

# Dynamics of a multihost pathogen in a carnivore community

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## Summary

1. We provide the first theoretical analysis of multihost disease dynamics to incorporate social behaviour and contrasting rates of within- and between-group disease transmission.

2. A stochastic susceptible–infected–recovered (SIR) model of disease transmission involving one to three sympatric species was built to mimic the 1994 Serengeti canine distemper virus outbreak, which infected a variety of carnivores with widely ranging social structures. The model successfully mimicked the erratic and discontinuous spatial pattern of lion deaths observed in the Serengeti lions under a reasonable range of parameter values, but only when one to two other species repeatedly transmitted the virus to the lion population.

3. The outputs from our model suggest several principles that will apply to most directly transmitted multihost pathogens: (i) differences in social structure can significantly influence the size, velocity and spatial pattern of a multihost epidemic; and (ii) social structures that permit higher intraspecific neighbour-to-neighbour transmission are the most likely to transmit disease to other species; whereas (iii) species with low neighbour-to-neighbour intraspecific transmission suffer the greatest costs from interspecific transmission.

**Key-words:** African lion, canine distemper virus, disease transmission, multihost model, social structure

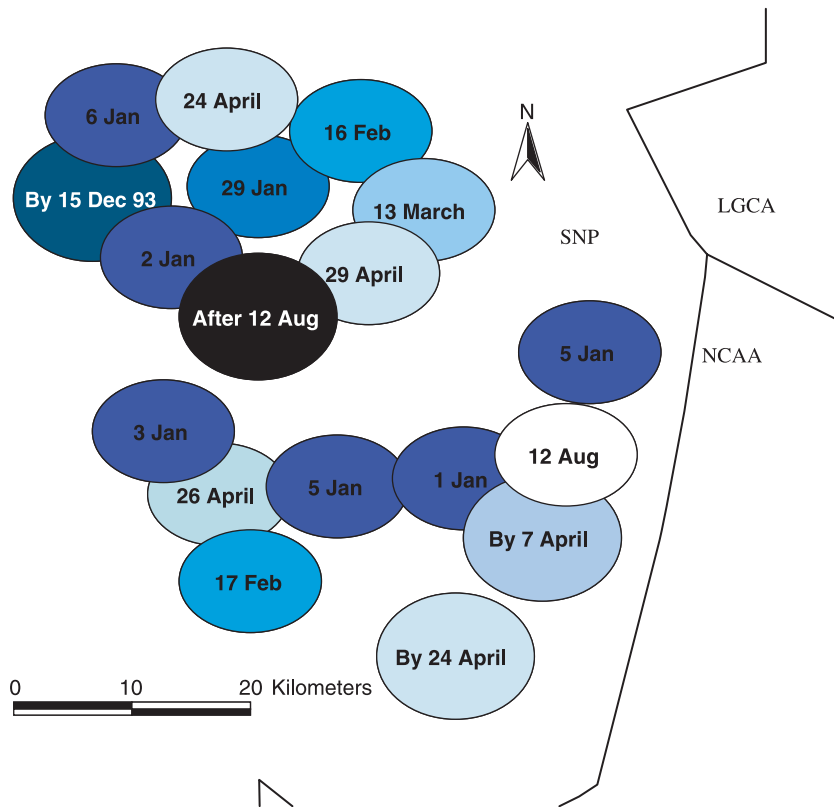
## Introduction

Multihost pathogens are likely to exhibit spatiotemporal dynamics different from those of pathogens that infect only a single host species. From one perspective, multiple hosts could be considered an additional form of heterogeneity that divides the total host population into subpopulations, between which transmission occurs at a different rate from that within each subpopulation. Single-species ‘subpopulation’ approaches (with multiple scales of mixing) have been successfully developed to examine disease transmission between sexes in the case of sexually transmitted diseases (May & Anderson 1987; Anderson 1991); between children of different ages (measles, mumps, rubella) (Anderson & May 1985); people living in regions, cities and villages of different sizes (measles, influenza) (May & Anderson 1984; Grenfell & Bolker 1998; Grenfell, Bjornstad & Kappey 2001; Viboud *et al.* 2006); and hosts living as a metapopulation in different patches of habitat (Swinton *et al.* 1998; McCallum & Dobson 2002; McCallum & Dobson 2006).

