

RISK OF DIFFUSION OF A HIGHLY PATHOGENIC AVIAN INFLUENZA VIRUS BETWEEN WILD AND DOMESTIC AVIAN COMPARTMENTS THROUGH WILD BIRDS IN ZIMBABWE

Caron A DVM PhD, Grosbois V PhD, Etter E DVM PhD, de Garine-Wichatitsky M DVM PhD

UPR AGIRs, Cirad, Montpellier, France; E-mail Alexandre.caron@cirad.fr

The role of wild birds in the ecology of Avian Influenza viruses (AIV) has been investigated in recent decades and has recently attracted efforts from the research community due to the panzooty of the Highly Pathogenic Avian Influenza (HPAI) H5N1 and its threat to human health. Up to now, no HPAI H5N1 has been detected south of the equator in Africa despite some endemic areas on the continent. However, outbreaks of HPAI H5N2 have occurred in farmed ostriches in South Africa and Zimbabwe in 2004 and 2005. The role of wild birds and more particularly waterfowl in the maintenance and spread of AIV has been intensively investigated in recent years. However, the role of wild birds as spreader of AIV at a local scale from waterfowl to domestic species (namely potential bridge species) has received little attention. Here we use the risk analysis approach to answer the question: what is the risk of spread of a HPAI strain through bridge species in four avian compartments in a Zimbabwean ecosystem once it has been introduced in one of the compartments. The four avian compartments are: waterfowl community on two lakes (Chivero and Manyame) 35 km west of Harare; intensive poultry farms; backyard chicken systems; and ostrich farms, all in a 10 km radius of the lake. In order to estimate the epidemiological interactions between bird compartments, we use bird census data (counting of wild birds in 15 to 34 wild and domestic sites every two months for 1 to 3 years). We calculate indices of shared community of wild birds between sites at the same time and can compare the transmission probability from one compartment to the next. We observed high inter-annual and intra-annual variability in the index calculated, indicating that these epidemiological interactions are difficult to predict from one year to another, despite some relatively regular peak season. However, our findings suggest that in this Zimbabwean ecosystem, there are only a few key species visiting the ecosystem at specific time of the year which constitutes the majority of the epidemiological interactions between compartments (e.g., barn swallow, *Hirunda rustica*, red-billed quelea, *Quelea quelea*). This has direct implications for the management of the HPAI risk if it was introduced in this ecosystem. It shows that management options to limit contact between production stock and these key bridge species during high risk seasons are possible. From a more theoretical point of view, it would be interesting to investigate bridge species communities in other ecosystems to assess if our findings are site-specific or not. If not, in addition to offer a framework to identify potential bridge species at the ecosystem level, our approach could help exploring potential general rules characterising bridge species communities in different ecosystems.