A model-based approach for investigation and mitigation of disease spillover risks to wildlife: Dogs, foxes and canine distemper in central India

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ABSTRACT

Multi-host pathogens can pose a serious conservation threat when free-ranging domestic animal populations occur alongside susceptible populations of wild species. An example is canine distemper virus (CDV), which can occur at high prevalence in domestic dog (*Canis familiaris*) populations from which it may be transmitted (spillover) into wild carnivore populations. Effective management of such disease threats is hindered by our limited understanding of the the dynamics of interspecific CDV transmission in natural settings. We used a modeling approach to better understand CDV spillover threats to wild Indian foxes (*Vulpes bengalensis*) occurring in a protected grassland habitat in central India. An agent-based stochastic simulation model was built, and parameterized with data from ecological and epidemiological studies. Based on the sensitivity analyses of the model, the CDV incidence rate in dogs was most influenced by the proportion of roamer dogs in the dog population. The CDV incidence rate in dogs was also sensitive to the CDV introduction frequency in the dog population. The proportion of roamer dogs in the dog population also influenced the number of CDV spillover events. The basic reproductive number (R_0) for CDV in the model fox population was 0.85, indicating that CDV could not be independently sustained in the fox population. We used the model to explore potential management strategies to mitigate the risk of CDV spillover. Vaccination of local dog populations was an ineffective disease control strategy, while fox vaccination was highly effective. Interventions potentially resulting in lower contact rates between dogs and foxes, like reduction in village dog density and restricting dog movements in fox habitat, implemented in a sustained and integrated manner would be most effective in mitigating disease threats to foxes. Such modeling approaches can be used to better understand disease threats for other species of management concern, and to contrast potential management interventions.

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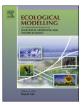
1. Introduction

Large populations of free-ranging domestic animals, such as dogs (*Canis familiaris*), occur in most of the developing world, and these free-mixing, mostly unvaccinated populations provide opportunities for the persistence and transmission of multi-host pathogens. Transmission of viruses from dog reservoirs has resulted in population declines and local extirpations in many threatened carnivore species, including both wild canids and non-canids (reviewed by Funk et al., 2001; Woodroffe et al., 2004; Cleaveland et al., 2006; Knobel et al., 2014). While vaccination of the dog reservoir or the target wildlife population have been

suggested as potential management options to protect wild carnivore species from such multi-host pathogens (Bronson et al., 2008; Bryan et al., 2011; Flacke et al., 2013; Laurenson et al., 1997), choosing appropriate management action is hindered by an incomplete understanding of the relative role of different host species in maintaining the pathogen within the broader multi-host species community.

Canine distemper virus (CDV) is one of the most important infectious microparasites of domestic and free-ranging carnivores worldwide. Dogs are often considered to be a primary reservoir of CDV and a source of infection for wild species, although CDV can persist in carnivore populations independent of dogs (Almberg et al., 2010). Epidemics in species such as African wild dogs (*Lycaon pictus*), African lions (*Panthera leo*), Caspian seals (*Phoca caspica*) and Lake Baikal seals (*Pusa sibirica*) have been attributed to CDV derived from dogs (Cleaveland et al., 2006). Mass

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vaccination of dogs has been successful in controlling the incidence of viruses such as rabies in free-ranging dogs and preventing transmission of dog rabies to other host species (Hampson et al., 2009; Kaare et al., 2009). Although CDV vaccination of dogs has been incorporated in some conservation management programs, its effectiveness in controlling CDV in dog populations remains to be fully evaluated (Prager et al., 2012; Belsare and Gompper, 2014).

An example of such difficulties in fully understanding the dynamics of interspecific CDV transmission in natural settings is observed in domestic canid–wild canid CDV transmission in rural Maharashtra, India. High prevalence of exposure (>72%) to CDV has been documented in free-ranging dog populations around the Great Indian Bustard Wildlife Sanctuary (GIB WLS), Nannaj in central India (Belsare and Gompper, 2013; Belsare et al., 2014). Indian foxes (*Vulpes bengalensis*) sampled in the same locale were also exposed to CDV (18%), and CDV-related mortalities were documented for multiple radiocollared foxes (Vanak et al., 2007; Belsare et al., 2014). To address this concern, the Maharashtra Forest Department (MFD), which oversees the GIB WLS, undertook mass dog vaccinations in the villages surrounding the GIB WLS as an approach to protecting wild carnivores inhabiting the protected area. Along with the mass vaccination programs, a study was undertaken to evaluate the applicability and efficacy of dog vaccination (against CDV, canine adenovirus and canine parvovirus) in free-ranging dog populations. The results indicated that vaccination failed to increase the proportion of dogs with antibodies against enzootic pathogens because a large proportion of unvaccinated adult dogs (the primary cohort that received targeted vaccination) were already antibody positive for these pathogens and therefore protected against these pathogens (Belsare and Gompper, 2014). Vaccination of adult dogs against CDV in such populations would be unnecessary, and would escalate the cost-benefit ratio of dog disease control programs. Further, given that most adult dogs are not infectious, it is not entirely clear how CDV could repeatedly move from the dog to the low density fox population.

