

we did not find the medium segment or a homologue gene. Lastly, we describe the nearly complete sequence of the Wuhan Tick Virus-like (WTV-like), which is comprised of one negative-sense single stranded RNA molecule, with 11,208 nucleotides. This virus was classified into Chuviridae family and encodes the polymerase, glycoprotein, nucleoprotein, and VP4. Interestingly, the tick pools from all the four sites of collection were positive for MGTV, LT2V-like, and WTV-like viruses, indicating that these viruses can be found in the tick population of a large area of the Brazilian territory, which is an important cattle producing region in the country and one of the leading regions in animal produce exportation. On the other hand, only the MGTV was simultaneously detected in 19.4 per cent (7/36) serum cattle, indicating viremia in these animals. In summary, we have identified three potentially novel tick-borne viruses with broad distributions in South of Brazil, which include potential novel pathogens for cattle.

A59 Expansion of genetic diversity and interspecies transmission dynamics of swine influenza viruses in China

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Swine influenza viruses (SIVs) pose a continuous threat to agriculture and public health, as indicated by the emergence of 2009 pandemic H1N1 virus (pdm/09). Our previous evolutionary studies of SIVs isolated from long-term surveillance in China during 1998–2010 revealed co-circulation of four major swine lineages, all of which were introduced from North America or Europe. The introduction and reassortment of pdm/09 with these major swine virus lineages have led to the expansion of genetic diversity in the study area. Frequent influenza virus transmission from human to swine also drives evolution of SIVs, facilitating the genesis of novel variants with increased human infectious potentials, as evidenced by the human cases caused by infection of zoonotic H3N2 variants. Repeated transmission of H3 human influenza viruses (huIVs) to pigs has been observed in China since 1998, but their long-term impact on the ecology and development of SIVs were not systematically explored. Using whole-genome sequences of 1,631 SIVs isolated from our influenza surveillance program during 1998–2015, we aim to investigate the following scientific questions: 1) the continuous development of pdm/09-like and huIV-like H3 viruses in pigs; 2) population dynamics of co-circulating swine lineages in China; 3) global migration of SIVs of various origins; 4) viral determinants of increasing diversity and human-to-swine transmissibility. Phylogenetic analyses in this project may provide insights into the risk posed by circulating SIVs and understanding of the mechanism of interspecies transmission.

A60 Molecular epidemiology of canine parvovirus type 2 (CPV-2) in Italy

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In this study, we performed phylodynamic analysis of 107 VP2 sequences of CPV strains detected in dogs showing clinical

signs of gastroenteritis, collected during the period 1994–2013. The age of these animals ranged between two months and ten years, with or without vaccination history from different breeds and both genders. The majority of faecal samples were collected in the continental area of North and Central Italy and twenty-nine faecal samples came from Sicily. VP2 genes were sequenced and a variety of statistical analyses of nucleotide polymorphism and sequence variability were performed on the sequence data. Maximum likelihood phylogenetic trees were estimated using PAUP* version 4.0, with the best-fit model of nucleotide substitution determined using JModeltest 2. The HKY + I + Γ substitution model was optimal for all the sequence data (including reference strains), whereas the GTR + I + Γ substitution model was used for the sequences analysed in this study; the key parameter values (the HKY and GTR substitution matrix, the proportion of invariant sites I and the gamma distribution of rate variation with eight categories) were estimated from the data. To assess support for individual nodes, bootstrap resampling values were estimated with 1,000 neighbor-joining trees, again employing PAUP*. Molecular phylogenetic analysis of the amino acid sequences with a maximum likelihood method was carried out using the software PHYLIP version 3.695. The best substitution model for amino acid sequences was estimated using MEGA version 5.2.2. The JTT + Γ substitution model was optimal for the protein dataset and used to build phylogenetic trees. Typing of CPV strains detected fifty-six CPV-2a strains, twelve CPV-2b strains, and thirty-nine strains characterized as CPV-2c. Sixty-one genetically distinct sequences or nucleotide sequence types (ntSTs) and nineteen amino acid sequence types (aaSTs) were identified among the 107 viruses sequenced. In the ten-year observation period, the frequency of the CPV variants showed rapid oscillations.

A61 High prevalences and a wide genetic diversity of simian retroviruses in non-human primate bushmeat in rural areas of the Democratic Republic of Congo

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Like the majority of emerging infectious diseases, HIV and HTLV are of zoonotic origin. Here, we assess the risk of cross-species transmissions of their simian counterparts, SIV and STLV, from non-human primates (NHP) to humans in the Democratic Republic of Congo (DRC). A total of 331 samples, derived from NHP bushmeat, were collected as dried blood spots ($n=283$) or as tissue samples ($n=36$) at remote forest sites mainly in northern and eastern DRC. SIV antibody prevalences in dried blood spots were estimated with a novel high throughput immunoassay with antigens representing the actual known diversity of HIV/SIV lineages. Antibody-positive samples were confirmed by PCR and sequence analysis. Screening for STLV infection was done with universal primers in tax, and new strains were further characterized in LTR. SIV and STLV infection in tissue samples was done by PCR only. Overall, 5 and 15.4 per cent of NHP bushmeat was infected with SIV and STLV, respectively.