71°

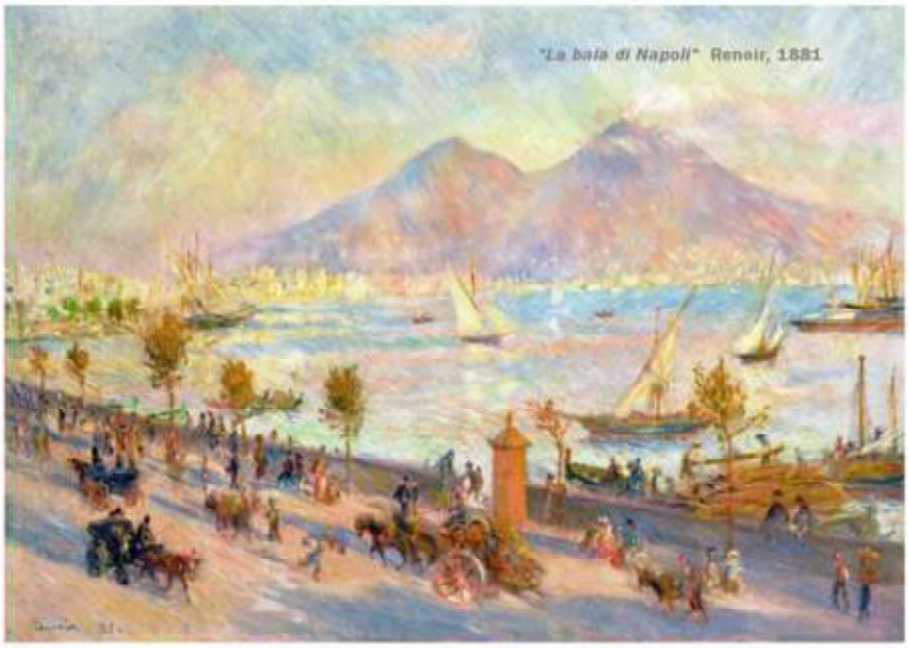
SOCIETÀ ITALIANA DELLE SCIENZE VETERINARIE

CONVEGNO SISVET

In collaborazione con

Dipartimento Medicina Veterinaria Produzioni Animali

Istituto Zooprofilattico Sperimentale del Mezzogiorno



XVII Convegno SICV

XV Convegno SIRA

XIV Convegno AIPVET

XII Convegno SOFIVET

IV Convegno RNIV

I Convegno ANIV

28 Giugno - 1 Luglio 2017

Università degli Studi di Napoli "Federico II"

Corso Umberto I, 40 - 80138 - Napoli

I contributi presenti negli Atti del 71° Convegno SISVet 2017

potranno essere citati utilizzando il codice ISBN 9788890909245

MONITORING OF BOVINE VIRAL DIARRHOEA VIRUS INFECTION IN WILD RUMINANTS AND IN CATTLE BY PCR ON FAECAL SAMPLES: A PRELIMINARY STUDY

Sara Ricci (1), Federico Morandi (2), Massimo dell'Orso (2), Corrado Corradini (3), Rino Spighi (1), Silvia Preziuso (1)

(1) Università di Camerino, Scuola di Bioscienze e Medicina Veterinaria, Italia. (2) Parco Nazionale dei Monti Sibillini, Italia. (3) Veterinario libero professionista, Italia.

Bovine Viral Diarrhoea Virus (BVDV) is a Pestivirus responsible for severe economic losses in cattle farms and it has also been discovered in some wild ruminants. Blood, milk, saliva, ear notch and tissue samples are usually used for diagnosis of BVDV infection in cattle [1]. However, these samples could be not easily collected when wild ruminants or beef cattle are tested.
The aim of this work was to investigate if BVDV can be detected by PCR in fecal samples from wild ruminants and cattle.
Fecal samples (n=60) were collected in 2 bovine farms with a history of seropositivity for BVDV-1 (A, n=40; B, n=20). In addition, faecal samples from red deer (*Cervus elaphus*, n=16), Appennine chamois (*Rupicapra pyrenaica ornata*, n=13), fallow deer (*Dama dama*, n=6), and roe deer (*Capreolus capreolus*, n=5) were collected from the environment. RNA was obtained from pool samples (10 individual samples = 1 pool) of bovine faeces and from individual samples from wild ruminants. Aliquots of faecal samples were stored at 4°C and tested after 3 months. Real time PCR for Pestivirus [2,3], nested PCR for BVDV [4] and PCR for 5'-UTR sequencing [5] were carried out.
BVDV-1 was detected in all 4 pool samples from cattle in farm A, in 4 samples from red deer, in 3 samples from chamois and in one sample from fallow deer. Positive results were obtained also by the faecal samples stored and tested after 3 months. The sequences obtained showed highest identity with BVDV-1 types 1a and 1c.
These preliminary findings suggest that faecal samples can be used for monitoring the molecular epidemiology of BVDV-1 in cattle and in wild ruminants. This approach allows to perform diagnosis of BVDV-1 infection in situations where is not possible to catch nor to kill the animals, such as in protected environments.
Further investigation are required for evaluating the sensitivity of the method and for detecting BVDV-1 types infecting wild ruminants in Italy.

[1] Lanyon SR, Hill FI, Reichel MP, Brownlie J. Bovine viral diarrhoea: pathogenesis and diagnosis. Vet J., 199(2):201-9, 2014. [2] Baxi M, McRae D, Baxi S, Greiser-Wilke I, Vilcek S, Amoako K, Deregt D. A one-step multiplex real-time RT-PCR for detection and typing of bovine viral diarrhea viruses. Vet Microbiol., 25;116(1-3):37-44, 2006. [3] Rodríguez-Prieto V, Kukielka D, Rivera-Arroyo B, Martínez-López B, de las Heras AI, Sánchez-Vizcaíno JM,Vicente J. Evidence of shared bovine viral diarrhea infections between red deer and extensively raised cattle in south-central Spain. BMC Vet Res., 14;12:11, 2016. [4] Letellier C, Kerkhofs P, Wellemans G, Vanopdenbosch E. Detection and genotyping of bovine diarrhea virus by reverse transcription-polymerase chain amplification of the 5' untranslated region. Vet Microbiol., 64(2-3):155-67, 1999. [5] Vilcek S, Herring AJ, Herring JA, Nettleton PF, Lowings JP, Paton DJ Pestiviruses isolated from pigs, cattle and sheep can be allocated into at least three genogroups using polymerase chain reaction and restriction endonuclease analysis. Arch Virol. 136: 309–323, 1994.