However, using subpopulation approaches on multihost pathogens is not as straightforward as it seems; different host species might vary in their response to infection, have varying contact patterns based on social behaviour, and have different spatial distributions across the landscape (Dobson 2004). Due to these complexities, previous work on multihost models has made simplifying assumptions and assumed that each host population is well mixed, and specifically ignored heterogeneities due to social organization (Dobson 2004; Fenton & Pedersen 2005; McCallum & Dobson 2006). We have, therefore, developed a general stochastic, spatial model of a disease outbreak in two and three host-species communities with widely ranging social structures. Our model structure is based on a 1994 outbreak of canine distemper virus (CDV) in the Serengeti ecosystem that killed one-third of the lion population (*Panthera leo*) (Roelke-Parker *et al.* 1996; Kock *et al.* 1998; Packer *et al.* 1999). CDV is a contagious multihost virus spread by aerosol inhalation, which affects all carnivore families. Infected animals either die or obtain lifelong immunity (Appel 1987; Williams 2001).

Because lions are territorial, and most opportunities for disease transmission between social groups involve immediate neighbours (M.E.C., unpublished data), the erratic and

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**Fig. 1.** The observed dynamics of a canine distemper outbreak in the Serengeti lion study population in the southeast Serengeti National Park (SNP) near the Ngorongoro Conservation Area Authority (NCAA) and Loliondo Game Controlled Area (LGCA). Each oval represents a lion pride. The time course was determined by either (a) date of first observed death in a pride; or (b) date of sampling for the first seropositive individual in the pride. Prides infected early in the epidemic are coloured dark blue, those infected later in the epidemic grade through to white. One pride remained uninfected (black).

discontinuous spatial pattern of CDV spread in the 1994 epidemic seems unlikely to have resulted solely from lion-to-lion transmission (Fig. 1). During the 1994 outbreak, the same CDV variant was responsible for deaths in spotted hyenas (*Crocuta crocuta*) (Haas *et al.* 1996; Roelke-Parker *et al.* 1996; Carpenter *et al.* 1998), while jackals (*Canis adustus*, *Canis aureus*, *Canis mesomelas*) also showed CDV-like symptoms and subsequently tested positive for CDV antibodies (Alexander *et al.* 1994; Roelke-Parker *et al.* 1996).

Hyenas and jackals had the potential to transmit CDV to lions, as the two species are more abundant than lions (Campbell & Borner 1986), and frequently interact with lions at kills (Schaller 1972; Cleaveland *et al.* 2008). While lions, hyenas, jackals, bat-eared foxes (*Otocyon megalotis*) and potentially many other carnivore species (e.g. leopards, *Panthera pardus*) were affected by the 1994 CDV outbreak (Roelke-Parker *et al.* 1996), our most detailed data come from the long-term monitoring of the Serengeti lions (Packer *et al.* 2005). We therefore treat lions as the sentinel species when comparing the observed pattern of infection in the 1994 lion population with the model's CDV spatial spread.

#### QUESTIONS

We developed a stochastic simulation model to capture the general spatial and temporal patterns observed in the 1994 CDV outbreak. Although the model is based on the lion outbreak, it has been developed to provide more general insights into disease outbreaks in other communities, where multiple host species are susceptible to infection by the same

pathogen. In particular, we ask whether differences in territorial social structure affect the spatial and temporal pattern of disease outbreaks, and if the time course of the epidemic is sensitive to different rates of within- vs. between-species interaction. Social organization due to territorial behaviour divides intraspecific transmission into two major components: within and between groups. Within-group transmission can occur during normal social interactions (feeding, grooming), whereas between-group transmission can occur during fights over food and territory, or during immigration events. Interspecific transmission occurs when multiple species feed together or during intraguild predation events.

We performed a set of simulations that examine the epidemic dynamics of a directly transmitted pathogen involving multiple host species with contrasting social organizations (e.g. isolated vs. well connected territorial structures), characterized by different within- and between-group transmission rates. After exploring the epidemic dynamics for each species in isolation, we examine the consequences of coexistence between pairs of species using high and low rates of interspecific transmission. Finally, we ask whether the coexistence of three hosts differs in any substantive way from any two-species scenario.

We use the simulation to ask:

How do within- and between-group contact patterns affect the incidence, rate of spread, probability and spatial pattern of infection in multiple hosts with coexisting pathogens?

How do the model results compare with the observed outbreak?

## MODELLING APPROACH

The model describes the spatial and temporal dynamics of a pathogen in a spatially structured, multihost community. The habitat is divided into a two-dimensional grid of 625 patches, with each patch containing a local population of each species. Because of the natural boundaries of the Serengeti ecosystem, we chose not to wrap the edges of the simulated habitat. Infection is spread within local populations, between different species occupying the same patch, and between any populations/species occupying the eight neighbouring patches. The pathogen is modelled in a stochastic, density-dependent, susceptible–infected–recovered (SIR) framework. The model was programmed in C.

