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Carnivore Viral Disease Studies in the Serengeti

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Abstract:

Introduction

Although habitat loss, persecution and over-exploitation are thought to have been the most important endangering process for wild carnivores in the past, disease has now emerged as a central issue in carnivore conservation. In the Serengeti, epidemics of rabies and canine distemper virus over the past 15 years have led to major declines in several carnivore species, including African wild dogs (*Lycaon pictus*) {GASCOYNE, KING, et al. 1993 32 /id} {Kat, Alexander, et al. 1995 1765 /id}and lions (*Panthera leo*) {RoelkeParker, Munson, et al. 1996 41 /id}{Kock, Chalmers, et al. 1998 313 /id}{Packer, Altizer, et al. 1999 237 /id}.

Rabies and canine distemper virus have been the cause of a disproportionately large number of recent wild carnivore epidemics of conservation concern {Funk, Fiorella, et al. 2001 43 /id}{Woodroffe, Cleaveland, et al. 2004 149 /id}and typify the pathogens that currently pose the greatest threat to wild carnivore populations in many parts of the world; they are viruses that cause high mortality in adults as well as juveniles, and can infect a wide range of host species. Understanding the epidemiology of these diseases and identifying appropriate measures to reduce disease threats has therefore considerable relevance beyond the Serengeti alone.

Several major reviews have recently focussed on diseases of wild carnivore and wild canid populations ({YOUNG 1994 47 /id}{Woodroffe, Ginsberg, et al. 1997 61 /id}; Murray et al., 1999; {Funk, Fiorella, et al. 2001 43 /id}; (1)). In this article, we focus

on data generated from studies of rabies and canine distemper in the Serengeti, highlighting the importance of long-term studies and collaborative approaches for investigating (a) the dynamics of rabies and canine distemper virus in the Serengeti, (b) the impact of these viral diseases in Serengeti's wild carnivore populations, (c) the design of cost-effective disease control strategies and (d) the integration of conservation measures with strategies to improve community health and welfare.

Disease and African Wild Dogs – Lessons for Conservation

Disease first emerged as a major conservation concern in the Serengeti-Mara ecosystem in the late 1980s and early 1990s, when a succession of disease outbreaks resulted in the decline and local extinction of African wild dogs{Kat, Alexander, et al. 1996 234 /id}{GASCOYNE, KING, et al. 1993 32 /id}. Following confirmation of rabies as the cause of death in both Serengeti and Masai Mara packs, a vaccination programme was implemented in the Serengeti using inactivated rabies vaccine that was administered through dart-inoculation of all individuals (n=34) in two known packs {GASCOYNE, KING, et al. 1993 32 /id}. Despite vaccination, all wild dogs in these packs died or disappeared 5-12 months after vaccination, as did a third pack that had been identified (Moru Track pack) {Woodroffe 1997 60 /id} but could not be located for either radio-collaring or vaccination.

Following the local extinction of this population, the association and putative causal relationships between disease outbreaks, handling of dogs (for radio-collaring and rabies vaccination) and their ultimate disappearance was widely debated and reviewed {Woodroffe 1997 60 /id}. Several hypotheses were proposed to account for the emergence of disease outbreaks in the population, briefly: (a) outbreaks of rabies in wild dogs reflected the re-emergence of rabies in neighbouring domestic dog populations (which was absent between 1953 and 1977), with the final extinction caused by canine distemper transmitted from domestic dogs during an outbreak in 1991 {Alexander & Appel 1994 489 /id}{Cleaveland, Appel, et al. 2000 29 /id}; (b) the final demise of the wild dogs was due to rabies, which occurred despite vaccination because of the failure of a single dose to protect wild dogs from rabies {Woodroffe 1997 60 /id}{Woodroffe 2001 156 /id} and (c) the stress of handling/vaccinating dogs re-activated a latent form of rabies, which re-entered an incubation phase before causing disease and death several months later {BURROWS,

Hofer, et al. 1995 241 /id}. The continuing debate surrounding the fate of the wild dogs results from a number of factors. First, temporal associations between events have been used to provide support for each hypothesis (summarized in Fig. 1), but there are insufficient data to demonstrate a causal relationship. Second, no samples were obtained from the packs that disappeared in the final extinction event in 1991 and therefore no diagnosis was possible to distinguish hypothesis (a) from either (b) or (c). However, given the rarity of latent rabies, the > 5month interval between vaccination and the disappearance of wild dogs, and the failure to detect adverse effects of handling in other wild dog populations, it is considered highly improbable that vaccination – or any other form of handling- caused the extinction of the Serengeti wild dog population (Macdonald et al., 1992, Creel et al., 1996, Woodroffe 2001a,b).

The uncertainties generated from these events had widespread implications for conservation and science, both in the Serengeti and further afield, with important lessons for carnivore disease management. Key to these is the need for good design in any intervention, with inclusion of appropriate controls and adequate resources to monitor the population and to establish cause of any deaths post-intervention, factors that were inadequate in the Serengeti study. It is recognised that these elements can be difficult to achieve, particularly in 'crisis' situations involving small populations. But the experience of recent rabies vaccination trials in the Bale Mountain Ethiopian wolf populations (*Canis simensis*) demonstrates that a robust study design is possible, even with critically-endangered endangered popualations (ref). A particular problem is that of confounding data; for example, in the Serengeti study, insufficient survival data were available for the unvaccinated Moru Track pack (as it was not radio-collared). As a result, this 'control' pack, which also disappeared in 1991, was excluded from subsequent survival analyses {BURROWS, Hofer, et al. 1994 250 /id}.

