

IN FOCUS

## Cross-disciplinary demands of multihost pathogens



M.E. Craft, P.L. Hawthorne, C. Packer & A.P. Dobson (2008). Dynamics of a multi-host pathogen in a carnivore community. *Journal of Animal Ecology*, 77, 1255–1262.

**The dynamics of infectious disease spread depend on host population contact structure. Heterogeneities in this contact structure can arise from various forms of demographic and spatial phenomena. Craft *et al.* (this issue) have constructed an exploratory simulation model of the spread of canine distemper virus through a multispecies carnivore community. Each species in this community is modelled with a contact structure reflecting host social organization, ranging behaviour, and likely interspecific contact patterns. The results are used to infer the possible roles of different species in determining the observed spatio-temporal incidence of canine distemper virus in Serengeti lions during an outbreak in 1993–94.**

The primary driver of infectious disease dynamics is transmission between individuals. Yet, in most important respects, we know remarkably little about this subject. Talk to any epidemiological modeller, and they will usually wave their arms in a reasonably informed way about prior expectations for the values of parameters in their models, until it comes to the rate of transmission between susceptible and infected individuals: the notorious  $\beta$  parameter (de Jong 1995; de Jong,

Diekmann & Heesterbeek 1995). At this point, they will look sheepish and admit that  $\beta$  can only be estimated by fitting the model to any available data. This is true even of well-studied pathogens in ‘simple’ observable systems like populations of cows, sheep, bacteria, and small children (Olsen, Truty & Schaffer 1988; Woolhouse *et al.* 1999; Burroughs, Marsh & Wellington 2000; Ferguson, Donnelly & Anderson 2001). When a pathogen can infect multiple host species, the transmission rate between species is an additional critical determinant of whether the pathogen can successfully invade

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a multispecies host community. Of course, it is even harder to collect empirical data on interspecific transmission rates, particularly when the host species are wild populations, and sick individuals rarely observed. So what progress can be made in advancing our understanding of the epidemiology of multihost pathogens in wildlife communities? The central premise underlying Craft's article is that epidemiological models in combination with studies of animal behaviour can inform our understanding of the spread of wildlife pathogens.

In 1993–94, a substantial epidemic of canine distemper virus (CDV) spread through lions in the Serengeti National Park, Tanzania, resulting in a 30% reduction in the lion population (RoelkeParker *et al.* 1996). Fortunately, this outbreak included Craig Packer's study population – which is by far and away the most intensively studied lion population ever. As a result, detailed data were collected on the dates that individuals in prides first seroconverted. Analysis of these data revealed a patchy, uneven progression of the infection through the population. The detailed observations on the movement of individual lions around this population (based in part on tracking VHF radiocollared individuals and in part through recognition of individually unique whisker-spot patterns) suggested that the movement patterns of lions could not account for the progression of disease through the population. Consequently, suspicion fell on alternative hosts that could potentially vector the virus between prides.

The Serengeti is home to a uniquely diverse community of competent host carnivore species. CDV isolates similar to those circulating in lions were recovered from spotted hyenas, a bat-eared fox, and a domestic dog (Carpenter *et al.* 1998). It is almost certain that a larger range of carnivores such as jackals, leopards, and other small carnivores are also competent host species (Alexander *et al.* 1994; RoelkeParker *et al.* 1996; Williams 2001). Craft *et al.* focus on the spread of disease through different combinations of lions, jackals and hyenas. They build a model that uses the accumulated understanding from decades of research on the social organization and movement of these species to speculate on different plausible contact structures, and then compare epidemic trajectories and spatial autocorrelation analyses of the resulting outbreaks with what is known about the actual spread of disease in the lions. While not enabling the identification of any unique combination of species, the simulation results suggest that only a mixed-species host assemblage could give rise to the patchy and sporadic incidence of CDV observed among the lion prides. In order to emulate the 1994 outbreak, the social structure of the alternative hosts should include high intraspecific transmission, while transmitting disease to lions at a low rate.