The importance of group size to pathogen persistence is well known (Swinton *et al.* 2001; Park, Gubbins & Gilligan 2002; McCallum & Dobson 2006), so we held group size constant across species and across social groups in order to isolate the effect of social organization. Each patch begins with 10 individuals of each species. An individual may be categorized in one of three states: S (susceptible), I (infected) or R (recovered). All individuals, except an initially infected source, begin the simulation in state S. Transitions occur from S → I (infection) and from I → R (recovery). During each time-step, we determine the probability of a susceptible individual becoming infected,  $p_{S \rightarrow I}$ , and of an infected individual recovering (either dying or obtaining lifelong immunity),  $p_{I \rightarrow R}$ . The number of actual transitions is drawn from a binomial distribution,  $B(n, p)$ . For the infection transition,  $n$  is the number of susceptible individuals in the group, while for the recovery transition,  $n$  is the number of infected individuals.

The probability that a susceptible individual  $i$  will be infected depends on the number of infections in its own social group, interspecific transmission within the same patch, and intra- and interspecific transmission from neighbouring patches. Two ‘who acquires infection from whom’ matrices (WAIFW; Anderson & May 1991) characterize the force of infection between individuals of each group; let  $\beta_{w,ij}$  represent within-patch transmission and  $\beta_{B,ij}$  represent between-patch transmission. The total probability of infection is given by:

$$1 - \exp \left[ - \left( \sum_{j \in S_L} \beta_{w,ij} I_j + \sum_{j \in S_N} \beta_{B,ij} I_j \right) \right]$$

where  $S_L$  is the set of groups sharing the local patch and  $S_N$  represents the groups in neighbouring patches and  $I_j$  is the number of infected individuals in group  $j$ . Each infected individual has a fixed probability,  $\mu$ , of recovering.

Interspecific  $\beta$  values are taken as a weighted average of the intraspecific values so that

$$\beta_{ij} = \beta_{ji} = \frac{1}{2}c(\beta_{ii} + \beta_{jj}),$$

where  $c$  describes the level of interspecific interactions (or coupling). We used two different values of  $c$ , designated ‘high’ and ‘low’ (0.2, 0.01, respectively) for the multispecies simulations.

**Table 1.** Relative rates of within- and between-group transmission

Resembles	$R_0$ within-group	$R_0$ between-group
Lion	>1 (1.9)	<1 (0.3)
Hyena	>1 (1.1)	>1 (1.1)
Jackal	>1 (1.5)	<1 (0.7)

Within- and between- $R_0$  values are calculated by  $n(1 - e^{-\beta/\mu})$ , where  $n$  is the number of susceptible individuals that might be contacted by the initially infected individual,  $\beta$  is the infection rate per susceptible individual, and  $\mu$  is the recovery rate. The model treats transmission from the initial infected to each susceptible as an independent Poisson process with rate  $\beta$  and duration  $1/\mu$ . The probability that each susceptible individual is infected is then  $p_i = 1 - P[\text{no infection}]$ , and the expected total number is  $np_i$ .

$n_{\text{local}} = 9$ ;  $n_{\text{nbr}} = 80$ ;  $\mu = 0.1$ .

The value of the average reproductive rate of the pathogen is defined as  $R_0$ . In general, a pathogen can persist only when  $R_0$  is >1 (when each infected individual infects at least one other individual). Species’ within- and between-patch transmission rates were chosen so that the  $R_0$  values in a single-species habitat equalled 2.2. CDV is closely related to phocine distemper virus, for which the empirically estimated  $R_0$  is 2.8 (Swinton *et al.* 1998). Different social systems were modelled by choosing different relative rates of within- and between-group transmission (Table 1).

In the Serengeti, the African lion lives in territorial social groups (prides) consisting of related females and their dependent offspring. Before the 1994 epidemic, average pride sizes (excluding cubs <3 months) were 10 individuals (M.E.C., unpublished data) defending territories ranging from 15 to 150 km<sup>2</sup> (Mosser 2008). Lions form fission–fusion groups where prides are in frequent physical contact, but only occasionally contact their neighbours during territorial defence or fights over food (Schaller 1972; M.E.C., unpublished data). Thus the within-patch (or within-pride) transmission rate for lions will be far higher ( $R_0 > 1$ ) than between-patch transmission ( $R_0 < 1$ ).

