

A47 **Reconstructing the evolutionary history of pandemic foot-and-mouth disease viruses: The impact of recombination within the emerging O/ME-SA/Ind-2001 lineage**

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Foot-and-mouth disease (FMD) is a highly contagious disease of livestock affecting animal production and trade throughout Asia and Africa. Understanding FMD virus (FMDV) global movements and evolution can help to reconstruct the disease spread between endemic regions and predict the risks of incursion into FMD-free countries. Global expansion of a single FMDV lineage is rare but can result in severe economic consequences. Using extensive sequence data, we have reconstructed the global space-time transmission history of the O/ME-SA/Ind-2001 lineage (which normally circulates in the Indian sub-continent) providing evidence of at least fifteen independent escapes during 2013–7 that have led to outbreaks in North Africa, the Middle East, Southeast Asia, and the Far East and the FMD-free islands of Mauritius. We demonstrated that sequence heterogeneity of this emerging FMDV lineage is accommodated within two co-evolving divergent sublineages, and that recombination by exchange of capsid-coding sequences can impact upon the reconstructed evolutionary histories. Thus, we recommend that only sequences encoding the outer capsid proteins should be used for broad-scale phylogeographical reconstruction. These data emphasize the importance of the Indian subcontinent as a source of FMDV that can spread across large distances and illustrates the impact of FMDV genome recombination on FMDV molecular epidemiology.

A48 **Identification and full-genome characterization of Alpha- and Beta-Coronaviruses viruses from bats in Italy**L. De Sabato,^{1,2} G. Vaccari,¹ D. Lelli,³ A. Lavazza,³ M. R. Castrucci,¹ and A. Moreno³

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Bats are the natural reservoir of Coronaviruses (CoVs). Human CoVs cause mild respiratory diseases worldwide, but, in the last decade, two Beta-CoVs [Middle East respiratory syndrome (MERS)-CoV and severe acute respiratory syndrome] caused thousands of deaths and cases worldwide. Phylogenetic analysis suggested the evolutionary origin of mammalian CoVs is derived from bats. In this study, we characterized three Alpha-CoVs and two Beta-CoVs demonstrating the circulation of bat strains in Italy. Isolates were sequenced using a next-generation sequencing approach and genomes reconstructed using the online tool Galaxy Aries. Phylogenetic analyses were conducted using MEGA7 and MrBayes. Similarity plots were generated using SSE v1.2. The structure of the receptor binding domain (RBD) in the S protein was predicted by sequence-homology method using the protein data bank. Bioinformatics analysis permitted the identification of 2 Beta-CoV complete genomes of 30 kb and three Alpha-CoV of 28 kb (named BatCoV-ITA1-5). BatCoV-ITA1 and 2 formed a monophyletic group with MERS-CoV sequences. The comparison of the concatenated domains within ORF1ab confirmed their classification into the MERS-CoV species. The 3D structure of RBD of Italian strains showed two amino acid deletions located in a region corresponding to the external subdomain of MERS-RBD. BatCoV-Ita3 and BatCoV-Ita4/5 were classified into two novel Alpha-CoV species by comparison of concatenated domains within ORF1ab. Due to the high divergence with the Alpha human spike protein strains, it was impossible to establish the protein structure and the potential affinity to human receptor. The Italian strains showed the typical organization of Alpha and Beta-CoVs. We reported two Beta-CoVs closely related to MERS-CoVs from bats belonging to common Italian species (*Pipistrellus kuhlii* and *Hypsugo savii*). The analysis of the RBD in the spike protein indicates significant differences from human RBD known to date. The three Alpha-CoV strains were classified into two novel species, confirming the high heterogeneity of CoV strains in bats. Although the studies conducted cannot confirm a risk for humans, surveillance studies are needed to investigate the genetic diversity of CoVs in bats. Because this exceeds what is known for other hosts, it is

compatible with bats being the major reservoir of mammalian CoVs.

A49 **Emerging rodent-borne viral pathogens in Italy: Overview of seroprevalence and genomic investigations**

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Rodents play a key role as reservoirs of many zoonotic pathogens which represent an emerging public health threat worldwide. Among these, Dobrava-Belgrade virus (DOBV) is the most pathogenic hantavirus in Europe with a case-fatality rate of up to 12 per cent, while Lymphocytic choriomeningitis virus (LCMV) has a mortality rate below 1 per cent. Both viruses are predominantly transmitted to humans through the inhalation of infected particles in aerosolized urine, feces, or saliva that are shed in the environment by chronically infected hosts, such as the yellow-necked mouse *Apodemus flavicollis*. Although no human cases of DOBV or LCMV have been reported in the Province of Trento (northeastern Italy) thus far, in order to evaluate the human hazard for these viruses, the prevalence of antibodies to DOBV and LCMV has been monitored using a specific immunofluorescence assay test in a wild population of *A. flavicollis* since 2000. These investigations have shown that the two RNA viruses circulate silently in this species in the study area. In particular, a sudden increase (up to 12.5%) in DOBV seroprevalence was observed in this rodent species between 2010 and 2012. Several efforts have been undertaken to isolate these viruses and characterize their genomes, but it has not yet been possible to detect viral RNA from seropositive mice using traditional methods such as RT-PCR. Since RNA viruses are very diverse and often difficult to isolate, innovative molecular methods based on viral targeted enrichment and high-throughput sequencing have been applied. We intend to report on this long-term seroprevalence study and provide an overview of the molecular approaches adopted in the attempt to confirm the presence of these viruses, and identify which variants are circulating in the region, as well as their pathogenicity.

A50 **Whole-genome sequencing of African swine fever isolates from Sardinia**C. Torresi,¹ F. Granberg,² L. Bertolotti,³ A. Oggiano,⁴ B. Colitti,³ M. Giammarioli,¹ and G. M. De Mia¹

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In order to assess the molecular epidemiology of African swine fever (ASF) in Sardinia, we analyzed a wide range of isolates from wild and domestic pigs over a 31-year period (1978–2009) by genotyping sequence data from the genes encoding the p54 and the p72 proteins and the CVR. On this basis, the analysis of the B602L gene revealed a minor difference, placing the Sardinian isolates into two clusters according to their temporal distribution. As an extension of this study, in order to achieve a higher level of discrimination, three further variable genome regions, namely p30, CD2v, and I73R/I329L, of a large number of isolates collected from outbreaks in the years 2002–14 have been investigated. Sequence analysis of the CD2v region revealed a temporal subdivision of the viruses into two subgroups. These data, together with those from the B602L gene analysis, demonstrated that the viruses circulating in Sardinia belong to p72/genotype I, but since 1990 have undergone minor genetic variations in respect to its ancestor, thus making it impossible to trace isolates, enabling a more accurate assessment of the origin of outbreaks, and extending knowledge of virus evolution. To solve this problem, we have sequenced and annotated the complete genome of nine ASF isolates collected in Sardinia between 1978 and 2012. This was achieved using sequence data determined by next-generation sequencing. The results showed a very high identity with range of nucleotide similarity among isolates of 99.5 per cent to 99.9 per cent. The ASF virus (ASFV) genomes were composed of terminal inverted repeats and conserved and non-conserved ORFs.