Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

ranged from 19–40 years (Median: 30 years). Most common signs and symptoms were rashes (100%), fever (96%), and body weakness (45%). Of the 806 specimens collected, 437 (54%) urine and 369 (46%) serum. Specimens were collected less than one day to 36 days (Median:2 days) from rash onset. Fourteen (3%), of the 437 urine were Zika positive, 47 (11%) for Dengue, and eight (2%) for Chikungunya. Of the 369 serum, 39 (11%) were Dengue positive and 19 (5%) for Chikungunya. No serum was positive for Zika virus. No pregnant case was positive for Zika virus. Also, no case was positive for multiple viruses and had travel history outside the country.

Conclusion: Our findings highlight ongoing local transmission of Zika virus in the country. Co-circulation of Zika, Dengue, and Chikungunya was also noted. An intensified community awareness campaign for the control and prevention of vector-borne diseases was then recommended.

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0553

Effect of sylvatic signature in the genetics of *Aedes aegypti* on its vector competence for viruses of public health significance

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Background: Arboviral diseases are, after malaria, the most important vector-borne causes of mortality and morbidity around the world. In the last five years, dengue has continued to expand its geographic range and 390 million dengue infections occur every year (95% confidence interval 284–528 million). Accidentally, or as a result of domestication and adaptation, some arboviruses are introduced to human settlements and if their ecological requirements (vector and hosts) are met, they can become established and cause outbreaks. The process involves introduction, adaptation, establishment and dispersal. *Aedes aegypti* is the most dangerous mosquito vector since it is competent to transmit more than 15 arboviruses, some of which are among the most important arboviruses of medical concern; and it is an aggressive feeder in the urban environment where it lives in close proximity to man. Two subspecies constitute the polymorphic *Aedes aegpyti* species: *Aedes aegypti formosus* and *Aedes aegypti aegypti*. Moreover, populations with individual mosquitoes having both genetic signatures were found in Argentina (formosus/aegypti). Those populations may represent an intermediate stage in the domestication process of *Aedes aegypti*. The aim of this work was to evaluate the effect of sylvatic genetic signature formosus in *Aedes aegypti* on its vector competence in the infection and transmission of arboviruses.

Methods and materials: A total of 6 populations (formosus signature: Gabon, Kenya; aegypti signature: Miami, Vero Beach; formosus/aegypti signature: Tartagal, Iguazu) were exposed perorally to chikungunya, dengue, Yellow fever and Zika viruses. Infection, dissemination and transmission rates were estimated at 3 time points (7-, 14- and 21-days post exposition).

Results: Differences between populations belonging to a genetic signature were high especially comparing Gabon and Kenya. Argentinean populations (Tartagal and Iguazu) developed infection, dissemination and transmission rates similar to those found in African populations for ZIKV and CHIKV. On the contrary, Kenya was the most susceptible population for yellow fever virus.

Conclusion: Preliminary data suggest there is not a clear association between genetic signature and vector competence. There are differences by population within the groups having the same genetic signature as well as beween groups with different genetic signatures. Differences between the two populations with formosus signature were the greatest.

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0555

Prevalence and genetic diversity of Coronavirus in human in Bangladesh

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Background: Coronaviruses (CoVs) are the causative agents of significant diseases resulting in a substantial impact on human and animal health. Both SARS-CoV and MERS-CoV originated from an animal reservoir and in recent years has caused a major burden on human health and health infrastructure globally. This study was conducted to detect and molecularly characterize known and novel coronaviruses in humans at high-risk animal-human interfaces in Bangladesh.

Methods and materials: From October 2017 to January 2019, we interviewed 862 participants using a questionnaire that examined behavioral risk factors associated with spillover and collected biological specimens from communities in Dhaka, Madaripur, and Dinajpur and one hospital, Faridpur Medical College Hospital, twice (dry and wet season). We enrolled participants from the hospital with symptoms that are associated with Influenza-like illness (ILI), Severe Acute Respiratory Syndrome (SARS), encephalitis, or fever of unknown origin (FUO) and from the community, apparently healthy participants who had a history of domestic or wild animal contact. We tested blood, oral and rectal swabs using consensus PCR targeting RNA-Dependent RNA Polymerase (rdrp) gene. Positive PCR products were confirmed by sequencing.

Results: Overall coronaviruses positive in 13 (95% CI: 0.8–2.5); among them 7 CoV-OC43, 4 CoV-HKU1 and 2 CoV-222E were detected. Coronavirus identified 3 in influenza-like illness ($n = 372$), 2 in fever of unknown origin ($n = 78$), 2 in encephalitis ($n = 90$), and 6 in apparently healthy participants ($n = 295$). Detecting CoVs was not associated with age or gender of the participants; however, virus detection was associated with samples collected in the dry sea-

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.

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0558

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 Southeast 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.

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0559

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.

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