The spotted hyena lives in social groups (clans) averaging about 45 individuals per clan (Hofer & East 1995). These hierarchical clans consist of related females and immigrant males who defend exclusive group territories (16–55 km<sup>2</sup>) and encounter their neighbours during territorial clashes, or when feeding at the same carcass (Hofer & East 1993a). Additionally, Serengeti hyenas have a unique feeding adaptation where they commute to migratory prey and associate with non-clan members at waterholes and resting sites (Hofer & East 1993b). Thus hyenas are expected to have high within-patch transmission (but contact each other less than lions), as well as high between-patch transmission.

Jackals live in small family groups of two to four, who are in close contact with each other (Moehlman 1983). Serengeti golden and black-backed jackals actively defend discrete territories ( $\approx 2\text{--}4$  km<sup>2</sup>) from neighbours; they also make extra-territorial forays to water sources and large mammalian kills (Moehlman 1983). We therefore consider each ‘patch’ of 10 individuals to consist of two to five loosely connected groups of jackals. Although they interact with each other less

frequently than pridemates, jackals contact individuals from neighbouring patches more frequently than lions.

Infections were introduced in a single individual at the edge of the grid to mimic a pathogen introduced from domestic dogs at the edge of the park (Cleaveland *et al.* 2000). We ran 150 simulations for each combination of species. To check whether changes in disease dynamics were due to social structure rather than to a simple increase in overall population size, we ran controls where the same species was coupled with itself within separate partitions of the same patch. Each simulation ran until all infections disappeared. For each species, we also varied the within- and between-group transmission rates to confirm that the results presented here were representative of the overall range of possible outcomes.

We used the package *NCF* (Bjornstad & Falck 2001) for R (R Development Core Team, 2006) to evaluate the spatial pattern in both simulated and observed outbreaks. For each time-step (day) in the simulated outbreaks, we entered the number of active infections per grid square (pride) into the nonparametric correlation function (*ncf*). Because of the coarse-grained resolution of within-pride mortality in 1994, we constructed within-pride epidemic curves from the simulated outbreaks by aligning the simulated start dates, averaging the number of infections at each time-step, and rounding the values into discrete integers. We combined these simulated within-pride epidemic curves with the observed first death date per pride and spatial location, to create a complete time-series for the observed outbreak.

## Results

### SINGLE-SPECIES MODELS

Depending on contact structure, single-species epidemics produced epidemic curves that varied in impact (average cumulative number of infected hosts by the end of an outbreak), velocity (cumulative number infected per unit time), and probability and persistence of an outbreak (Figs 2 and 3). The outbreaks in hyenas produced the most infected individuals, spread with the highest velocity, and had the highest percentage of runs with epidemics (defined as lasting longer than 200 time-steps). In contrast, lions had the fewest infected individuals and slowest velocity; the disease generally burned out (few runs caused epidemics, and those that did were of shorter duration). Jackals produced values intermediate between lions and hyenas, except that infection persisted the longest in jackals (Fig. 2).

### MULTISPECIES MODELS

Compared with single-species models, any representation of a multihost system inevitably involves an increased number of susceptible hosts with a concomitant effect on disease transmission and persistence. We isolated the impact of an increased number of susceptibles by constructing a series of controls that effectively doubled or tripled the number of individuals in the single-species simulations. We could then

highlight the effects of social system *per se* by contrasting a lion-plus-lion model (which doubled the number of lions) to a lion-plus-hyena model (with the same number of individuals as the doubled-lion model, but with two different social systems).

