Among the conserved ORFs, B385R, H339R, and O61R-p12 showed 100 per cent amino acid identity. The same was true for the hypervariable ORFs, with regard to X69R, DP96R, DP60R, EP153R, B407L, I10L, and L60L genes. The EP402R and B602L genes showed, as expected, an amino acid identity range of 98.5 per cent to 100 per cent and 91 per cent to 100 per cent, respectively. In addition, all of the isolates displayed variable intergenic sequences. As a whole, the results from our studies confirmed a remarkable genetic stability of the ASFV/p72 genotype I viruses circulating in Sardinia.

A51 Genetic variability of small ruminant lentiviruses in sheep and goats from single-species flocks from Poland

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Previous phylogenetic analyses of small ruminant lentivirus (SRLV) sequences found in Poland revealed the circulation of subtype A1 in both sheep and goats, subtypes B1 in goats, and subtypes B2, A12, and A13 in sheep only. This study aimed to analyze the genetic nature of SRLV circulating in sheep and goats from single-species flocks. In order to analyze the degree of genetic variability, the fragments of *gag* and *env* genes of 24 SRLV strains were amplified by PCR, cloned into plasmid vectors, sequenced, and consensus sequences were aligned to each other and to reference sequences available from GenBank. Phylogenetic analysis was performed using the Geneious tree-builder tool, and phylogenetic trees were constructed using Mr Bayes (using the general time reversible substitution model) within Geneious Pro 5.3. Pairwise genetic distances were calculated in MEGA 6. Phylogenetic analysis revealed that the strains were highly heterogeneous and represented ovine strains belonging to subtypes A12 and B2 and caprine strains grouped in subtypes B1, B2, A1, and A12. In addition, two novel subtypes, A16 and A17, were found in goats. The mean pairwise genetic distances of *gag* and *env* sequences of both clusters were above 15 per cent nucleotide divergence when compared to all other subtypes within group A, which is a criterion required to distinguish a new subtype. Additionally, the existence of two separated clusters was confirmed by high bootstrap values. Co-infections with strains belonging to different subtypes within A and B groups were detected in one sheep and four goats originating from four flocks. Since the co-infection with more than one lentivirus genotype offers an opportunity for viral recombination, the possible recombination events were tested based on RDP analysis. For all co-infected animals, no evidence of recombination was found within the *gag* gene; however, *env* sequences showed some recombination patterns in three samples. In conclusion, we have demonstrated extended genetic variability of SRLV in sheep and goats from Poland with the existence of co-infection and recombination events.

A52 MERS coronaviruses from camels in Africa exhibit region-dependent genetic diversity

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Middle East respiratory syndrome coronavirus (MERS-CoV) causes a zoonotic respiratory disease of global public health concern, and dromedary camels are the only proven source of this zoonotic infection. Although MERS-CoV infection is ubiquitous in dromedaries across Africa and the Arabian Peninsula, the continuous appearance of zoonotic MERS cases in humans is confined to the Arabian Peninsula. MERS-CoV from Africa has hitherto been poorly studied. Here, we report the genetic and phenotypic characterization of MERS-CoV from dromedaries in African countries. Phylogenetically, viruses from dromedaries in Africa formed a monophyletic clade, which we have provisionally designated as virus clade C. Molecular dating analyses of MERS-CoV, including clade C viruses, suggests that the ancestral MERS-CoV in dromedaries could have spread to the two continents within a short timeframe. Camel MERS-CoVs from west and north African countries form a subclade (C1) that shares genetic signatures of a major deletion in the accessory gene ORF4b. Compared with human and camel MERS-CoV from Saudi Arabia, virus isolates from Burkina Faso (BF785) and Nigeria (Nig1657) had lower virus replication competence in Calu-3 cells and in *ex vivo* cultures of human bronchus and lung, and BF785 replicated to lower titer in lungs of human DPP4-transduced mice. However, it is still inconclusive whether ORF4b deletions may lead to the reduced replication competence of BF785 and Nig1657. Genetic and phenotypic differences in West African viruses may be relevant to the zoonotic potential of MERS-CoV.

A53 MERS-CoV in East African dromedary camels

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Human Middle East respiratory syndrome is a zoonotic respiratory disease caused by Middle East respiratory syndrome coronavirus (MERS-CoV) originating from camels in the Arabian Peninsula. While there are a large number of camels in East Africa, often traded to the Arabian Peninsula, no autochthonous human MERS-CoV case is reported in East Africa. Furthermore, there is limited information of MERS-CoV in East Africa. In this study, MERS-CoV in dromedary camels from Ethiopia was detected using RT-qPCR. Next-generation sequencing was used to obtain the full genome of MERS-CoV. MERS-CoV antibodies were also detected through MERS-spike pseudoparticle neutralization assay. Phylogenetic analysis of full-genome sequences and spike-genome antibodies indicates that MERS-CoV in East Africa is genetically distinct from those in the Arabian Peninsula. The results from this study show that MERS-CoV circulating in dromedary camels in East Africa are genetically distinct from those in the Arabian Peninsula. Further studies are needed to evaluate the risk of zoonotic transmission in East Africa.

A54 Genomic analysis of camel-HKU23 in Nigeria dromedary camels reveals strain-specific cross-species recombination

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Coronaviruses (CoVs) are enveloped, single stranded, positive-sense RNA viruses with a large genomic size of 26–32 kilobases. The first human CoV identified in the 1960s was isolated from patients presenting with common cold symptoms. Subsequent epidemic outbreaks of novel zoonotic CoV transmission were reported, examples including HCoV-229E (229E), HCoV-OC43 (OC43), severe acute respiratory syndrome, and Middle East respiratory syndrome (MERS). The ongoing outbreak of MERS in the Middle East is originating from a zoonotic source of dromedary camels. Surveillance later revealed that three CoV species—HCoV-229E (229E), camel-HKU23, and MERS-CoV—were co-circulating in Saudi Arabia dromedary camels. Camel-HKU23 belongs to Group 2a CoV, which also includes human coronavirus OC43, bovine coronavirus, and porcine hemagglutinating encephalomyelitis virus. Recombination, resulting in the generation of different novel genotypes, has been reported previously among these CoVs. Our surveillance of dromedary camels slaughtered in a major abattoir in Nigeria identified camel-HKU23 from nasal swab samples with a prevalence of 2.2 per cent. Phylogenetic analysis showed Nigeria camel-HKU23 is distinct from those previously identified in Saudi Arabia, while still genetically similar, as they share a monophyletic origin. Recombination analysis of Nigeria camel-HKU23 revealed two recombination breakpoints at positions of 22774–24100 base pairs (bp) and 28224–29362 bp. Recombination breakpoint at position 22774, encoding the Group 2a CoV-specific hemagglutinin esterase gene, exhibited high bootstrap support for clustering with RbCoV HKU14, which was previously detected in