

01.003

**Satisficing control options for influenza**

G.M. Leung

*The University of Hong Kong, School of Public Health, Hong Kong/CN*

Drawing on real-life examples from past influenza outbreaks, particularly 2009 H1N1pdm and 2013 H7N9, this talk will highlight the state of the science in influenza preparedness research, in mitigation of annual epidemics, the next pandemic and newly emerging outbreaks otherwise. It will draw on the multiple disciplines of ecology, evolutionary biology, virology, epidemiology, and mathematical sciences. A “One Health” approach that recognises the zoonotic driver of epidemics will be emphasised. Particular attention will focus on the multiple strands of global health initiatives contributing to the common goal of health and human security against influenza and its sequelae.

<http://dx.doi.org/10.1016/j.ijid.2016.11.015>

01.004

**Zoonotic diseases at the human-domestic animal - Wildlife interface in Southern and Eastern Africa**

R.R. Kazwala

*Sokoine University of Agriculture, Public health, Morogoro/TZ*

Southern and East African Countries are rich in ecosystems where human, livestock and wildlife populations are in close proximity and serviced by the ecosystems services such as water, land and fauna resources. In the course of mingling there are possibility of sharing pathogens which consequently may lead to outbreaks of zoonotic agents in the concern populations. In Tanzania various studies were conducted in the past decade which were determining the presence of zoonotic agents, the burden in individual populations, the dynamics and drivers of disease transmissions at the human-livestock-wildlife interfaces..

Using serological and molecular biological techniques, a cross sectional studies were conducted in human and animal populations at an various ecosystems neighbouring wildlife conservation areas of Tanzania. The selected agents studied included bacterial and viral zoonotic agents.

Microscopic Agglutination Test (MAT) was carried out to test for leptospira antibodies in 1,351 livestock and 42 wildlife. The overall seroprevalence was 26.35% and 28.57% with serovars of *Leptospira interrogans*; Hardjo, Hebdomadis, Grippotyphosa, Sokoine and Lora were common. Similarly, 30% of 267 human samples tested positive, for almost similar serovars. Sequencing alignment on 16S ribosomal DNA gene, suggested that serovars of *Leptospira interrogans* were common among human and animal populations. Using Rose bengal as a screen test, a total of 5.57% and 11.9% of sera from domestic animal and wild animals were found to be positive respectively. The IDEXX Q Fever ELISA for the detection of antibodies against *Coxiella burnetii* was employed and 40 of 587 (6.8%) cattle and 15 of 22 (68.2%) of wild animals were found to have antibodies against *C. brunetti*. RVF virus testing conducted IgG and IgM ELISA revealed, thirty two out of 800 (4%) and eight out of 42 (19%) from domestic animals and wildlife tested positive for IgG respectively. Of the 440 sera from domestic animal tested for IgM only 15 (3.4%) had IgM, while all wild animal samples were negative. Under the PREDICT Project protocol, a total of 268 wildlife animal species (Bats, Rodents and Non human primates) were subjected

to molecular virology diagnostic tests and revealed the presence of 64 viruses including 48 novel viruses. The identification of the novel viruses is still underway to determine the peculiar genus and species. Using the geographical information system, the locations for infected animals and humans congregated at same coordinates putatively indicate cross infections between two populations.

Findings from the present studies are providing important insight on presence of zoonotic agents which potentially may cause febrile illness among persons in frequent contact with animals and their products in the poor resources rural communities not only of Tanzania but across the developing world.

<http://dx.doi.org/10.1016/j.ijid.2016.11.016>

01.005

**Global early warning signs for health threats at the human animal ecosystem interface**

J. Pinto

*FAO, Rome/IT*

Diseases are emerging and reemerging rapidly in different ecosystems and regions. Disease surveillance is an approach widely used for detecting new pathogens through event-based or indicator surveillance efforts. We should ask ourselves why, as a global community, do we not implement a robust global surveillance and early warning system capable of detecting early signals of disease emergence? In addition, why is it that we continue to incur high costs of crisis mitigation, as in outbreaks of H5N1 HPAI, Nipah, MERS-CoV, Zika, Ebola, etc., particularly in regions associated with poor indicators of development and high vulnerability?

A new mindset is required to change the way that the international community coordinates and manages disease emergencies. Lessons learned from HPAI H5N1 outbreaks indicate that many affected countries continue to suffer disease impacts because of failures in implementation of technical strategies, poor practices and inadequate policies for disease prevention and control. A better understanding of the drivers of disease emergence is needed to help identify prompt actions that will tackle the issues at their source. A multidisciplinary approach is required to build a strong network of institutions and coordinate incidents at the complex human/animal/ecosystem interface. This approach also necessitates local capabilities and networks with epidemiologists or public health specialists capable of conducting disease outbreak investigations with the support of national or regional laboratory networks. Strengthening local capacities in epidemiological analysis, and the use of open analytical tools and GIS platforms, and new technologies (e.g. mobile devices, rapid diagnostics) are opening a new window of opportunities to enhance the quality and speed on how disease information is reported, detected, verified and communicated.

Disease information is available and circulating every day from the media, social networks, informal surveillance systems and official systems. Health information should be recognized as a public good and we should all practice due diligence to share publicly our data and information collectively. The international community should no longer wait for official reports to respond to disease threats. This new approach, however, requires a coordinated and joint effort among governments, communities, donors and international networks to invest in prevention systems with capability to identify early signals for the emergence, spill over and spread of animal pathogens (livestock production dynamics, trade issues and markets, climate change, civil unrest, consumer behaviors, etc.). A global and intelligent early warning system is needed to capture, analyze and transform data and information that can be used