the most relevant species to monitor the circulation of WNV but seroprevalence studies carried out on different animals reported WNV infection in different African countries, however, their role in the transmission cycle is not well understood. Only few countries have reported WNV from dogs in Africa with very scarce information from North Africa.

Conclusion: Future research on WND is urgently needed in Libya.

DENGUE PROGNOSTIC BIOMARKERS PREDICT DENGUE HAEMORRHAGIC FEVER WITH HIGH SENSITIVITY AND SPECIFICITY

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Intro: Ninety-six million people are symptomatically infected with Dengue globally every year. Under the current standard-of-care, up to 20% of Dengue patients may be hospitalized, while only 500,000 develop Dengue Haemorrhagic Fever (DHF) and require hospitalization. This leads to unnecessary overwhelming of hospitals in tropical countries during large Dengue epidemics, especially when healthcare systems are grappling with large numbers of COVID-19 patients. Our research team set out to discover biomarkers to prognosticate Dengue patients, and augment the infectious disease clinician's decision-making process to hospitalize Dengue patients.

Methods: Host biomarkers with concentrations significantly different between pooled serum samples of Dengue Fever (DF) patients and DHF patients were identified using protein array. The prognostication capabilities of selected biomarkers were then validated over 283 adult Dengue patients recruited from three Singapore tertiary hospitals, prior to the diagnosis of DHF.

Findings: Three biomarkers (A2M, CMA1 and VEGFA) were identified that provide independent prognostication value from one another, and from clinical parameters commonly monitored in Dengue patients. The combination of all three biomarkers was able to identify from as early as Day 1 after the onset of fever, DF patients whose conditions will deteriorate into DHF. The biomarkers are robust and able to predict DHF well when trained on different AI/ML algorithms (logistic regression, support vector machine, decision tree, random forest, AdaBoost and gradient boosting). When stacked, prediction models based on the biomarkers were able to predict DHF with 97.3% sensitivity, 92.7% specificity, 66.7% PPV, 99.6% NPV and an AUC of 0.978.

Conclusion: To the best of our knowledge, our panel of three biomarkers offers the highest accuracy in prognosticating Dengue to date. Further studies are required to validate the biomarkers in different geographical settings and pilot their implementation as part of the standard-of-care workflow for Dengue patients.