son (p = <0.001). This study revealed, HCoV-229E and HCoV-HKU1 were circulated in Madaripur and Dhaka, respectively whereas HCoV-OC43 was detected in diverse locations. Phylogenetic analysis demonstrated that HCoV-229E was closely similar to CoV strains detected in China; HCoV-HKU1 in the USA and Thailand, and HCoV-OC43 in France and China.

Conclusion: This study demonstrates the diverse strains of CoVs are circulating in the study areas. Based on our research this is the first report of molecular characterization of coronavirus strains in humans in Bangladesh. Continued viral surveillance is recommended to better understand the CoV viral diversity in Bangladesh and serological assays to determine the spillover events at human-animal interfaces.

https://doi.org/10.1016/j.ijid.2020.11.045

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Dengue geography in Vientiane Capital, 2012–2019: Combining multiple datasets to understand virus spread in an endemic city

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Background: Dengue is a vector borne disease transmitted by *Aedes* mosquito species. The disease affects all major cities in South-east Asia. Urbanization of the world is a clear factor that led to *Aedes* and dengue spread during the past decades. In Lao PDR, two epidemics hit the country in 2010 and in 2013, affecting respectively more than 22,890 and 44,171 individuals. However, if some researches were conducted in some localities of Vientiane (Vallée and al, 2011), the overall dengue context and its geography are little known.

This presentation has two aims: 1° to present dengue epidemiology and its geography in Vientiane Capital using surveillance system implemented by Institut Pasteur du Laos 2° to uncover what drives the dengue force of infection among built up, socio-economic, local temperature and more innovative data which allow to describe commuting pattern of millions of individuals.

Methods and materials: To study the link between environmental disparities and incidence rate of cases, we rely on several data: (i) Global Human settlement, which allows to quantify the sprawl of built-up areas, (ii) surface temperature detected trough Landsat 8, (iii) census data which will help us to qualify the social economic disparities (iv) commuting patterns of Facebook users to understand the migration flow in the city and its link with dengue spread.

Results: A total of 2699 cases were recorded and could be located at village level. The effect of village typology (i.e. urban core, 1st, 2nd peripheries and rural areas) on dengue incidence was investigated using a Poisson regression. We could underline that the main risk factors in Vientiane Capital are not linked with poverty but are associated with the percentage of individuals that recently migrated to the city. The second risk factor stands precisely in the degree of urban centrality of a village.

Conclusion: This research suggest that risk factors do not only depend on the local context but are also impacted by the structure and intensity of connectivity between villages composing Vientiane Capital. This results underline that dengue could be better model by introducing mobility of individuals at city level.

https://doi.org/10.1016/j.ijid.2020.11.048

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Identification and validation of plasma proteins associating with severe dengue by quantitative proteomics and biochemical approaches

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Background: Four serotypes of dengue virus (DENV1-4) from the family *Flaviviridae* cause dengue, a mosquito-borne disease that results in major epidemics in tropical and sub-tropical regions of the world with an estimated 3.9 billion people at risk. Most primary infections lead to generation of type-specific neutralizing antibodies with or without sub-neutralizing cross-reactive antibodies which may contribute to enhanced infection upon secondary infections with a heterologous dengue serotype. Enhanced viremia, exaggerated immune response leading to cytokine storm and inflammation are some of the factors associated with severe dengue. Data from recent studies suggest that antibody-independent pathways may also contribute to disease manifestations observed in severe dengue however very few of the host proteins have been identified as potential players in this event.

Methods and materials: o Blood samples were obtained from children aged between 4–14 years presenting to AIIMS with clinical symptoms suggestive of dengue.

o We adopted a multiplexed quantitative proteomics approach by tandem mass spectrometry using isobaric tags for relative and absolute quantitation (iTRAQ) of plasma samples from convalescent, mild and severe dengue patients ($n = 5$ each). Differentially expressed proteins were further validated using multiple-reaction monitoring (MRM) and biochemical methods such as ELISA, HPLC and flow-cytometry.

Results: We identified 310 proteins that were differentially regulated in dengue infection by iTRAQ. 54 of these proteins were significantly up or down-regulated (>1.5 fold or <0.5 fold with a P value of <0.05) in at least two sets. Some of the prominent pathways that were differentially regulated in severe dengue infection included complement cascade, platelet degranulation and plasma lipoprotein assembly, remodeling and clearance suggesting the involvement of apolipoproteins.

Conclusion: Our study has identified plasma proteins that suggest an association between the innate immune components and severe dengue disease. Further characterization of these pathways will be useful to understand the physiological relevance of these pathways either as a cause of severe dengue or as an effect of disease manifestation. In either case, these pathways could serve as targets for intervention for clinical management of severe dengue.

https://doi.org/10.1016/j.ijid.2020.11.049