sequences. Our findings highlight ongoing genetic evolution and high diversity of circulating strains, locally and globally, with potential antigenic differences. Taken together, these provide a possible explanation on the nature of recurrent local RSV epidemics.

### A50 The emergence of G8P[8] rotavirus group A across Vietnam

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*Authors contributed equally to this work.Group A rotaviruses (RoV) are highly transmissible, globally ubiquitous, and are the principal cause of acute gastroenteritis in children. RoV are non-enveloped double-stranded RNA viruses comprised of 11 independent gene segments, encoding six structural proteins (VP1–VP4, VP6 and VP7) and five nonstructural proteins (NSP1–NSP5/6). Reassortment of viral segments can occur when a single cell is co-infected with two or more viruses, yielding mixed progeny with gene segments derived from multiple parental strains. Within a hospital-based study conducted to determine the etiology of diarrhea in five provincial hospitals located across Vietnam from 2012 to 2015, we detect RoV in 50.2% of all cases (678 RoV-positive/1,350 diarrhea cases). Determination of G- and P-type combinations using standard VP7/VP4 genotyping methods revealed that the common human G1P[8] (32.2%) and G2P[4] (13.0%) strains were most prevalent, whilst the less commonly described G8P[8] strain (10.5% of all RoV) showed a relatively high detection rate. The G8P[8] lineage was not detected in samples until 2014, when it was detected in 5.2% of all rotavirus sequences. By 2015, 44.8% of all RoV collected in our study were of the G8P[8] genotype. Full genome sequencing and phylogenetic analysis of G8P[8] sequences reveals that this lineage represents a non-reassortant, monophyletic clade closely related to other G8P[8] strains isolated recently in Europe and Asia, and has experienced an unprecedented spread across Vietnam within a very short time period. Future work will be conducted to document the arrival and spread of this lineage across Vietnam, to determine the potential impact of the arrival of this lineage on RoV epidemiology and disease burden, and to contrast the dynamics of G8P[8] to those of the more common endemic human genotypes (G1P[8] and G2P[4]) in Vietnam.

### A51 Dengue virus multi-strain models as hypotheses for serotype interaction

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Dengue virus (DENV) is endemic in the city of Rio de Janeiro, Brazil, with the four serotypes having been previously found circulating. Surveillance efforts include sequencing of the RNA virus collected in human sera, which allow identification of the currently circulating DENV serotypes and genotypes. Phylogenetic analyses estimate how circulating viruses relate to previously circulating genotypes in the same region or to viruses circulating in other parts of the country and the world, as well as indicating new introductions or reemergence of particular lineages [1–3]; however, sequence data has not been related to incidence dynamics in the region. Several mathematical models with a great range of detail have been proposed to describe the dynamics of DENV transmission [4], but almost always they rely on forward simulation only. One of the rare instances of model fitting and comparison used vietnamese DENV-1 data to compare variations of an SIR model with and without vectors and/or structure [5]. We have developed models of two serotype transmission to account for serotype co-circulation and interaction that is suitable for Brazilian multi-serotype surveillance data. We show how to incorporate more than one tree in a Beast2 implementation under a single model of disease transmission, and describe the performance of the single, and multiple independent or interacting serotypes. We also compare the estimation to that based on classical epidemiological data such as incidence time series, and point to the perspectives in model development and data collection.

### A52 Development and evaluation of a viral-specific random PCR and next-generation sequencing based assay for detection and sequencing of hand, foot, and mouth disease pathogens

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Hand, foot, and mouth disease (HFMD) has become a major public health problem across the Asia-Pacific region, and is commonly caused by Enterovirus A, including enterovirus A71 (EV-A71) and coxsackievirus A (CV-A) 6, 10, and 16. The ability to generate pathogen whole-genome sequences is essential for understanding their genetic diversity and phylodynamics. The frequent replacements among serotypes of Enterovirus A and a limited number of whole-genome sequences available in GenBank hinder the development of overlapping PCRs for whole-genome sequencing. We developed and evaluated a viral specific random PCR (rPCR) and next generation sequencing based assay for sequence independent whole-genome amplification and sequencing of HFMD pathogens. A total of 14 EV-A71/CV-A6/CV-A10/CV-A16 PCR positive rectal/throat swabs (Cp values: 20.9–33.3) were used for assay evaluation. Our assay evidently outperformed the normal rPCR in terms of the total number of EV-A71 reads and the percentage of EV-A71 reads: 3% (3,055/105,000 reads) vs. 0.1% (113/148,000) and 6% (4973/81,000) vs. 0.91% (1,054/116,000) for the samples with Cp values of 30 and 26, respectively. In addition, the assay could generate genome sequences with the percentages of coverage of 94–100% of 4 different HFMD causing enteroviruses in 73% of the tested rectal/throat swabs, representing the first whole-genome sequences of CV-A6/10/16 from Vietnam, and could assign correct serotyping results in 100% of the tested specimens. In all but one the obtained consensuses of two replicates from the

same sample were 100% identical, suggesting that our assay is highly reproducible. Phylogenetic analysis of the obtained sequences in the present study suggested that the EV-A71 strains sampled in 2012 belonged to subgenogroup C4, whereas the viruses collected in 2013 belonged to subgenogroup B5. All CV-A16 sequences belonged to genogroup B1a, and showed a close relatedness to the viruses circulating in the Asia-Pacific region. In contrast, the CV-A6 and CV-A10 strains were closely related to the corresponding HFMD-causing viruses from various parts of the world including Europe and Asia. We have successfully developed a viral specific rPCR and next-generation sequencing based assay for sensitive detection and direct whole-genome sequencing of HFMD pathogens from clinical samples.