over the years. EV-A71 C4 displayed low activity during 2015 – early 2018 and then emerged in late 2018, early 2019 and late 2020. Compared with B5, C4 was more likely to be associated with severe HFMD. During the study period, the proportion of CV-A6 and CV-A16 increased in 2017 followed by a drop in 2018, and then went up again between 2019 and 2021

Conclusion: Our data have provided significant insights into important aspects of HFMD over seven years (2015–2021) in Vietnam, and emphasize active surveillance for pathogen circulation remains essential to inform the local public health authorities in the development of appropriate intervention strategies to reduce the burden of this disease. Multivalent vaccines are urgently needed to control HFMD

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LONG TERM CIRCULATION OF SARS-COV-2 RELATED LINEAGES IN BATS IN CAMBODIA

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Intro: Recent evidence shows the Greater Mekong Subregion to be a hotspot for Sarbecoviruses in bats, especially insectivorous Horseshoe bats (genus Rhinolophus). However, prevalence, maintenance, and evolution of these viruses in Rhinolophids is still poorly understood. Sampling efforts are still limited and generally only cover cross-sectional surveillance at single points in time. Following the detection of Severe Acute Respiratory Syndrome coronavirus 2 (SARS-CoV-2)-related viruses in Rhinolophus shameli from 2010 in Steung Treng, Cambodia, further active longitudinal surveillance in the same area between 2020-2021 continued the detection of these viruses.

Methods: Live bat capture and sampling has been implemented in several sites located in Stung Treng province. All rectal swabs of bats were tested for the detection of SARS-CoV-2 or Sarbecoviruses by real time RT-PCR. RNA samples from positive RT-PCR bats were then sequenced using a highly multiplexed PCR amplicon approach using new designed primers set guided by the ARTIC Network multiplex PCR primers set (https://artic.network/ncov-2019), on Oxford Nanopore technology.

Findings: The sarbecoviruses were detected in four Rhinolophus shameli bats, a percentage of similarity ranging at the nucleotide level between 98.8% - 99.1% when compared to two other Cambodian bat sarbecoviruses from 2010 and between 92.4% - 94.5% when compared to human SARS-CoV-2 across the whole genome.

Discussion: The bat SARS-CoV-2 related virus recently detected in four positive bats in 2020-2021 are genetically homologous with the virus detected in 2010, indicating a geographically/host limited population that is stable over time in the past ten years.

Conclusion: Overall, our findings indicate further complexity in the diversity and evolution of sarbecoviruses and add intricacy to the search for the origins of the Coronavirus Disease 2019 (COVID-19) pandemic.

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SIDEROPHORE RECEPTOR PROTEIN FROM KLEBSIELLA PNEUMONIAE AS A PROMISING IMMUNOGEN FOR SEROTYPE-INDEPENDENT THERAPEUTIC LEAD DEVELOPMENT

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Intro: Klebsiella pneumoniae causes wide range of infections including urinary tract infections, sepsis, bacteremia, pneumonia and liver abscesses. The emergence of multi drug resistance in this bacterium led to a major setback for clinical management. WHO also endorsed need for finding alternative therapy to antibiotics for the treatment of these infections. Development of vaccines and passive antibody therapy has been proven as a potent alternative to antibiotics in case of MDR, XDR and PDR Klebsiella infections.

Methods: Antigen isolation, characterisation and identification through ultracentrifugation, SDS-PAGE and Triple-TOF Mass spectrometry. Cloning and expression of Fep A gene was done. Mice immunisation and challenge study with Klebsiella pneumoniae bacteria accomplished.

Findings: Clinical strains of Klebsiella pneumoniae were grown in iron deficient conditions and the iron regulated outer membrane proteins were extracted and characterized through mass spectrometry for specific identification. The gene for identified protein was cloned in pET- 28a vector and expressed in E. coli. The native protein and the recombinant protein were isolated and purified and used as antigens for generation of immune response in BALB/c mice. The native protein of Klebsiella pneumoniae grown in iron deficient condition was identified as FepA (Ferrienterobactin receptor) and other siderophore receptors. This 80 kDa protein generated a significant immune response in BALB/c mice. The antiserum from mice after subsequent booster doses was collected and showed binding with FepA protein in western blot and phagocytic uptake assay of K. pneumoniae. From animal studies after bacterial challenge post immunisation in mice, signifant bacterial clearance was observed. The antiserum from mice showed binding and clearance of the Klebsiella pneumoniae bacteria in vitro and in vivo.

Conclusion: The antiserum from immunised mice with FepA showed binding and clearance of the Klebsiella pneumoniae bacteria in vitro and in vivo.This study demonstrates the potential signifance of FepA as an immunogen or a therapeutic agent.

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