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to identify the sources of infection, and the virus evolution as well as host/virus interaction. In our study, using 454/Illumina sequencing, we have obtained large amount of whole genome sequences. We designed a preliminary bioinformatics analysis pipeline to classify these NGS reads. First we mapped our nucleotide reads to GenBank reference sequences using BLAST, and classified them by their taxonomic family, such as host, virus and unclassified. Then, for a specific type of virus (e.g. influenza virus, MERS coronavirus), we conducted de novo and reference based assembly of the reads to obtain the full genome sequences for further phylogenetic study. In the future, through advanced bioinformatics tools, we hope to get more detailed information from our large amount of NGS sequences of field/clinical samples, experimental data, especially in the following areas: (i) finding novel pathogens in unclassified sequences; (ii) virus/virus interactions; (iii) pathogen/host interaction.

A25 Phylogenetic analysis of the nucleocapsid and RNA-dependent RNA polymerase fragments of the first imported case of middle east respiratory syndrome coronavirus (MERS-CoV) infection in the Philippines from Saudi Arabia, February 2015

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We report the first laboratory-confirmed case of Middle East Respiratory Syndrome Coronavirus (MERS-CoV) infection from a patient returning to the Philippines from the Kingdom of Saudi Arabia (KSA). MERS-CoV was first identified in 2012 circulating in Middle Eastern countries with outbreaks occurring in KSA, the United Arab Emirates (UAE), and South Korea, plus sporadic imported cases in at least 20 other countries. The Philippines is at risk for MERS-CoV transmission from frequent travelers, such as overseas Filipino workers and Hajj pilgrims, coming from Middle Eastern countries. Throat swabs, sputum samples, and a rectal swab were collected from the index case within 13 to 22 days after the onset of symptoms. MERS-CoV testing was performed using a real-time reverse transcription polymerase chain reaction (RT-qPCR) screening assay targeting regions upstream of the envelope gene (upE) and the nucleocapsid gene (N2), a confirmatory RT-qPCR assay targeting regions within the open reading frame 1a gene (ORF1a) and another region of the N gene (N3), and Sanger sequencing of regions of the N and RNA-dependent polymerase (RdRp) genes. The index case tested weakly positive for MERS-CoV in a sputum sample until day 19 of illness. Sequences of the N and RdRp gene regions reveal 100 and 99% similarity with MERS-CoV sequences obtained in KSA and UAE, respectively, confirming that the infection originated from Middle Eastern strains. Two unique synonymous/silent mutations (T15259A and T15265C) were identified in the RdRp sequence fragments. Whole genome sequencing of the strain may identify other mutations across the genome and determine the most probable origin of the strain.

A26 Transmission patterns and evolution of RSV in a community outbreak identified by genomic analysis

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Detailed information on the source, spread and evolution of respiratory syncytial virus (RSV) during seasonal community outbreaks remains sparse. Molecular analyses of attachment (G) gene sequences from hospitalised cases suggest that multiple genotypes and variants co-circulate during epidemics and that RSV persistence over successive seasons is characterized by replacement and multiple new introductions of variants. No studies have defined the patterns of introduction, spread and evolution of RSV at the local community and household level. We present a whole genome sequence analysis of 131 RSV group A viruses collected during six-month household-based RSV infection surveillance in Coastal Kenya, 2010 within an area of 12 km^2. RSV infections were identified by regularly screening of all household members twice weekly. Phylogenetic analysis revealed that the RSV A viruses in 9 households were closely related to genotype GA2 and fell within a single branch on the global phylogeny. Genomic analysis allowed the detection of household-specific variation in seven households. For comparison, using only G gene analysis, household-specific variation was found only in 1 of the 9 households. Nucleotide changes were observed intra-host (viruses identified from same individual in follow-up sampling) and inter-host (viruses identified from different household members) and these coupled with sampling dates enabled partial reconstruction of the within household transmission chains. The genomic evolutionary rate for the household dataset was estimated as 2.307×10^{-3} (95% highest posterior density: 0.93513–4.1636×10^{-3}) substitutions/site/year. We conclude that (i) at the household level, most RSV infections arise from the introduction of a single virus variant followed by accumulation of household specific variants and (ii) analysis of complete virus genomes is crucial to better understand viral transmission in the community. A key question arising is whether prevention of RSV introduction or spread within the household by vaccinating key household members in these functions would lead to a reduced onward community wide transmission.

A27 Using whole genome sequence data and minority variant profiles to elucidate transmission patterns during RSV household outbreaks

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Reconstructing transmission chains for outbreaks is important in understanding how viruses spread. Furthermore, defining the main underlying determinants of transmission chains is important for developing effective interventions. Whole