An important outcome of this work was the realization that effective management of diseases in free-ranging populations requires a better understanding of the conditions favoring persistence of the pathogens in the system under study. Identifying a reservoir population and the mechanism of transmission between the reservoir hosts and the target hosts would help determine where the control efforts need to be directed. But undertaking experimental interventions to identify a reservoir host population, especially when wildlife species are involved, is a legally, ethically, and logistically difficult proposition. For instance, determining the mechanisms of disease transmission and estimating disease transmission rates in field situations pose serious challenges, as it depends upon repeated interventions requiring capture and handling of statistically large numbers of free-ranging animals. Thus, unequivocal identification of disease reservoirs and the underlying transmission mechanisms is often nearly impossible when the host populations are free-ranging.

Given the substantial uncertainty about the disease dynamics, a modeling approach can increase our understanding of the disease processes and define interventions that are epidemiologically and ecologically sound. Here we use an agent-based model of CDV dynamics in a two host system. We model CDV transmission between dogs and foxes in and around the GIB WLS based on our current best understanding of the system. The model provides opportunities to play out various scenarios under different assumptions, and explore potential disease control strategies. The modeling exercise also indicates the areas where further research could be directed.

2. Methods

2.1. Biological background

CDV is a multi-host pathogen with a global distribution, and causes severe, life-threatening diseases in dogs and wild canid species (Day et al., 2010). Canid species are the principal reservoir hosts for CDV (Greene and Appel, 2006). Several studies from across the globe have documented high seroprevalence of anti-CDV antibodies in free-ranging dogs, implying that CDV is endemic in such populations (Acosta-Jamett et al., 2011; Belsare and Gompper, 2013; Bronson et al., 2008; Fiorello et al., 2004; Kelly et al., 2005; Millán et al., 2013). In areas with large, free-ranging dog populations, most adult dogs have developed immunity to the pathogen (Belsare and Gompper, 2014). A constant supply of puppies ensures availability of susceptible dogs in the population, and persistence of CDV in dog populations is attributed to contact among recently infected and susceptible dogs (Greene and Appel, 2006). From 25 to 75% of susceptible dogs get subclinical CDV infection, while clinical disease is mostly seen in pups following loss of maternal antibody at 3–6 months of age (Williams, 2001). The infectious phase starts 1 week post-infection when the infected dogs start shedding the virus and may last 60–90 days, although shorter periods of virus shedding are more common. The virus is unstable in the environment and is rapidly destroyed outside the host (Greene and Appel, 2006).

The daily activity pattern of free-ranging dogs in areas bordering wildlife reserves or natural areas may involve ranging in wildlife habitat which brings dogs into contact with wildlife. Free-ranging dogs interact with native wildlife in a variety of ways (Gompper, 2014) and so the potential exists for transmission of pathogens from the abundant reservoir host (dogs) to sympatric wildlife. In the case of CDV, transmission of viral particulates between animals is via aerosol or contact with bodily excretions. The likelihood of such contact between infectious and susceptible animals can be mediated by resource distributions (e.g., food waste, crops, water sources) (Knobel et al., 2014). Furthermore, chasing, fights and simultaneous and sequential feeding events at carcasses have also been suggested as mechanisms facilitating contact and pathogen transmission (Kapil and Yeary, 2011).

Large fluctuations of Indian fox populations have been documented, and although disease has been suspected it has never been properly investigated (Manakadan and Rahmani, 2000; Vanak and Gompper, 2009). A study undertaken in the GIB WLS in 2006–2007 revealed a putative epizootic of CDV in Indian foxes, and the combination of low seroprevalence of anti-CDV antibodies in the population as a whole, but high mortality among recently exposed individuals, suggests high susceptibility and low probability of survival of foxes after exposure (Belsare et al., 2014).

2.2. Model description

The model was developed in NetLogo version 5.0.2 (July 27, 2012) (Wilensky, 1999). Here we provide the overview, general concepts underlying the model's design and details as per the ODD (overview, design concepts, and details) protocol for describing individual- and agent-based models (Grimm et al., 2006, 2010).

2.2.1. Purpose

The purpose of this model is to explore the transmission dynamics of CDV in a two-host system, comprised of an abundant dog population and a relatively low density Indian fox population in central India. Given the paucity of data, the modeling exercise was undertaken to elucidate the parameters that are most important for disease transmission in this system, suggest potential management strategies and prioritize future research.