

According to the passages, and the other investigators' findings, we can declare that the new vaccine (RB51) is potentially suitable for being used in the control and prevention program of bovine Brucellosis and its usage has been satisfactory in Iran over these years and is a successful replacement for S19 vaccine.

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18.015

Trans-border Transmission of Rabies Between South Africa, Zimbabwe and Mozambique Resulted in the Re-emergence of Rabies in Northern South Africa

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Despite the effectiveness and the availability of vaccines for animal and human use, the largely populated rural areas of South Africa are still haunted by rabies. In these areas the dog is the main vector species transmitting rabies to humans. In one such rural area, the Limpopo province in northern South Africa, canine rabies has been under control for the past two decades. However, in 2005 an unexpected and drastic increase of dog rabies cases in this area was observed. Laboratory confirmed cases increased from 5 cases in 2004 to 35 cases in 2005 and 100 cases in 2006 and this increase was paralleled by human rabies outbreak during 2005/2006. In order to determine the origin of this outbreak, a panel of 60 rabies viruses obtained from South Africa, Zimbabwe and Mozambique were genetically characterised by sequencing an 850bp amplicon spanning the cytoplasmic domain of the glycoprotein gene and the non-coding G-L intergenic region of each of these viruses. Through phylogenetic analysis of the nucleotide sequence data, it was demonstrated that the virus variant associated with the recent outbreak in Limpopo was genetically related to rabies viruses from southern Zimbabwe indicating that this lineage could have been introduced from Zimbabwe. Furthermore the results showed that common rabies cycles exist among South Africa, Zimbabwe and Mozambique highlighting the transboundary transmission of rabies in southern Africa. The porous nature of the African borders enables translocation of infected animals across national borders. The re-emergence of dog rabies in Limpopo highlighted the importance of continuous and sustained animal vaccination programs and further underlined the importance of multi-national collaboration in the control of animal movement across national borders.

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Evolution of H5N1 Virus NS1 Gene Isolated from Human (2006–2007) as Next Pandemic Threat

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During the past two years highly pathogenic avian influenza viruses H5N1 spread to 60 countries and fall into distinct clades VTM, INDO and EMA. Continued transmission to humans has been raised in Indonesia and Egypt, causing pandemic concern. To address questions relevant to virus evolution and adaptation; NS1 sequence data of EMA and INDO H5N1 viruses isolated from human between 2006–7 were downloaded from GenBank and aligned with MUSCLE. The ENC and GC3S values for NS1 gene in both clades were less biased. No selection pressure for EMA NS1 was found whereas the NS1 gene of INDO clade was under positive selection ($=1.22$). The rate of NS1 evolution in INDO has faster than EMA suggests a possible change in the adaptation of the H5N1 virus to human. To explain the change pseudoknot loops were identified within NS1 gene using RNA folding path. Among them formation of a pseudoknot due to mismatches at the top and the bottom of a conserved sequence (5-GAGGAU-3/5-GUCCUC-3) was questionable. Stability of the pseudoknot was compared between the two clades by energy estimation. According to free energy the pseudoknot destabilizes in Indonesia H5N1 human viruses (-11.1 kcal/mol vs -13.6 kcal/mol) indicating changes in RNA secondary structure. The change may lead to increase adaptation of NS1 gene to human population.

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Acute Fibrinosuppurative Hemorrhagic Pneumonia Caused by *S. equi* Subsp. *Zooepidermidis* in the Shelter Dogs in Korea

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Background: Canine infectious respiratory disease (CIRD) is a common distress in the kennels and shelters housed with dense population. The CIRD is associated with the several viruses and bacteria. In case of bacteria, *B. bronchiseptica* is predominant pathogen, but other bacterial species have also been associated with CIRD. Although *Streptococcus sp.* is the commensal of the upper respiratory tract, there was only few report of streptococcal pneumonia as a primary pathogen except *S. canis*. We have diagnosed the fatal hemorrhagic pneumonia case associated with *S. equi* subsp. *zooepidermidis* and described the pathologic and bacteriologic results.

Methods: A veterinarian of the shelter informed us that the sudden death of dogs was increased within a few days