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Wild birds as carriers of antimicrobial-resistant and ESBL-producing *Enterobacteriaceae*

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Purpose: Extended-spectrum β -lactamases (ESBLs) has been studied widely in *Escherichia coli* and *Salmonella* spp. from humans and livestock in Europe. In contrast, information on this phenomenon in wild animals is poor, although the close interaction between wildlife, other animals and human-influenced habitats potentially allows bacterial exchange. Moreover, migratory behaviour of wild birds make these animals potential carriers of antimicrobial-resistant bacteria from human-influenced environments over long distances. Thus, the aim of this work was to provide data on the prevalence and characterization of ESBL-producing *E. coli* and *Salmonella* spp. from wild birds in Northern-Italy.

Methods & Materials: One hundred-three cloacal samples from wild birds (belonging to the Accipitridae, Anatidae, Strigidae, Apodidae, Corvidae, Falcoidea, Fringillidae, Scolopacidae, Laridae, Columbidae, Picidae, Strigidae, Sylviidae and Turdidae Families) were tested to detect *E. coli* and *Salmonella* spp. using the classical bacteriological procedure. Single colonies were plated on Brilliance-ESBL Agar (Oxoid) and presumptive ESBL-producers were confirmed by combination disk diffusion tests. Susceptibility to the non-beta-lactams was determined by the disk diffusion method according to the CLSI guidelines.

Results: Thirty-five animals (33.9%) were carriers of *E. coli* and 1 (0.9%) of *Salmonella* spp. Of the 77 strains isolated (diverse bacterial colonies from the same animal were stored if they showed differences in morphology), 4 (5.2%) were ESBL-producing *E. coli*. The *E. coli* ESBL-producers were isolated from 2 *Accipiter gentilis*, 1 *Falco Linnaeus* and 1 *Trichoglossus haematodus*. The *Salmonella* spp. isolate was not ESBL-producing. A considerable number of strains, including 3 of the 4 ESBL-producing strains, were also classified as multidrug-resistant, showing resistance especially to aminoglycosides, sulfonamides and tetracycline. All the isolates were susceptible to the quinolones tested and the unique *Salmonella* spp. strain was susceptible to all the compounds tested.

Conclusion: The presence of antimicrobial-resistant and ESBL-producing *Escherichia coli* in wild birds highlight the potential roles of these animals as source of resistant bacteria to critically important drugs. The migratory behaviour of some of these animals, together with the close contact with urban and peri-urban areas, suggests that wild birds can contribute to the global dissemination of resistance among different ecosystems.

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Seroprevalence and risk factors for equine arboviral infections (Eastern Equine Encephalomyelitis, Western Equine Encephalomyelitis, Venezuelan Equine Encephalomyelitis and West Nile Fever) in Costa RicaS. Hutter^{a,*}, M. Baldi^b, C.L. Firth^a, B. León^c, A. Käsbohrer^d, C. Jimenez^e^a *University of Veterinary Medicine, Vienna, Institute of Veterinary Public Health, Vienna/AT*^b *Institute of Wildlife Ecology, University of Veterinary Medicine, Vienna/AT*^c *Servicio Nacional de Salud Animal, Ministerio de Agricultura y Ganadería, Heredia/CR*^d *University of Veterinary Medicine Vienna, Institute of Veterinary Public Health, Vienna/AT*^e *Universidad Nacional, Virology, Heredia/CR*

Purpose: To gain a better understanding of the epidemiological situation of arboviral infections in horses in Costa Rica, a national IgG seroprevalence study was performed in 2013. In Costa Rica, equine arboviral infections are caused by *Alphaviruses* such as Eastern equine encephalomyelitis virus (EEV), Western equine encephalomyelitis virus (WEV) and Venezuelan equine encephalomyelitis virus (VEV), as well as a *Flavivirus*: West Nile Virus (WNV).

This study was carried out in response to a number of lethal disease outbreaks in horses, which were primarily caused by VEV, but also WNV and EEV. Arboviruses, which are transmitted to horses and humans through blood-sucking mosquitoes, may cause pyrexia, neurological disease and even death in both animals and humans.

Methods & Materials: The representative sample size with respect to the national horse population was calculated to be 196, assuming a total population of 140,000, using a precision of 7%, a confidence level of 95% and an expected seroprevalence of 50%. In the absence of horse distribution data, a convenience sampling approach was required, collecting serum from 3 horses per canton.

Samples were evaluated for IgG at a single dilution of 1:100. *Alphaviruses* were assessed by indirect ELISA, antibodies to WNV were determined using a capture monoclonal, recombinant protein. Risk factors such as mosquito density, housing system and location for these arbovirus infections were analysed.

Results: A total of 241 horse serum samples from 80 cantons were collected and analyzed.

The highest seroprevalence was determined for EEV (61%), followed by WNV (58%), VEV (with 43%) and WEV (16%). Detected risk factors were primarily related to the location (province), but also management (housing system).

Conclusion: The present study was the first nationwide seroprevalence study of equine arboviruses in Costa Rica. The high seroprevalence of IgG to these viruses demonstrates that horses are highly frequently exposed to these pathogens. However, we have not yet been able to distinguish individual responses from cross-reactions to these or other viruses of the genus, which might be resolved by serum neutralisation test. Nevertheless, this is an important finding which may have consequences for both veterinary and human public health authorities in the country.

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