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Objective: Sheep pox is endemic in most parts of Northern Africa and has the potential to cause severe economic problems. Live attenuated vaccines are used in Morocco, and in many other countries, in order to control the disease. Sheep pox virus (SPPV) re-appeared in 2010 causing a nodular clinical form previously not observed in Morocco. The severe clinical signs observed during the course of this outbreak and initial reports citing similarity in nucleotide sequence between the Moroccan vaccine strain and field isolates warranted a more in depth analysis of this epizootic. It was the purpose of this study to (1) look more closely into the epizootic of 2010 in Morocco (2) investigate the possible link between the Moroccan vaccine used in that period and the virus isolated from the field by exploring sequence similarity in different regions of the genome and by developing PCR methods to differentiate between vaccine and wild-type virus.

Methods: Samples collected from 19 flocks located within four provinces the eastern region of Morocco during the 2010 Outbreak were analysed using real-time PCR panel and an in-house monolayer Elisa. Isolates from different geographic regions were phylogenetically analysed and compared to each other and to the vaccine used in the region. DIVA PCRs were developed to analyze a possible link between the isolates and vaccine.

Results: Aside from scab material, blood was the sample type which most frequently gave a positive result (98% positive) followed by buccal and ocular swabs, 93% and 91% positive, respectively. However, most variability was seen in blood samples when using the Haegeman PCR panel, ranging from 64%, 69% to 85% positivity. Seroconversion for Capx was detected in 80.5% of the animals and in each flock.

Sequence analysis of two genomic regions showed that all isolates obtained from four the provinces of Eastern Morocco were identical and were clearly different from the Moroccan vaccine strain. Using two newly developed DIVA PCRs no trace of wild type SPPV was found in the vaccine and no trace of the vaccine was found in the sampled animals.

Conclusion: Supporting the published findings ocular swabs were found to be a useful sample type to test with a detection rate of the Haegeman PCR-panel of 91%. For rectal and nasal swabs the detection rates were noticeably probably due to a greater sensitivity to the timing of sampling relative to the course of infection. Buccal swabs (detection rate of 93%) were found to be an interesting alternative with the added advantage of being easier to take than ocular swabbing. The PCR-panel detection rate in blood was found to be 98%. However, this sample type may be less suited as the individual PCR detection rates of the PCR-panel were more variable.

Based on the sequences data from the different isolates, it can be stated that a single SPPV strain was responsible for the 2010 epizootic. In addition, no evidence was found linking the vaccine (vaccine strain or presence of wild type virus) directly to the epizootic. However, further analysis is needed to clarify the epidemiological picture in relation to recombination, re-introduction or re-emergence. The two newly developed PCRs, able to differentiate between the RM-65 vaccine strain and wild type SPPV, can be a useful tool in future epidemiological investigations during vaccination programs.

Prevalence of antibodies to selected viral pathogens in wild boars (*Sus scrofa*) in Serbia

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Objective: There has been a worldwide increase in the number and geographical spread of wild boar populations in recent decades leading to an increase in both the circulation of disease agents and greater contact with domestic animals and humans. Knowledge of diseases circulating among wild boars can be important not only for production and health of domestic pigs, other livestock and wild animals but also for public health. The risk of transmission of pathogens from free-ranging wild boars (*Sus scrofa scrofa*) to outdoor domestic pigs (*S. scro-*

fa domesticus) is of increasing concern in many European countries. In Serbia, the wild boar is one of the most important big game species. However, information on the prevalence and distribution of potentially important infectious disease agents among wild boar populations in Serbia is currently very limited, or doesn't exist. The aim of the current study was to investigate the presence of selected viral pathogens in wild boars populations in Serbia, and to assess possible role of wild boars in the epidemiology as reservoirs of these viruses for domestic pigs and other domestic and wild animals and for human population in Serbia.

Methods: Blood samples from 381 wild boars from 53 hunting grounds and 13 out of 25 counties in Serbia, that are 3.66% of predicted number of wild boars (10 409) on the observed territory, and 1.91% of predicted number of wild boars (19 908) from all 12 districts and 142 hunting grounds of Serbia, were collected during the hunting season from October 2011 until March 2012. Blood samples were taken by hunters or by veterinarians from the heart after the wild boars had been shot. Collected blood sera were tested by commercial enzyme-linked immunosorbent assays (ELISAs) for the presence of antibodies against Aujeszky's disease virus (ADV), H1N1 and H3N2 swine influenza viruses (SIV), and hemagglutination inhibition (HI) test was used for detection of antibodies against porcine parvovirus (PPV).

Results: Out of 381 analyzed blood sera samples, antibodies against ADV, SIV H1N1, SIV H3N2 and PPV were detected in 27.03% (103), 4.73% (18), 5.51% (21), and 61.68% (125) samples, respectively. The prevalence of seropositive wild boars to ADV (102/32.38%); SIV H1N1 (18/5.71%); SIV H3N2 (20/6.35%); and PPV (209/66.35%) from 34 hunting grounds on the northern part of the country (315 samples from Vojvodina province) was higher than those found among wild boars (66) from 19 hunting grounds from south part of the country (ADV (1/1.52%); SIV H1N1 (0/all negative); SIV H3N2 (1/1.52%); and PPV (26/39.39%)). Anti-PPV antibodies were detected in wild boars originated from all counties from where the samples were collected. Seropositive wild boars to ADV were detected in all (6 out of 6) tested counties on the northern part and in just one out of 7 counties on the southern part of Serbia. Seropositive wild boars to SIV H1N1 were found just on the northern part of the country in 4 and 3 out of 6 examined counties, and seropositive wild boars to SIV H3N2 were found in 3 out of 6 and in 1 out of 7 examined counties on the northern and southern part of Serbia, respectively.

Conclusion: Our results indicate that wild boar populations throughout the Republic of Serbia are exposed to PPV. Also, our results show that ADV is highly prevalent, especially among wild boars from northern part of Serbia, the area of higher density and intensive pig production. In addition, our results indicate presence of both H1N1 and H3N2 swine influenza virus infections that are more prevalent at the northern part of the country. This is the first comprehensive serologic study on selected viral diseases in wild boars in Republic of Serbia. Our results provide information on the current disease exposure to selected viruses and health status of wild boars in Serbia. The obtained results point on the possibility that wild boars in Serbia may play a significant role in the epidemiology of studied viral diseases and act as a potential reservoir and source of infection for domestic, especially free range pigs, and other animals as well as humans. Further and more comprehensive research is needed including testing of wild boar samples from the whole country and from a few hunting seasons on antibody and virus presence to obtain more conclusive results on presence and role of examined viruses in wild boars on the epidemiology of disease in Serbia.

Keywords: ADV, SIV (H1N1/H3N2), PPV, wild boar, seroprevalence, Serbia

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Is *Ornithodoros erraticus* able to transmit the Georgia2007/1 African Swine Fever virus isolate to domestic pigs?

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