

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

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Abstract

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^{3,5,6}. 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 2005⁴. The role of wild birds and more particularly waterfowl in the maintenance and spread of AIV has been intensively investigated in recent years³. 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 attention¹.

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 compartments² are: waterfowl community on two lakes (Chivero and Manyame) 35kms west from Harare; intensive poultry farms; backyard chicken systems; and ostrich farms, all in a 10kms 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.

Selected literature

1. Caron A, de Garine-Wichatitsky M, Gaidet N, Chiweshe N, Cumming GS 2010 Estimating dynamic risk factors for pathogen transmission using community-level bird census data at the wildlife/domestic interface 2010 *Ecology and Society* 15: 25
2. Caron A, Gaidet N, de Garine-Wichatitsky M, Morand S, Cameron EZ 2009 Evolutionary biology, community ecology and avian influenza research 2009 *Infection, Genetics and Evolution* 9: 298-303

3. Olsen B, Munster VJ, Wallensten A, Waldenstrom J, Osterhaus AD, Fouchier RA 2006 Global patterns of influenza A virus in wild birds 2006 *Science* 312: 384-388
4. Sinclair M, Bruckner GK, Kotze JJ 2009 Avian Influenza in ostriches: epidemiological investigation in the Western Cape Province of South Africa 2009 *Veterinaria Italiana* 42: 69-76
5. Webster RG, Bean WJ, Gorman OT, Chambers TM, Kawaoka Y 1992 Evolution and Ecology of Influenza A Viruses 1992 *Microbiological Reviews* 56: 152-179
6. Webster RG, Peiris M, Chen H, Guan Y 2006 H5N1 outbreaks and enzootic influenza 2006 *Emerging Infectious Diseases* 12: 3-8