

# An investigation of social dynamics in Cape buffalo and implications for disease transmission at wildlife/domestic interfaces in the Great Limpopo Transfrontier Conservation Area

ALEXANDRE CARON<sup>1,2,3\*</sup>, MICHEL DE GARINE-WICHATITSKY<sup>1,2,6</sup>, EVE MIGUEL<sup>1</sup>, VLADIMIR GROSBOIS<sup>1</sup>, CHRIS FOGGIN<sup>4</sup>, MARKUS HOFMEYR<sup>5</sup> & DANIEL CORNELIS<sup>1,2</sup>

<sup>1</sup> CIRAD, UPR AGIRs, Montpellier, France

<sup>2</sup> CIRAD, RP-PCP, Harare, Zimbabwe

<sup>3</sup> Mammals Research Institute, University of Pretoria, Pretoria, South Africa

<sup>4</sup> Wildlife Veterinary Unit, Governmental veterinary Services, Zimbabwe

<sup>5</sup> South Africa National Parks, Kruger National Park, South Africa

<sup>6</sup> Department of Biological Sciences, University of Zimbabwe, Zimbabwe

---

**Abstract:** In southern Africa, TransFrontier Conservation Areas (TFCAs) are promoting the sustainable coexistence between Mankind and Nature, and are seeking to find a balance between wildlife conservation, agricultural production and natural resource use. In these TFCAs, the various land use types include wildlife/domestic interfaces prone to create human/wildlife conflicts. Amongst those conflicts, disease transmission between buffalo and cattle (and potentially to human for zoonoses) is a serious concern. In this study, we GPS-tracked buffalo and cattle herds in the Great Limpopo TFCA in order to understand disease transmission and estimate the risk of emerging pathogen spillover. This protocol makes it possible to investigate inter-species contacts along multiple spatiotemporal windows, and thus risks of transmission of various pathogens. Regarding buffalo specifically, Adult females were shown to range within stable home ranges, displaying little overlap with adjacent buffalo herds. However, inter-individual association patterns strongly challenged the standard concept of herd. Interestingly, two of the young GPS-tracked females displayed long-range (70-90kms) movements in a few week times, linking distant buffalo populations across communal lands. This shed light on a poorly described behaviour that has major implications in disease ecology in the GLTFCA. We conclude by discussing the implication of buffalo/cattle interactions for disease transmission, particularly in the context of transboundary disease transmission and by listing some hypotheses that will require testing in the near future to manage the health issue at buffalo/cattle interfaces in Africa.

---