genetic sequences has a fundamental role in the study of a virus with high sequence variability, such HRSV. This methodology could also be used for genome sequencing of other RNA viruses.

A33 Respiratory syncytial virus group B evolutionary trends in the attachment (G) glycoprotein in Kilifi, Kenya, 2003–2015

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Respiratory syncytial virus (RSV) attachment (G) protein mediates virus binding to cells and is a target for human neutralising antibodies. Understanding its evolutionary patterns is relevant to design of vaccines or antiviral therapy. RSV group B genotype BA, characterised by a sixty-nucleotide duplication, was first detected in 1999 in Buenos Aires, Argentina, and has since been spread and become the globally dominant RSV B genotype. BA viruses were first detected in Kilifi, coastal Kenya in 2003 and soon achieved high prevalence, replacing all other RSV-B genotypes. We present in detail, evolutionary patterns of the genotype BA G protein from >600 BA viruses obtained during twelve successive RSV epidemics in Kilifi. Phylogenetic analyses revealed extensive diversification of the BA genotype viruses into multiple genetically distinct variants (~58), some of which persisted locally across sequential epidemics while others were re-introductions into the community. The most recent common ancestor dated back to 1990, and the mean evolutionary rate over their G ectodomain region was 6.51×10^{-4} substitutions/site/year (95 per cent CI $5.65–7.42\times10^{-4}$). Demographic analysis demonstrated two main phases: an early rapid expansion and subsequent seasonal fluctuations of BA populations. Putative positive selection was detected in six codon sites, all located in the second hyper-variable G protein region. Nucleotide substitutions introducing alternative termination codons were observed resulting in up to five different protein lengths. Two potential N-glycosylation sites were conserved in 89.3 per cent sampled viruses while eight other sites were detected in a small proportion of the viruses. Further, four codons tended to revert to previous states over successive epidemics, an indication of adaptive mechanism for immune evasion. These results provide insights into the local genotype BA viral evolutionary dynamics and highlight the importance of continuous molecular surveillance to inform on changes in proteins that may be important to vaccine design.

A34 Spread and evolution of respiratory syncytial virus A genotype ON1, coastal Kenya, 2010–2015

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In February 2012, the novel respiratory syncytial virus (RSV) group A, genotype ON1, was detected in Kilifi County, coastal Kenya. ON1 is characterized by a seventy-two-nt duplication within the highly variable G gene (encoding the immunogenic attachment surface protein). Cases were diagnosed through surveillance of pneumonia in children at the county hospital. Analysis of epidemiologic, clinical, and sequence data of RSV-A viruses detected over five RSV seasons (2010/2011 to 2014/2015) indicated the following: 1) replacement of previously circulating genotype GA2 by ON1, 2) an abrupt expansion in the number of ON1 variants detected in the 2014/2015 epidemic, 3) recent accumulation of amino acid substitutions within the ON1 duplicated sequence, and 4) no clear evidence of altered pathogenicity relative to GA2. The study demonstrates the public health importance of molecular surveillance in defining the spread, clinical effects, and evolution of novel respiratory virus variants.

A35 Molecular epidemiology of respiratory viruses

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Respiratory viruses cause a high burden of disease worldwide. The attributed morbidity and mortality is especially high in infants and young children with lower respiratory tract illness. In contrast to influenza virus, little is known about the circulation patterns of other pathogens that commonly cause respiratory disease in humans, such as respiratory syncytial virus and the human parainfluenza viruses. The recently proposed source-sink and globally migrating metapopulation models have improved our understanding of circulation patterns of influenza virus. We thus aim to investigate the molecular evolution of non-influenza respiratory viruses and understand their geographical transmission dynamics by sequencing viruses and combining them with sequences from public databases. Temporal phylogenetic trees are then inferred within a Bayesian framework to characterise the evolutionary and population dynamics of these viruses. Finally, we use phylogeographic methods to infer global migration patterns. For human parainfluenza virus 3 (HPIV-3), our preliminary analysis indicates that multiple virus lineages co-circulate globally and regionally, with introductions into specific locations that are followed by expansion and endemic circulation within each given location. We find that the HPIV-3 phylogeny displays geographical structuring that may be related to regional outbreaks. However, HPIV-3 can also be transmitted globally as reflected by the inter-mixing of different geographical locations.

A36 Circulating strains of human respiratory syncytial virus in Belgium during six consecutive respiratory seasons (2011–2017)

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Human respiratory syncytial virus (HRSV) is the most common cause of acute respiratory infection in young children. HRSV belongs to the Pneumoviridae family within the order of the Mononegavirales and can be divided into two subtypes: HRSV-A and HRSV-B. The two subtypes co-circulate during the annual HRSV season, which occurs between November and March in Belgium. The aim of this study was to determine the circulating HRSV subtypes and genotypes between the seasons of 2011–2012 to 2016–2017. With this information, we intend to understand the temporal phylogenetic relationships better between the circulating strains over the six seasons. Between October 2011 and February 2017, 1,272 HRSV positive patient samples from the University Hospitals of Leuven were collected. In order to