Previous studies have suggested that recombination breakpoints of FMDV are mostly located in the boundaries between capsid and non-capsid proteins. Here, we investigated the recombination patterns of viral lineages (determined by VP1 phylogeny) known to be endemic to Southeast Asia (SEA): FMDV serotype O lineages PanAsia and Mya-98, and serotype A lineage Sea-97). We analyzed ninety-three full ORF sequences from SEA countries and reference sequences from other Asian regions. Of these, thirty sequences were generated by our laboratory and the remaining were obtained from GenBank. We used maximum likelihood phylogenetic reconstruction for each of the protein coding regions and RDP4 to detect recombination. Specific recombinant viruses were further analyzed using RIP to visualize their mosaic patterns. Three specific mosaic viruses of lineage A/Sea97 and O/Mya98 sequences were detected. Reconstruction of the phylogenies revealed a closer relationship between O/Mya98 and A/Sea97 lineages in the non-structural proteins. We further analyzed intra-lineage recombination, using homoplasy test (after removal of mosaic sequences), revealing hot spots of recombination regions that differ depending on the lineages A/Sea97 (hotspots in VP2, 2 C, and 3 D), O/Mya98 (in Lpro, VP1, 3 C, and 3 D), and PanAsia (in Lpro and 2 C). This study integrates knowledge of molecular FMD epidemiology and the specific implications of viral recombination. Furthermore, these results suggest novel understanding of the evolutionary interdependence of FMDV serotypes and lineages. Unveiling the evolutionary mechanisms of FMDV may help predict emergence of new lineages, and inform the risk posed by co-circulating lineages in FMD-endemic regions.

### A57 Clinical features and virology of hand, foot, and mouth disease in southern Vietnam from July 2013 to July 2015

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In Asia, hand, foot, and mouth disease (HFMD) is associated with large and sometimes severe outbreaks since 1997, and is caused by enterovirus A (EV-A), in particular EV-A71. Monitoring the pattern of replacement between EV serotypes, its associated clinical profile and pathogen evolutionary process are essential for understanding the progress of outbreak/epidemics and development of intervention strategies. A large prospective study has been conducted at three referral hospitals in southern Vietnam since July 2013: Children's Hospital 1, Children's Hospital 2 and Hospital for Tropical Diseases in Ho Chi Minh City. For each participant, clinical data, throat and rectal swabs were collected. Multiplex real-time and nested RT-PCRs were employed to detect and identify specific EV serotypes in clinical specimens. Selected EV-A(71) positive swabs were then subject to whole-genome deep sequencing. During two years, there were 1,547 cases enrolled into the study. The most commonly detected pathogens included CV-A6 (21.8 per cent), EV-A71 (24.4 per cent), CV-A16 (10.8 per cent), and CV-A10 (7.9 per cent), followed by CV-A2/A4/A12 and Echovirus. Temporally, the four common enterovirus genotypes (including EV-A71, CV-A6, CV-A10, and CV-A16) replaced each other during the entire study period. A total of 295 genome sequences were obtained, including 156 EV-A71 sequences. EV-A71 B5 ($n = 156$) was the predominant subgenogroup. Phylogenetic analysis showed that all Vietnamese CV-A16 ($n = 25$), CV-A2 ($n = 7$), CV-A5 ($n = 3$), CV-A8 ($n = 4$), CV-A12 ($n = 10$), and CV-A14 ($n = 1$) were closely related to those from China and the region, while CV-A4 ($n = 10$), CV-A6 ($n = 26$), and CV-A10 ($n = 43$) clustered with viruses belonging to genogroups collected from worldwide, and CV-A4 were imported into Vietnam from two independent events. Clinically, there was no significant difference between CV-A6, CV-A16, and CV-A10 groups. Patients with EV-A71 infection were older than those with non-EV-A71 infection (21.7 vs. 17.3 months old, $P < 0.001$). Other differences included myoclonus (21 vs. 13 per cent, $P = 0.001$), irritability (17 vs. 70 per cent, $P < 0.001$), and location of erythema. There was a trend toward EV-A71 detection rate and clinical severity: 23 per cent grade 1, 17 per cent (2 A), 39 per cent (2B group 1), 71 per cent (2B group 2), 64 per cent (3), and 67 per cent (4). Our study represents the most comprehensive descriptive HFMD study in Vietnam. The analysis of 1,547 patients has revealed interesting and important insights into epidemic patterns, pathogen-associated clinical phenotypes, and viral evolution, which are essential for public health and of clinical significance.

### A58 Identification of novel viruses in the families Flaviviridae (Jigmenvirus), Chuviridae, and Bunyaviridae (phlebovirus-like) in ticks from the south of Brazil

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Tick-borne viruses are transmitted to humans and animals by tick bites and include many important emerging and re-emerging viruses. In addition, recent studies based on high-throughput sequencing have revealed an unprecedented diversity of tick-borne viruses. The objective of this project was to investigate the viral diversity present in ticks in South of Brazil. To this end, we sampled ~600 ticks (*Rhipicephalus microplus*) and 36 serum from cattle collected in six farms in the South of Brazil between October of 2015 to June of 2016. Samples were distributed in twelve pools based on sample (ticks or serum cattle) and site of collection. Viral RNA was extracted, followed by synthesis of double-stranded cDNA and was sequenced using the Illumina platform. Sequence reads were quality-filtered, the adapter sequences removed and the remaining reads were assembled with *de novo* methods using the MetaVIC pipeline. We identified and characterized the complete genome sequence of three RNA viruses, which were classified into the families Flaviviridae, Bunyaviridae, and Chuviridae. The genome of Mogiana Tick virus (MGTV) comprised four positive sense single stranded RNA molecules, named as segments one to four with 2,672 to 2,994 nucleotides, which encodes five proteins (NSP1, VP1, NSP2, VP2, and VP3). This virus was classified as a member of Jigmenvirus, a possible new genus in the Flaviviridae family. The Lihan Tick 2 virus-like (LT2V-like) possesses two segments, the small segment encodes the nucleoprotein and the large segment encodes the RNA-dependent RNA polymerase. Despite this virus being classified as a phlebovirus-like (Bunyaviridae),