Middle East Respiratory Syndrome Coronavirus (MERS-CoV) causing infections in humans is genetically indistinguishable from the virus found in Arabian camels (dromedaries) in the Middle East. Although no primary human case of MERS was reported outside the Arabian Peninsula, camel populations in Africa are known to have high prevalence of antibodies against MERS-CoV. We carried out surveillance for MERS-CoV in dromedaries in Africa and Central Asia. By MERS-CoV spike pseudoparticle neutralization assay we confirmed that camel serum samples from African countries have high prevalence of MERS-CoV antibodies. Using RT-qPCR we detected MERS-CoV positives in camel nasal swabs from all different African countries from which samples were collected. However, dromedary serum and swab samples from Kazakhstan in Central Asia were negative for MERS-CoV by these assays. Phylogenetic analysis of the spike gene revealed that MERS-CoVs from Africa formed a cluster closely related to but distinct from the viruses from the Arabian Peninsula. Results from this study suggest that MERS-CoV is actively circulating in dromedary populations in Africa and the virus in Africa is phylogenetically distinct from that in the Middle East.

A47 Origin and possible genetic recombination of the middle east respiratory syndrome coronavirus from the first imported case in china: phylogenetics and coalescence analysis

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The Middle East respiratory syndrome coronavirus (MERS-CoV) causes a severe acute respiratory tract infection with a high fatality rate in humans. Coronaviruses are capable of infecting multiple species and can evolve rapidly through recombination events. Here, we report the complete genomic sequence analysis of a MERS-CoV strain imported to China from South Korea. The imported virus, provisionally named ChinaGD01, belongs to group 3 in clade B in the whole-genome phylogenetic tree and also has a similar tree topology structure in the open reading frame 1a and -b (ORF1ab) gene segment but clusters with group 5 of clade B in the tree constructed using the S gene. Genetic recombination analysis and lineage-specific single-nucleotide polymorphism (SNP) comparison suggest that the imported virus is a recombinant comprising group 3 and group 5 elements. The time-resolved phylogenetic estimation indicates that the recombination event likely occurred in the second half of 2014. Genetic recombination events between group 3 and group 5 of clade B may have implications for the transmissibility of the virus.

A48 Inference of biological functionality in individual genomic secondary structural elements found within capulavirus genomes

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The seeming simplicity of the iconic DNA double helix is deceptive. The genomes of single-stranded DNA and RNA viruses often contain numerous nucleic acid secondary structures. Whilst a number of these secondary structural elements have been found to play crucial roles during the life cycles of these viruses, the majority have neither any identified function nor known impact on viral fitness and evolution. Secondary structures can be predicted using nearest neighbour free-energy parameters that quantify the stability of a given secondary structure. Using an array of bioinformatic techniques we investigated the influence of inferred secondary structures on the sequence evolution of capulaviruses, a diverse genera of single stranded DNA viruses. We detected a significant association between structured regions of the genome and selective constraints on synonymous substitutions in coding regions. This is suggestive of either natural selection acting to preserve these structures or a predisposition toward lower mutation rates in base-paired regions of the genome. In addition, coevolution analyses revealed a significant tendency for nucleotides that are base-paired in predicted structures to coevolve in a complementary manner. Combined, these results highlight the pervasiveness of conserved genomic secondary structures within capulavirus genomes and support the notion that natural selection is favouring the maintenance of these structures, providing compelling evidence of their likely biological relevance. This structure-first strategy for comparative analysis of genome-wide secondary structures can be broadly applied to understand the contributions of higher-order genome structures to viral replication and pathogenicity.

A49 Molecular evolutionary dynamics of respiratory syncytial virus group A in recurrent epidemics in coastal Kenya

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The characteristic recurrent epidemics of human respiratory syncytial virus (RSV) within communities may result from the genetic variability of the virus and associated evolutionary adaptation, reducing efficiency of pre-existing immune responses. We analyzed the molecular evolutionary changes in the attachment (G) glycoprotein of RSV-A viruses collected over 13 epidemic seasons (2000–12) in Kilifi ($n = 649$), Kenya, and contemporaneous sequences ($n = 1{,}131$) collected elsewhere within Kenya and 28 other countries. Genetic diversity in the G gene in Kilifi was dynamic both within and between epidemics, characterized by frequent new variant introductions and limited variant persistence between consecutive epidemics. Four RSV-A genotypes were detected in Kilifi: ON1 (11.9%), GA2 (75.5%), GA5 (12.3%), and GA3 (0.3%), with predominant genotype replacement of GA5 by GA2, then GA2 by ON1. Within these genotypes, there was considerable variation in potential N-glycosylation sites, with GA2 and ON1 viruses showing up to 15 different patterns involving eight possible sites. Further, we identified 15 positively selected and 34 genotype-distinguishing codon sites, with six of these sites exhibiting both characteristics. The mean substitution rate of the G ectodomain for the Kilifi dataset was estimated at 3.58×10^{-3} [95% HPD: 3.04–4.16] nucleotide substitutions/site/year. Kilifi viruses were interspersed in the global phylogenetic tree, clustering mostly with Kenyan and European

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