

Genetic Characterisation of Rabies Viruses from NigeriaM.F. Ogo^{1,*}, L.H. Nel¹, C.T. Sabeta²¹ University of Pretoria, Pretoria, South Africa² Onderstepoort Veterinary Institute, Pretoria, South Africa**Keywords:** Molecular epidemiology; Rabies; Nigeria; Glycoprotein phylogeny

In Nigeria, rabies still poses the greatest public and veterinary health risks, similar to other countries in Africa and Asia. The disease remains one of the most neglected endemic zoonosis despite the availability of biologicals for its control. There is no active surveillance system for the disease; in addition, underreporting and misdiagnosis are common. A study was therefore undertaken to elucidate the molecular epidemiology of rabies in Nigeria. A cohort of 100 rabies viruses all recovered from dogs between 1989 and 2007 were included in this investigation. The samples were confirmed to be rabies using the direct fluorescent antibody test (FAT). Reverse transcription and amplification were performed on a partial region of the glycoprotein gene of each of viral RNAs of rabies isolates analysed. The PCR products were sequenced and a 592-nucleotide sequence encompassing the cytoplasmic domain of the glycoprotein and the G-L intergenic region using the Big Dye Terminator V3.1 cycle sequencing kit (Applied Biosystem). The phylogenetic analysis demonstrated that the panel of Nigerian rabies viruses were closely related with 93.2 - 100% sequence identity. However, despite this close genetic relationships, the viruses could be differentiated into one major group of viruses recovered from dogs from the North Central states of Nigeria, and the other two from the from the North East and South West regions respectively. The implication of the data on control of rabies in Nigeria will be discussed.

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Bacterial Causes of Ovine Abortion and Neonatal Mortality in Iran

M.H. Rad*, Z. Naseri

School of Veterinary Medicine, Ferdowsi University of Mashhad, Mashhad, Iran (Islamic Republic of)

Background: Abortion and prenatal lamb mortality is the major cause in lowering of productivity of sheep. The objectives of the present study were to explore the problem in lambs in Iran and to identify the causal bacteria.

Methods: During a one year survey a total of 45 aborted fetuses and 47 neonatal deaths from different farms were examined to determine the bacterial causes. Tissues were collected aseptically for microbiologic examination. Routine examination included aerobic and micro-aerobic culturing of lung, liver and stomach content. New diagnostic assays such as PCR was added to standard protocol for confirming Salmonella isolates by detecting *invA* gene which are specific for Salmonella.

Results: Bacterial agents were diagnosed on the basis of isolating an organism from several fetal tissues in pure or nearly pure culture. Bacterial agents associ-

tal death (36.17%). Bacteria responsible for abortion were: Salmonella spp. (9%), Brucella melitensis (4.5%), Campylobacter fetus subsp fetus (4.5%), Moraxella spp.(4.5%), Escherichia coli (4.5%), Corynebacterium spp.(4.5%). Bacteria responsible for neonatal mortality were: Salmonella spp(8.5%), Escherichia coli (8.5%), Pasteurella multocida (6.4%), Mannheimia haemolytica (6.4%), Campylobacter fetus subsp fetus (4.25%) and Brucella melitensis (2.12%).

Conclusion: Salmonella spp. was the most frequent bacterial species identified as cause of abortion and neonatal mortality in lambs in Khorasan province of Iran. We found other organisms in pure culture with low virulence related to abortion and neonatal deaths. Because of suppression of immune reaction at the junction of the fetal and maternal placentas, any infectious agent that is able to reach the junction of the maternal and fetal placentas could be free to multiply and cause lesions unhindered by immune reaction. Under these immunologic conditions, bacteria of low virulence may cause abortion and neonatal deaths.

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Prevalence of Feline Coronavirus Antibodies in Cats in Bursa (Turkey) by An Enzyme-Linked Immunosorbent AssayA. Pratelli^{1,*}, K. Yesilbag², E. Yalçın³, Z. Yilmaz⁴¹ Department of Public Health and Zootechnics, Valenzano - Bari -, Italy² Departments of Virology, Uluda - Bursa, Turkey³ Departments of Internal Medicine, Uluda - Bursa, Turkey⁴ Department of Internal Medicine, Uluda - Bursa -, Turkey

Since feline coronavirus (FCoVs) are ubiquitous pathogens, the seroprevalence was studied to monitor infection in Turkey. One hundred sera, collected from cats belonging to catteries or community shelters and to households, were tested. The VN test was performed and compared with ELISA. Each sample was heat-inactivated and serial two-fold dilutions starting from 1/2 were mixed with 100TCID₅₀/50 µl of FCoV type II strain 25/92. Subsequently, freshly trypsinized CRFK cells were added and the plates were incubated at 37 °C for 96 h. The VN antibody titer was expressed as the reciprocal of the highest serum dilution that completely inhibited viral cytopathic effect. Microtiter NUNC-polysorp immunoplates were coated with 25 µg/ml of FCoV type II antigen (purified whole virus) and incubated overnight at 4 °C with shaking. Each serum, diluted 1/50, was added and the plates were incubated for 90 min at 37 °C. Rabbit anti-cat IgG was added and then freshly prepared substrates were used. The OD were determined at 405 nm. The results were compared using the Cohen's kappa test for agreement and repeatability.

The VN revealed 79 sera as negative and 21 as positive. The negative sera were subsequently examined by ELISA which confirmed 74 as negative while 5 resulted positive. These 74 negative sera were also found to be free of FCoVs specific antibodies by western blotting. Using the VN test as the gold standard test, ELISA had a sensitivity of 100% and