### DO WITHIN- AND BETWEEN-GROUP CONTACT PATTERNS INFLUENCE THE IMPACT OF A PATHOGEN?

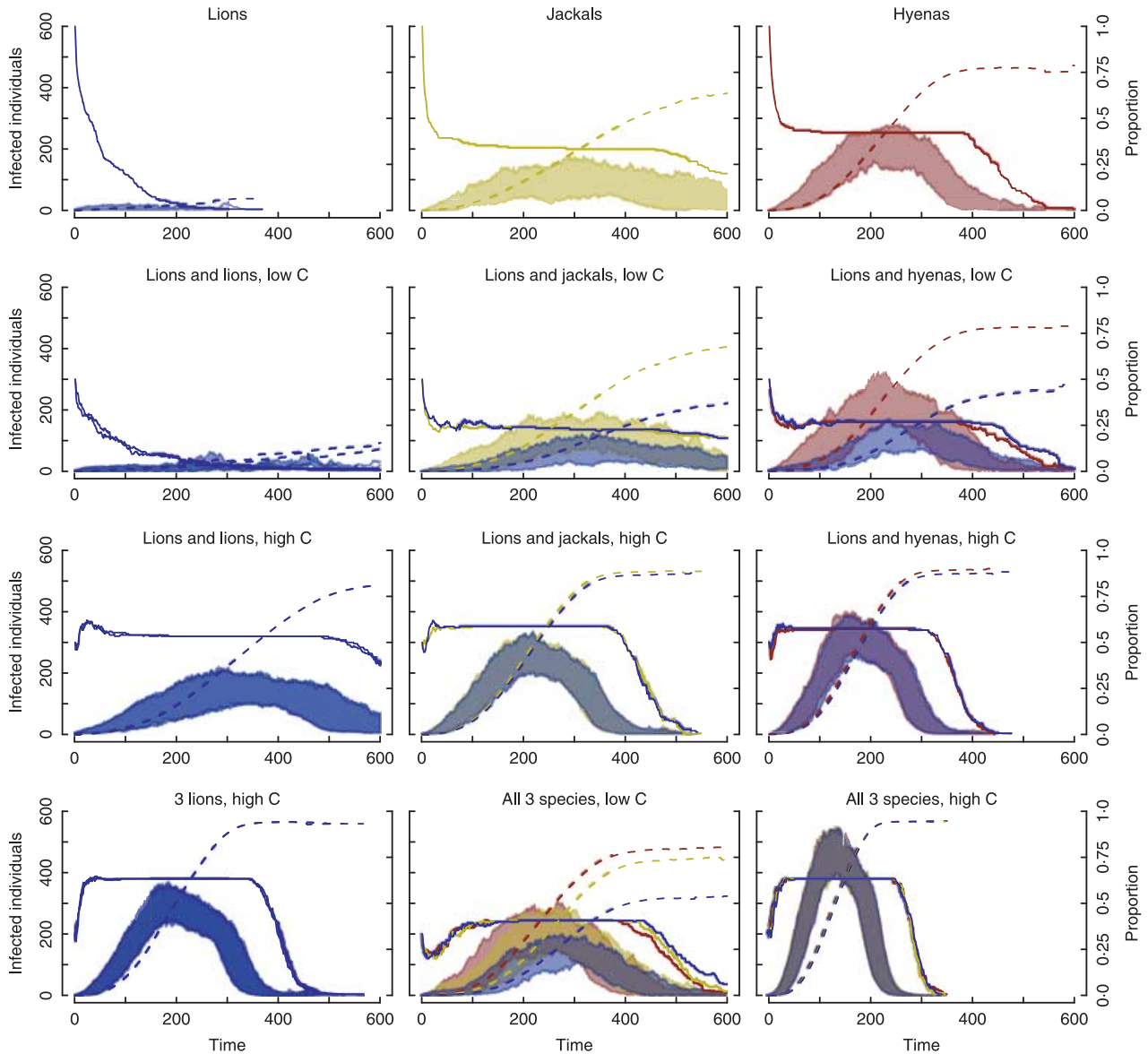
Adding a second or third host species (Figs 2 and 3a) increased the impact of the pathogen (average cumulative number of infected individuals in the first host species), although this was not always significant (see Supplementary material). For example, the number of infected hyenas did not increase significantly when hyenas were weakly coupled to another species, even to an overlapping control population of hyenas. However, many more lions were infected when weakly coupled with either hyenas or jackals than with a control population of lions. Note, though, that fewer jackals are infected when lions are weakly coupled with jackals, compared with the weakly coupled doubled-jackal control. This is due to the dilution effect of 'wasting' infections on less competent transmitters such as lions (Ostfeld & Keesing 2000). An amplification effect can be seen when hyenas (the most competent transmitters) are paired with lions, compared with the lion-plus-lion scenario. With high inter-specific connectivity, the overall increase in infecteds can largely be attributed to increased population size, because the doubled and tripled single-host-species scenarios are indistinguishable from the two- and three-host-species outputs.

### DO WITHIN- AND BETWEEN-GROUP CONTACT PATTERNS INFLUENCE THE RATE OF SPREAD OF THE PATHOGEN THROUGH THE SYSTEM OR THE PROBABILITY OF AN EPIDEMIC?

When additional species were added to a single-species epidemic with high coupling, the average velocity (number of infecteds per unit time) of the wave front increased, and there was a higher probability of an epidemic; but this was not always the case when species were loosely connected (Fig. 3b,c). For example, in hyenas, the velocity of infection and probability of an epidemic actually slowed down when weakly combined with one or two additional species. The controls illustrate that at high coupling, there are large effects of adding any additional species (regardless of social structure); but at low coupling, the social structure of the additional hosts can increase or decrease the velocity or probability of a large-scale epidemic.

