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First description of african horse sickness virus serotype 7 in healthy horses in northern Senegal

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Purpose: The purpose of the study was to survey African Horse Sickness (AHS) virus prevalence in healthy horses and identify the serotypes circulating in Senegal. This study was conducted one month prior to the notification of the first AHS clinical case in northern Senegal and before mass vaccination against eight serotypes took place.

Methods & Materials: Between 12–19 August 2007, 414 horses were randomly sampled in three zones in the Senegal River delta: St.-Louis, Ross Bethio and Richard Toll. The blood samples collected from 138 horses in each zone were centrifuged, stored at –20°C, and later tested by competitive ELISA. A random sample of 71 positive horse sera was analyzed by Plaque Reduction Neutralization Test (PRNT) on Vero cells against African Horse Sickness Virus (AHSV) serotypes. Cytopathogenic effects were read four days later. Statistical data analysis was done using R software.

Results: The overall true seroprevalence rate by ELISA test was 89.5% in 414 horse sera. In the subset of 71 infected horses, antibodies against AHSV 2 were detected in 67.5%, against AHSV 7 in 92.96% and against AHSV 9 in 100% of horses. AHSV 7 antibodies were found in 80.95% of the positive horses from Ross-Bethio, 95.45% from St.-Louis, and 100% in Richard-Toll zones.

Conclusion: Prior to this study, only the monovalent vaccine against AHSV serotype 9 was used on horses in the area. The polyvalent vaccine against eight types of AHSV was first used after our sampling. Our results reveal the presence of antibodies against AHSV 7, which suggests that Serotype 7 virus had been circulating prior to the mass vaccination. Chi-square test for the three serotypes showed that they are not independent. Based on these results we hypothesize that the vectors of AHSV 9 in the Senegal River delta may be the same vectors that introduced and spread AHSV 2 and AHSV 7. This work is the first description of AHSV 7 in Senegal.

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Pathogens in domestic cats and dogs in the Canary Islands, Spain

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Purpose: The aim of this work was to increase the knowledge about the range of pathogens affecting domestic cats and dogs in

the Canary Islands, Spain, due to the actual scarcity of data. Another purpose of this study was to assess through immunological methods whether dogs in the Canary Islands are coming into contact with the nematode *Angiostrongylus cantonensis*.

Methods & Materials: Between 2014 and 2015, 264 dogs and 60 cats were attended in different veterinary clinics in Tenerife and Lanzarote, two out of the Canary Islands. Faeces samples were obtained from each individual to determine the presence of *Cryptosporidium* spp., *Giardia* spp., *Toxoplasma* spp. and *Entamoeba* spp. by morphological methods, whereas Giemsa-stained blood smears were occasionally analyzed for the presence of *Babesia* parasites. On the other hand, sera samples were obtained from 59 dogs belonging to Tenerife to carry out the detection of IgG antibodies against a 31-kDa glycoprotein of *A. cantonensis* by ELISA technique.

Results: The protozoa *Giardia* spp., *Cryptosporidium* spp., *Cystoisospora* spp. and *Entamoeba* spp., and the helminths *Toxocara canis*, *Trichuris vulpis*, *Enterobius* sp., *Aelurostrongylus abstrusus*, *Dicrocoelium* sp., *Toxascaris leonina* and *Ancylostoma caninum* were found in domestic dogs. With regard to domestic cats, we found the protozoa *Giardia* spp., *Cryptosporidium* spp., *Entamoeba* spp. and *Toxoplasma gondii*, and the helminths *Toxocara cati* and *Aelurostrongylus abstrusus*. *Giardia* spp. was the most prevalent pathogen in both domestic cats and dogs. The presence of *Cryptosporidium* spp. in both cats and dogs was occasionally confirmed by amplifying the 18S small subunit ribosomal RNA (18S rRNA) gene by using genus-specific primers. On the other hand, 11.89% of the dogs analyzed carried IgG antibodies against *A. cantonensis*. Finally, *Babesia canis vogeli* was identified in a dog by PCR and sequencing of the 18S rRNA gene.

Conclusion: The finding of pathogens with zoonotic potential in domestic cats and dogs in the Canary Islands highlights the necessity of assessing whether zoonotic transmission events from pets to humans are taking place in this archipelago. Pet owners should be also taught appropriate hygiene measures to prevent the transmission of some of these zoonotic pathogens.

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Overwintering of epizootic hemorrhagic disease virus in white-tailed deer in Florida, USA: Unanticipated seroconversion and the case for alternative vectors

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Purpose: Hemorrhagic disease (HD) is a vector-borne disease of ruminants caused by two distinct but related viruses: epizootic hemorrhagic disease virus (EHDV) and bluetongue virus (BTV). HD is the most important viral disease of white-tailed deer in North America. In recent years, HD outbreaks have become more frequent, and HD has become a more global problem as the viruses have spread, causing infection in both domestic and wildlife hosts. The reasons for this incursion are not well understood but some hypotheses for this phenomenon include the expanding range of biting midge vectors (*Culicoides* spp.), potentially resulting in