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The effect of protected areas on pathogen exposure in endangered African wild dog (*Lycaon pictus*) populations

K.C. Prager [a,*], Jonna A.K. Mazet [a], Linda Munson [a,1], Sarah Cleaveland [b], Christl A. Donnelly [c], Edward J. Dubovi [d], Micaela Szykman Gunther [e,f], Robin Lines [g], Gus Mills [h], Harriet T. Davies-Mostert [i,j], J. Weldon McNutt [k], Gregory Rasmussen [j], Karen Terio [l], Rosie Woodroffe [a,m]

[a] Wildlife Health Center, University of California, One Shields Avenue, Davis, CA 95616, USA
[b] Boyd Orr Centre for Population and Ecosystem Health, University of Glasgow, Glasgow, United Kingdom
[c] MRC Center for Outbreak Analysis and Modelling, Department of Infectious Disease Epidemiology, Imperial College London, St. Mary's Campus, Norfolk Place, London W2 1PG, United Kingdom
[d] Animal Health Diagnostic Center, College of Veterinary Medicine, Cornell University, PO Box 5786, Ithaca, NY 14852-5786, USA
[e] Department of Wildlife, Humboldt State University, Arcata, CA 95521, USA
[f] Smithsonian Conservation Biology Institute, National Zoological Park, Front Royal, VA 22630, USA
[g] Zambian Carnivore Programme, PO Box 80, Mfuwe, Eastern Province, Zambia
[h] Kgalagadi Cheetah Project, Private Bag X5890, Upington 8800, South Africa
[i] Endangered Wildlife Trust, Private Bag X11, Modderfontein, Gauteng 1645, South Africa
[j] Wildlife Conservation Research Unit, Recanati-Kaplan Centre, Department of Zoology, Oxford University, Tubney House, Abingdon Road, Tubney, Abingdon OX13 5QL, United Kingdom
[k] Botswana Predator Conservation Project, Private Bag 13, Maun, Botswana
[l] University of Illinois, Zoological Pathology Program, Maywood, IL, USA
[m] Institute of Zoology, Regent's Park, London NW1 4RY, United Kingdom

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ABSTRACT

Infectious diseases impact African wild dogs (*Lycaon pictus*), but the nature and magnitude of this threat likely varies among populations according to different factors, such as the presence and prevalence of pathogens and land-use characteristics. We systematically evaluated these factors to assist development of locally appropriate strategies to mitigate disease risk. Wild dogs from 16 sites representing five unconnected populations were examined for rabies virus, canine distemper virus (CDV), canine parvovirus, canine coronavirus, and *Babesia* spp. exposure. Analyses revealed widespread exposure to viral pathogens, but *Babesia* was never detected. Exposure to CDV was associated with unprotected and protected-unfenced areas where wild dogs likely have a high probability of domestic dog contact and, in the case of protected-unfenced areas, likely reside amongst high wildlife densities. Our findings also suggest that domestic dog contact may increase rabies and coronavirus exposure risk. Therefore, domestic dogs may be a source of CDV, rabies and coronavirus, while wildlife may also play an important role in CDV transmission dynamics. Relatively high parvovirus seroprevalence across land-use types suggests that it might persist in the absence of spillover from domestic dogs. Should intervention be needed to control pathogens in wild dogs, efforts to prevent rabies and coronavirus exposure might be directed at reducing infection in the presumed domestic dog reservoir through vaccination. If prevention of CDV and parvovirus infections were deemed a management necessity, control of disease in domestic dogs may be insufficient to reduce transmission risks, and vaccination of wild dogs themselves may be the optimal strategy.

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1. Introduction

The African wild dog (*Lycaon pictus*) is one of the world's most endangered carnivores with <8000 animals, in <800 packs, remaining in the wild (IUCN/SSC, 2007, 2008). While habitat loss, reduced prey base and persecution were the major causes of historical decline and continue to be important threats to wild dog conservation (Woodroffe et al., 2007), evidence suggests that infectious disease may have also contributed to these declines (Woodroffe and Ginsberg, 1997). Currently, most wild dog populations are reduced to small numbers (⩽8 packs), and pathogens may now pose an even greater threat to long-term population viability due to stochastic extinction events (Ginsberg et al., 1995; Woodroffe and Ginsberg, 1997). Pathogens, such as rabies virus (Alexander et al.,

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[*] Corresponding author. Tel.: +1 530 752 4167; fax: +1 530 752 3318.
E-mail address: kcprager@ucla.edu (K.C. Prager).
[1] Posthumously.

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2010; Gascoyne et al., 1993b; Hofmeyr et al., 2000) and canine distemper virus (CDV: Alexander et al., 1996; Goller et al., 2010; van de Bildt et al., 2002), have been associated with die-offs and population declines. If pathogen impacts on wild dogs are similar to those seen in related species, other pathogens may also be of concern as they might undermine population viability by causing pup mortality (e.g., canine parvovirus (Mech and Goyal, 1995)), by acting as a co-pathogen that increases the severity of, or susceptibility to, other infections (e.g., *Babesia* spp. (Munson et al., 2008)) or by decreasing general health and hence ability to survive (e.g., canine coronavirus (McCaw and Hoskins, 2006)). Identifying the presence and prevalence of these pathogens in wild dog populations is a first step to evaluating the degree of exposure of different populations and the nature of potential disease threats. Further, identification of risk factors associated with pathogen exposure may help managers evaluate whether preventive measures are needed to reduce these risks, to determine what these measures may be, and to assess the suitability of potential wild dog reintroduction sites. For conservation managers, evaluating the degree of disease threat is challenging and must address both the likelihood of pathogen introduction into an endangered population and its potential impact on population viability. In this paper, we focus primarily on the probability of pathogen exposure as an important starting point, while recognizing that the effect of pathogens on population viability is the more important consideration.