### DO WITHIN- AND BETWEEN-GROUP CONTACT PATTERNS CHANGE THE SPATIAL SPREAD OF A PATHOGEN?

Spatial spread of single-species infections differed according to contact patterns (Fig. 4a). While the epidemic always travels in a wave-like pattern, the neighbour-to-neighbour transmission rate determined the extent of spatial spread.



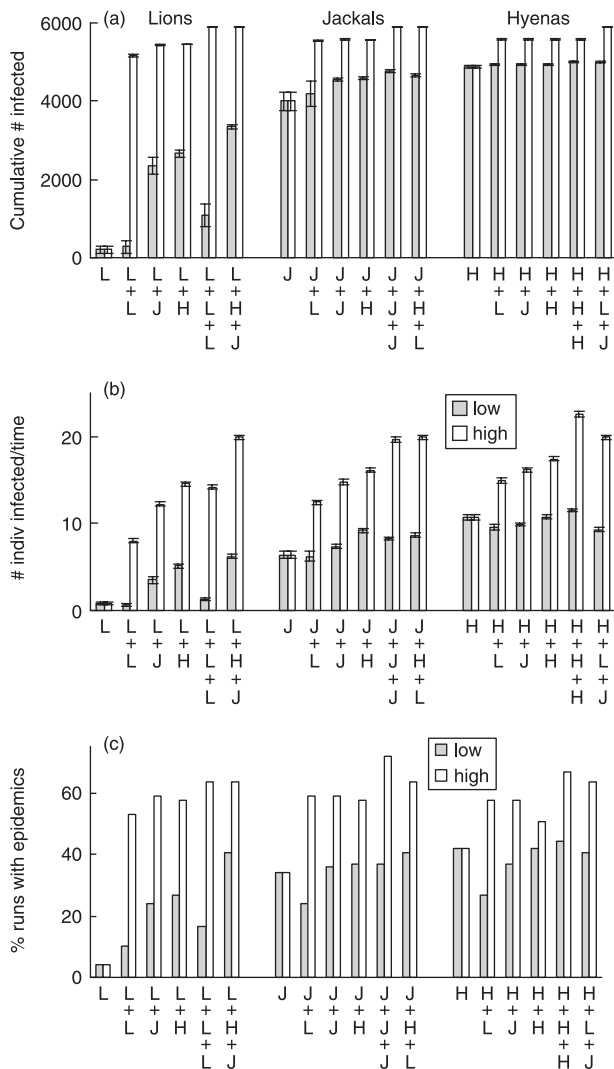
**Fig. 2.** Temporal dynamics of simulated epidemics. Single-species epidemics in lions, jackals and hyenas, and multiple-species epidemics when coexisting species are weakly vs. highly coupled (low  $C$  vs. high  $C$ ). Coloured zones indicate 10–90% quantiles of the number of infecteds in each species in runs where infections were still present (left  $y$ -axis). Solid lines, proportions of runs with an infection still present (right  $y$ -axis). Dashed lines, cumulative proportion of individuals that became infected during the course of the epidemic. Population size for each species, 6250 individuals.

Hyenas and jackals have high conspecific neighbour transmission, so there is extensive spatial spread no matter which other species is added to their community. Low neighbour-to-neighbour transmission in lions, however, limits the spatial spread of the pathogen unless the lions are tightly coupled with another species. When lions are loosely coupled with another species, occasional spill-overs from the more competent host cause smaller local outbreaks (Fig. 4b).

Overall, the finer resolution of spatial spread in two-host systems depended on the level of connectivity between species. With low coupling, most cells were infected by conspecific neighbours causing long chains of same-species infection; fewer cells were infected. With high coupling, each

species had a relatively equal chance of being infected by a different species, and more cells were infected (Fig. 4b). When the spatial nonparametric correlation function was plotted at low and high coupling, the spatial correlation was consistently higher with high coupling (Fig. 4c), indicating a more coherent, wave-like spread of infection. With the low coupling, correlation between infection times broke down only a few cells away, confirming a more local, patchy spread.