This paper serves to lift the curtain further on our ignorance of multihost infection dynamics. In single-species systems,  $\beta$ , the transmission parameter, can be estimated from data informative of disease incidence, and while the simple mixing processes often adopted by these models are certainly unrealistic, they may not be 'importantly wrong' in that they provide a usable guide to the fundamental dynamics of these epidemiological systems. However, it is almost never the case that incidence data can be collected from multiple-host

species in the same place, during the same time period, and therefore the 'who acquires infection from whom' matrix on which these dynamics are dependent remains inestimable. Consequently, debate about how to intervene in such multihost pathogen systems can rumble on largely uninformed for long time periods (witness the interminable debate regarding control of bovine tuberculosis in cattle and badgers in the UK).

One of the incalculable long-term benefits of funding an array of multidisciplinary research programmes in the same place is the unanticipated synergies that arise between these programmes. The extraordinary 'natural laboratory' that is the Serengeti-Mara ecosystem has attracted and inspired ecological study for over 60 years now (Sinclair & Arcese 1995; Sinclair *et al.* 2008). Different researchers studying lions, hyenas, jackals, their prey species, and the diseases that afflict them all, find themselves working in ever-shifting partnerships. For example, Craft's paper suggests a potentially productive liaison between behavioural ecologists and epidemiologists: if the relative contact frequency of these different carnivore species could be estimated through painstaking behavioural studies, then these relative contact patterns might be related to disease transmission through a single overall rate constant estimated by fitting the model to incidence-related data from perhaps just a single species. For example, the relative frequency of interactions between different carnivore species, and particularly the close encounters required to spread a disease like CDV, could be estimated from observations at the kill sites of prey. Of course, these interactions at kill sites may give a biased impression of a wider range of other forms of interactions. Furthermore, because we do not understand exactly which interactions result in the transmission of different pathogens, 'who contacts whom' matrices may not be exactly proportional to 'who acquired infection from whom' matrices. Such an approach also assumes that the behaviour of infected individuals is essentially the same as uninfected individuals, and we know this is not necessarily true. However, it is a good idea and definitely worth a try.

Seroprevalence data of the sort used in Craft *et al.*'s paper provides a rare keyhole through which to observe patterns of pathogen exposure in wild populations. However, our understanding of how these patterns are generated remains insufficient because issues of demographic flux, immunologic processes, and biases in exposure complicate using these often statically observed patterns of exposure. Models provide an obvious way of remedying this deficiency. Emerging access to new technologies will provide additional options for studying transmission. Genetic data on pathogens acquired from infected hosts can enable transmission trees to be estimated at much finer temporal and spatial scales than previously thought. This is certainly true of RNA viruses with their high mutation rates (Lembo *et al.* 2007; Cottam *et al.* 2008). Global positioning system (GPS) collars and other types of biotelemetry tags are now used with increasing effect to understand the movement of individuals (Patterson *et al.* 2008). In the next few years, we can expect advances in the physical technology (Prange *et al.* 2006), and the accompanying analyses (Morales *et al.* 2004), to be extended to study contact patterns within and between

different species. A further area that is likely to play a key role in advancing our understanding of transmission is statistical. Hidden state-space models can be fitted using Bayesian techniques such as Markov chain Monte Carlo and used to infer the dynamics of 'hidden' processes and variables, such as unobserved infections and latently infected individuals inevitable in the study of natural populations (Clark & Bjornstad 2004; Streftaris & Gibson 2004; Clark & Gelfand 2006).

Advancing our understanding of the dynamics and control of multihost pathogens requires overcoming particularly challenging problems at the interface of population biology, animal behaviour, community ecology, epidemiology, and statistics. Forming effective cross-disciplinary research collaborations to tackle these challenges will be exceedingly difficult. If we want to control multihost pathogens, it will be essential.

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