African wild dogs live at low density, including those inhabiting fenced reserves, and contact between packs is infrequent (Woodroffe and Donnelly, 2011); hence pathogens that cannot survive long outside of their hosts and require direct contact for transmission, such as CDV and rabies virus (Greene and Appel, 2006; Greene and Rupprecht, 2006) or contact with fresh infectious material, such as coronavirus (McCaw and Hoskins, 2006), may be spread rapidly within a pack but may rarely be transmitted to other packs. In addition, pathogens such as rabies virus and CDV that cause a high degree of mortality and/or induce life-long immunity are likely to go extinct within a pack once all susceptibles have been infected.

Although wild carnivore species such as bat-eared foxes (*Otocyon megalotis*) and black-backed jackals (*Canis mesomelas*) are thought to act as rabies virus reservoirs in southern Africa (Bingham, 2005; Hofmeyr et al., 2000), research suggests that, in most of Africa, domestic dogs (*Canis familiaris*) are the principal reservoir for rabies virus (Lembo et al., 2008; Prager et al., in preparation) and possibly CDV (Alexander et al., 1996; Cleaveland et al., 2000; Gowtage-Sequeira et al., 2009), from which these pathogens can spill over into wild carnivore populations. Proximity to domestic dog populations may therefore pose a significant exposure risk to African wild dogs. By contrast, pathogens such as parvovirus can survive in the environment for months (McCaw and Hoskins, 2006); thus opportunities for between-pack transmission are greater, and, once introduced, might be maintained in a wild dog population in the absence of an external reservoir. Similarly, pathogens with complex lifecycles involving invertebrate vectors, such as *Babesia* spp. (Taboada and Lobetti, 2006), might be able to persist in low-density host populations (Lloyd-Smith et al., 2005) such as those of wild dogs. Domestic dogs can transmit all of these pathogens to wild dogs, either through close contact (rabies virus, CDV), via feces (coronavirus, parvovirus), or through shared ectoparasites (*Babesia* spp.), and might therefore be the original source of infection to susceptible wild dog packs; however, once introduced into an ecosystem certain pathogens may be able to persist without subsequent domestic dog-to-wild dog transmission events. Nevertheless, contact with or proximity to domestic dogs, or other species that harbor these pathogens, may increase the level of exposure even when the pathogen is endemic.

Land-use characteristics of areas inhabited by wild dogs, such as fencing and protected status, are likely to influence wild dogs' probability of exposure to domestic dogs and may therefore be used as predictors for domestic dog contact. "Predator proof" fences separate wildlife from domestic animals in some areas, thus limiting domestic dog contact with the wildlife contained within. Wildlife species from unfenced protected areas are likewise expected to have a relatively low probability of contact with domestic dogs where dogs are actively excluded by park staff. However, domestic dogs may live at high densities on lands adjoining protected areas, thus creating a perimeter zone where opportunities for pathogen transmission from domestic dogs may be high (Butler et al., 2004). Protected areas may also allow wildlife to reach greater densities than those on unprotected areas where the threats of poaching and persecution may be greater. In the absence of fences, these high wildlife densities may facilitate pathogen transmission from high domestic dog densities at the periphery to wild dogs and other wildlife at the center of a reserve.

Our goal was to determine the presence and prevalence of four viral pathogens of concern (rabies virus, CDV, canine parvovirus and canine coronavirus) and one protozoal pathogen of interest (*Babesia* spp.) in African wild dog populations across much of their range. While exposure to some of these pathogens has been examined previously in a number of wild dog populations across Africa (Alexander et al., 1993a,b, 2010; Creel et al., 1997; Gascoyne et al., 1993b; Laurenson et al., 1997a,b; Van Heerden et al., 1995), differences between the serological methods and laboratories used precludes direct comparison of results across sites. We sought to reliably and comparably screen samples across multiple sites and populations to identify risk factors for pathogen exposure among wild dogs. In particular, we sought to understand whether large-scale land-use management characteristics, associated with varying probabilities of contact with domestic dogs, influenced infectious disease exposure in wild dogs. We hypothesized that, as the probability of contact with domestic dogs increased, exposure to directly transmitted pathogens would increase. In contrast, we hypothesized that pathogens with environmental persistence or complex lifecycles might be able to persist in wild dog populations in the absence of an external reservoir, such that wild dog exposure might not be as influenced by land-use type and probability of contact with domestic dogs. Data collected from wild dog populations across 16 sites in sub-Saharan Africa allowed us to test these hypotheses.

2. Methods

2.1. Samples

Blood samples, and associated background data, were collected between 1988 and 2009 from 268 individual African wild dogs distributed across 16 sites in five countries (Fig. 1, Table S1) (Gascoyne et al., 1993a; Osofsky et al., 1996; Rasmussen and Macdonald, 2012; Spiering et al., 2009; Van Heerden et al., 1995; Woodroffe, 2011). Where individual animals were sampled repeatedly, data from only a single sampling date were included in statistical analyses. This date was chosen by ordering individuals by ID and then alternately choosing the first, or second, sampling date to avoid collection bias. The majority of wild dog samples were tested between 2008 and 2010. All samples and data were collected in the course of wild dog monitoring projects. These 16 sites represented five unconnected wild dog populations; nine sites in South Africa were managed as a single connected metapopulation; Kruger National Park in South Africa was considered a single population, four sites fell within a very extensive connected population covering eastern Namibia, southern Angola, southern Zambia,

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