When all three species were loosely coupled together, the wave-like pattern was replaced by disconnected jumps in the spatial pattern of infection and uneven coverage of infection when viewed from the lion's perspective (there was still a



**Fig. 3.** (a) Average cumulative number of infected individuals for each of the species listed, in isolation and combined with one and two other species (L = lion, H = hyena, J = jackal). Grey bars, low-coupling; white bars, high-coupling; error bars, 95% CI. (b) Velocity of infection (number of infections per time-step) per combination of species. (c) Percentage of simulations ( $n = 150$ ) that cause an epidemic (defined as infection persisting longer than 200 time-steps).

strong wave formation in jackals and hyenas) (Fig. 4b). As in the two-host case, most cells were infected by their conspecific neighbour. But with high mixing, there was a high coverage of infecteds, most infections stemmed from interspecific contacts, and spatial pattern was more of a multispecies wave of infection than in the two-species case, although the timing of infection in lions was still slightly patchy. The ncf also showed higher correlation with high coupling, and less correlation with low coupling.

In addition, when we used different within- and between-group mixing parameters (species 1, 1·1, 1·1; species 2, 0·5, 1·7; species 3, 1·7, 0·5), our findings were consistent with the results obtained from the mixing parameters used in this model. Specifically, with the varied set of mixing parameters,

we also found that differences in social structure can significantly influence the size, velocity and probability of a multihost epidemic, especially with low interspecific coupling.

#### COMPARISON WITH OBSERVED OUTBREAK

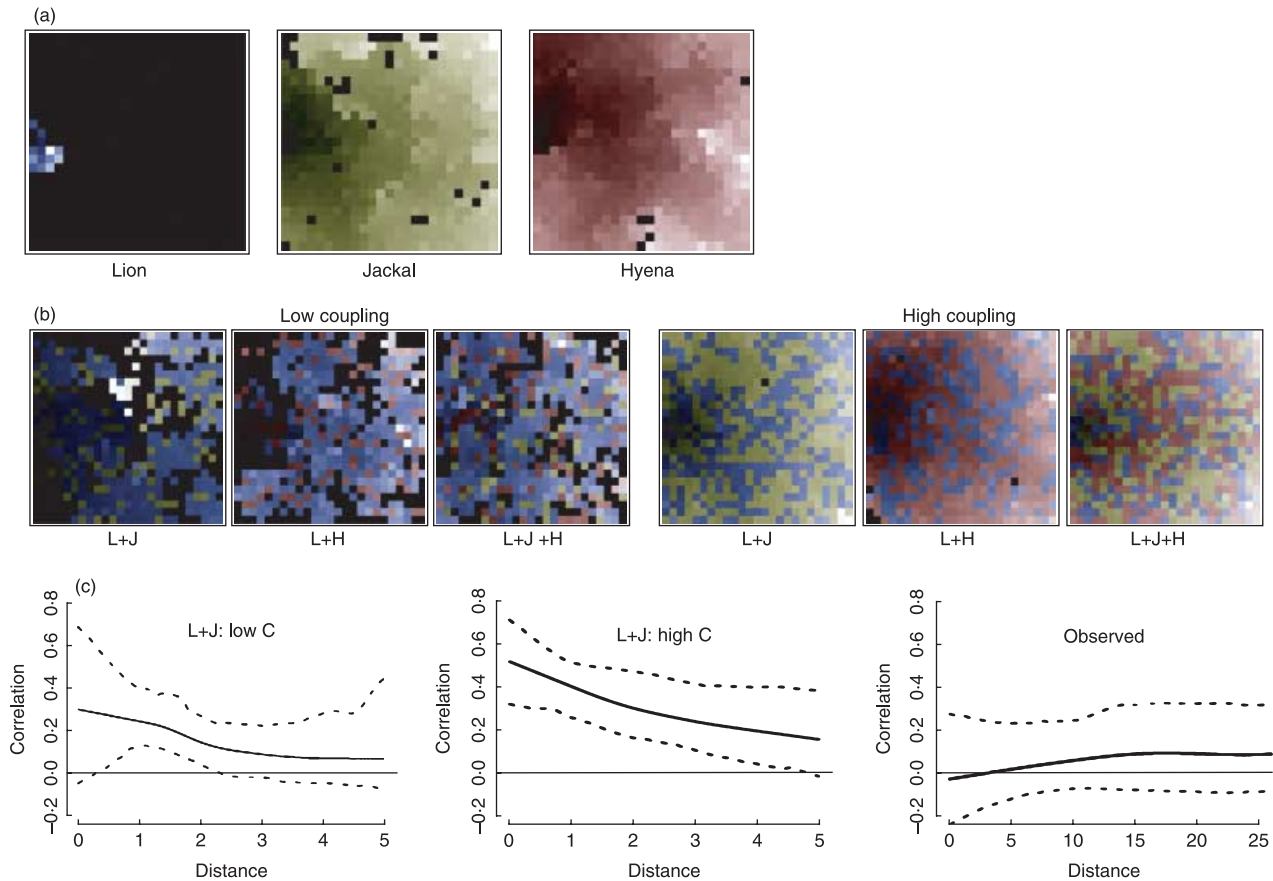
The low-coupling simulations generated spatial patterns that were more similar to the nonwave-like, patchy spread of CDV observed in the Serengeti lions. High-coupling models generated an obvious wave-like pattern with a high degree of spatial correlation that contrasted sharply with the observed outbreak (Fig. 4c).

