

Using the community of pathogens to infer inter-specific host epidemiological interactions at the wildlife/domestic interface

A tool for exploring and anticipating emerging disease processes in their hot spots

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The incidence of Emerging Infectious Diseases (EIDs) in human and domestic species has been increasing during the last decades (1-3). Zoonoses or domestic animal's pathogens linked with wildlife constitute a quarter of the list of pathogens in these studies. The sanitary surveillance is concentrated on human, domestic species and a few wildlife flagship species. As a result of this bias in surveillance the majority of EIDs' events remains unnoticed. From Jones et al. (3), EIDs' emergences can be described into 2 step process: 1) Emergence *sensus stricto*; 2) Amplification. We will concentrate on the first step, characterised by hot spots of biodiversity in tropical habitat where new pathogens emerge at the wildlife/domestic interface, in target species. The study of EIDs in these hot spots is practically difficult: necessity to work with multiple-host systems, in remote areas, required multidisciplinary – epidemiology, ecology, social sciences-, lack of governmental investment in animal or public health etc. How does one get prepared to EIDs' events in such conditions in these areas where emergence is likely to occur but when the spill-over to target species has not yet happened?

We define the concept of Epidemiological Interaction (EI) as any ecological interaction resulting in the transmission of pathogen between 2 hosts. EIs are defined by their frequency, intensity and direction. The use of host population dynamics, movements and contacts to determine *a priori* EIs has already been presented (4, 5). Here, we suggest a different "pathogen approach" based on the shared community of pathogens between populations or species in a particular ecosystem as an *a posteriori* indicator of EIs. The study of prevalence data and molecular phylogeny of pathogen strains can highlight EI and help drawing a network of EI between host populations. We explore this idea through the recent emergence of bovine tuberculosis (bTB) on the Zimbabwean side of the GLTFCA (6). Can some ecological and epidemiological data about other pathogens (FMD, Brucellosis, tick-borne diseases, RVF, etc.) in this ecosystem help stakeholders to predict the spread of bTB in this ecosystem? If yes, in a resource-limited environment, the surveillance and control options can be targeted. We conclude by investigating the possibility of identifying ubiquitous pathogens which could be indicators – patho-indicators – of the EI network in a given ecosystem.

References

1. Cleaveland S, Laurenson MK, Taylor LH. Diseases of humans and their domestic mammals: Pathogen characteristics, host range and the risk of emergence. *Philosophical Transactions of the Royal Society of London Series B Biological Sciences*. 2001; 356(1411): 991.
2. Jones KE, Patel NG, Levy MA, Storeygard A, Balk D, Gittleman JL, et al. Global trends in emerging infectious diseases. *Nature*. 2008; 451: 990-4.
3. Taylor LH, Latham SM, Wolhouse MEJ. Risk Factors for human disease emergence. *Philos Trans R Soc Lond B Biol Sci*. 2001; 356: 983-9.
4. Caron A, Gaidet N, de Garine-Wichatitsky M, Morand S, Cameron EZ. Evolutionary biology, community ecology and avian influenza research. *Infect Genet Evol*. 2009; 9(2): 298-303.
5. Caron A, De Garine-Wichatitsky M, Gaidet N, Chiweshe N, Cumming GS. Estimating dynamic risk factors for pathogen transmission using community-level bird census data 2010; Submitted.
6. de Garine-Wichatitsky M, Caron A, Gomo C, Foggin C, Pfukenyi D, Dutlow K, et al. Spread of wildlife tuberculosis across the Great Limpopo Transfrontier Conservation Area? ; Submitted.