

explaining the patterns observed, such as considerable gene flow and inbreeding probably due to anthropogenic activities in the light of population management and conservation programmes are discussed.

Identification of a new genotype of African swine fever Virus in domestic pigs from Ethiopia

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African swine fever (ASF) is an important emerging transboundary animal disease (TAD), which currently has an impact on many countries in Africa, Eastern Europe, the Caucasus and the Russian Federation. The current situation in Europe shows the ability of the virus to rapidly spread, which stands to threaten the global swine industry. At present, there is no viable vaccine to minimize spread of the disease and stamping out is the main source of control. In February 2011, Ethiopia had reported its first suspected outbreaks of ASF. Genomic analyses of the collected ASF virus (ASFV) strains were undertaken using 23 tissue samples collected from domestic swine in Ethiopia from 2011 to 2014. The analysis of Ethiopian ASFVs partial p72 gene sequence showed the identification of a new genotype, genotype XXIII that shares a common ancestor with genotypes IX and X, which comprise isolates circulating in Eastern African countries and the Republic of Congo. Analysis of the p54 gene also followed the p72 pattern and the deduced amino acid sequence of the central variable region (CVR) of the B602L gene showed novel tetramer repeats not previously characterized.

Development of broad-spectrum human monoclonal antibodies for rabies post-exposure prophylaxis

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Currently available rabies post-exposure prophylaxis (PEP) for use in humans includes equine or human rabies immunoglobulins (RIG). The replacement of RIG with an equally or more potent and safer product is strongly encouraged due to the high costs and limited availability of existing RIG. In this study, we identified two broadly neutralizing human monoclonal antibodies that represent a

valid and affordable alternative to RIG in rabies PEP. Memory B cells from four selected vaccinated donors were immortalized and monoclonal antibodies were tested for neutralizing activity and epitope specificity. Two antibodies, identified as RVC20 and RVC58 (binding to antigenic site I and III, respectively), were selected for their potency and broad-spectrum reactivity. In vitro, RVC20 and RVC58 were able to neutralize all 35 rabies virus (RABV) and 25 non-RABV lyssaviruses. They showed higher potency and breadth compared to antibodies under clinical development (namely CR57, CR4098, and RAB1) and commercially available human RIG. In vivo, the RVC20–RVC58 cocktail protected Syrian hamsters from a lethal RABV challenge and did not affect the endogenous hamster post-vaccination antibody response.

Phylogenetic analysis of Newcastle disease viruses isolated from commercial poultry in Mozambique, 2011 to 2016

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The complete sequence of the fusion (F) protein gene from eleven Newcastle disease viruses (NDV) isolated from commercial poultry in Mozambique between 2011 and 2016 has been generated. The F gene cleavage site motif for all eleven isolates was 112RRRKRF117 indicating that the viruses are virulent. A phylogenetic analysis using the full F gene sequence revealed that the viruses clustered within genotype VIIh and showed a higher similarity to NDVs from South Africa, China and Southeast Asia than to viruses previously described in Mozambique in 1994 to 1995 and 2005. The characterization of these new NDVs has important implications for Newcastle disease management and control in Mozambique.

Molecular characterization of orf virus from sheep and goats in Ethiopia, 2008–2013

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Orf is a contagious disease of sheep, goats and wild ungulates caused by orf virus (ORFV) a member of the genus Parapoxvirus, Poxviridae family. Although orf is endemic in Ethiopia, little attention has been given so far as it is not a notifiable disease by the World Organization for Animal Health. In this work, we have investigated orf