#### Discussion

These results have implications that extend beyond pathogens of Serengeti carnivores. Our model suggests a number of general principles that will apply to most directly transmitted pathogens that can infect multiple host species: (1) differences in social structure can significantly influence the size, velocity and probability of a multihost epidemic; (2) social structures that permit higher intraspecific neighbour-to-neighbour transmission are the most likely to transmit disease to other species; and (3) species with low neighbour-to-neighbour intraspecific transmission are most vulnerable to interspecific transmission.

Deterministic models by Holt & Pickering (1985); Begon & Bowers (1994); Woolhouse, Taylor & Haydon (2001); and Dobson (2004) have consistently emphasized the importance of multiple scales of mixing, specifically the relative rate of within- vs. between-species transmission in determining the transient dynamics of infection. When interspecific transmission is high, our stochastic spatial model shows that the presence of multiple-host species is essentially equivalent to a larger susceptible host population. More hosts are infected, and the pathogen may have a significantly higher impact in species that could not sustain an outbreak in isolation. The combined population of species essentially acts as a single super species, incorporating the strongest parameters of each species. Thus the rate of disease spread can increase with the number of coexisting host species; the rate of interspecific transmission increases the cumulative number of hosts infected in all susceptible host populations; the probability of an extensive outbreak increases; and the number of individuals infected (and potentially dying) may be higher in host populations that would otherwise be too small or too dispersed to sustain the pathogen by themselves. Furthermore, adding a second species that is more effective at transmission produces an amplification effect; while a less-effective second species can cause a dilution effect (Keesing, Holt & Ostfeld 2006).

In the observed 1994 outbreak, hyenas and/or jackals feasibly could have acted as amplifying species by spreading the CDV through the more isolated lion prides and causing long-distance leaps in infection among prides. When we compared the observed CDV outbreak with the simulations, results were reasonably similar to the low transmission-rate



**Fig. 4.** (a) Spatial spread of infection from a single example of a simulation in lions, jackals and hyenas, respectively; (b) simulated multispecies epidemics involving lions. The colour of each simulated grid cell represents the source of infection in lions in a single example (blue, lion; yellow, jackal; red, hyena); colours grade from early (dark) to late (light) infection; uninfected cells are black. (c) Spatial correlations for simulated and observed outbreaks. For simulated epidemics, each plot shows mean estimates (solid line) and 95% bootstrap CI (dashed lines) based on 1000 randomly chosen  $5 \times 5$  subgrids. For the observed epidemic, each plot shows distance (km) vs. spatial correlation for mean estimate (solid line) and 95% bootstrap CI (dashed lines). NCF figures were similar for the other two-species combinations and the three-species scenario.

scenario. Based on our simplified model, we cannot say whether an outbreak restricted to hyenas, jackals and lions, or a larger combination of susceptible species (e.g. leopards, bat-eared foxes), could have created the observed outbreak, but rather that low interspecific contact rates feasibly could have accounted for the extensive coverage of CDV infection and erratic spatial spread seen in the Serengeti lions.

Multihost pathogens have particular importance for the management of endangered species. First, numerically abundant species will usually act as reservoirs of infection for endangered species that are, by definition, rare (McCallum & Dobson 1995; Funk *et al.* 2001; Woolhouse, Taylor & Haydon 2001). Second, infections would normally die out in any single-species system where the host experiences low levels of intergroup contact, but the risk of a persistent outbreak increases dramatically when it is exposed to a well mixed host species. Disease threats from sympatric species historically have been overlooked when considering reintroduction and translocation of social carnivores (focusing instead on the negative effects of kleptoparasitism

and intraguild predation) (Gusset *et al.* 2008). But any highly territorial species will be especially susceptible to multihost diseases in the presence of less sedentary species such as hyenas or evenly distributed species such as jackals. These risks should be considered when translocating territorial social species for reintroductions.

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## Supplementary material

The following supplementary material is available for this article online:

**Table S1.** Pairwise comparison between means for 95% CIs.

This material is available as part of the online article from: <http://www.blackwell-synergy.com/doi/full/10.1111/j.1365-2656.2008.1410.x>

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