Canine distemper in Serengeti lions

In 1994, canine distemper virus caused a second major carnivore disease event in the Serengeti, with a dramatic epidemic affecting a range of carnivores including lions (*Panthera leo*), spotted hyaenas (*Crocuta crocuta*), bat-eared foxes (*Otocyon megalotis*) and domestic dogs (*Canis familiaris*). Although several cases of CDV had previously been confirmed in large cats in captivitiy {BLYTHE, SCHMITZ, et al.

1983 494 /id}{Fix, Riordan, et al. 2004 493 /id}{Appel, Yates, et al. 1994 492 /id}, the Serengeti outbreak was the first documented in free-living lion populations, and drew attention to the disease as a potential new threat for large felids. During the epidemic, 30% of lions in study areas of both the Serengeti and Masai Mara died or disappeared {RoelkeParker, MUNSON, et al. 1996 239 /id}{Kock, Chalmers, et al. 1998 313 /id} and it was estimated that, in the whole ecosystem, a total of approximately 1,000 individuals died as a result of the disease.

Carnivore Viral Infection Dynamics

In order to identify the need – or otherwise - for disease management and to evaluate alternative strategies for diseases control, we need to understand the dynamics of infection in host populations. The dynamics of viral pathogens depends on several key factors relating both to the virus (e.g. transmission characteristics), individual host responses (e.g. immunity, host survival) and host population characteristics (e.g. population size, density, contact patterns, birth and death rates, and spatial distribution) (Anderson and May, 1991). For generalist pathogens in complex, multi-host systems, such as the Serengeti, this poses a considerable challenge, requiring long-term data on different species and collaboration between disciplines.

A central objective of carnivore disease studies in the Serengeti has been the identification of reservoirs of infection, which is fundamental to the evaluation and design of appropriate disease control measures in multi-host systems{Haydon, Cleaveland, et al. 2002 20 /id}. In the Serengeti studies, we have adopted several approaches, using case-incidence patterns, phylogenetic analyses, seroprevalence and demographic data, disease modelling and intervention studies to explore the dynamics of infection and to identify reservoir systems.

Here we review case studies from the Serengeti, highlighting the relevance of long-term research findings to our understanding of the impact and epidemiology of rabies and CDV in the Serengeti ecosystem and the approach to disease control.

Canine Distemper Virus

(a) Case-incidence data

It is well-recognised that diagnosis and detection of pathogens is notoriously difficult in wildlife populations (Gulland, 1995). Isolation of virus from field samples is particularly challenging, given the logistic difficulties of collecting, storing and transporting samples from remote field site. Even in the visible and intensively-monitored study prides of the Serengeti, only 23 carcasses were retrieved from an estimated 75 (30%) [- CRAIG CHECK – Can't work it out from the Nature paper] lions that died during the CDV epidemic in 1994, and virus isolated from six of these {RoelkeParker, Munson, et al. 1996 421 /id}{Carpenter, Appel, et al. 1998 292 /id}. Although the number of confirmed cases was relatively limited, the spatial and temporal distribution of these cases provided important epidemiological information (Fig. 1). Thus, the epidemic spread from the Seronera area (the location of the index case) throughout the ecosystem at a consistent rate of about 20 km/month (check) and progressed southwards to affect domestic dogs of the Ngorongoro Conservation Area (NCA) after several months. The timing of the epidemic in Ngorongoro dogs demonstrated that the Maasai dog population was unlikely to be either the source or reservoir of CDV for wildlife.

(b) Phylogenetic analyses

Sequence analysis of CD viral PCR products from lions, hyaenas, a bat-eared fox and domestic dog demonstrated close phylogenetic homology among the Serengeti viruses, with a tendency for isolates to cluster according to geographic rather than host species origin {RoelkeParker, Munson, et al. 1996 421 /id}{Haas, Hofer, et al. 1996 413 /id} {Carpenter, Appel, et al. 1998 292 /id}. These findings suggested that a single virus strain caused mortality in a range species in the Serengeti and that this strain was transmissible between domestic dogs and wild carnivores. This provided important evidence for a link between domestic dogs and wild carnivores, but did not indicate the directionality of transmission or the role of different species in maintenance of infection.

(c) Serological studies

Difficulties in field diagnostics mean that much of the epidemiological information on wildlife populations has derived from serological studies (the measurement of antibodies in blood). While of great value, serological data have limitations in that that they demonstrate only that an animal has been exposed at some time in the past. To ascertain the precise timing of exposure and to distinguish epidemic and endemic patterns, longer-term data are needed in conjunction with detailed information on the age of individuals. The Serengeti lion project is a rare example of a long-term large-mammal study that combines both. As such, it has been possible to obtain precise information on the timing of CDV exposure in the lion population, with a consistent 'step-wise' pattern across the years providing clear evidence for an outbreak of CDV in 1981 and 1994, but no exposure in the intervening years {Packer, Altizer, et al. 1999 230 /id}. (Fig. 2). These results do not support the hypothesis that CDV was maintained in a wild carnivore reservoir during this period. If CDV was circulating in a wildlife reservoir, we would have expected evidence of sporadic exposure of the lion population, with occasional seropositive individuals detected throughout the period rather than a complete absence of exposure between 1981 and 1994.

In contrast to the long-term data set, a single cross-sectional survey, say in 1995 (Fig. 2), would be more ambiguous as a single 'step-wise' pattern could also be explained by continuous circulation of CDV in the lion population, but with differential exposure of different age classes (i.e. only older animals exposed). In this case, it would be difficult to exclude wildlife as reservoirs and different approaches to disease control might be needed.

A precise estimate of the timing of CDV outbreaks in Serengeti lions (i.e. in 1981 and 1994) coupled with survival data provides further important information about virus-host infection dynamics and potential strategies for disease control. Although pathogenicity and mortality in lions were both high during the 1994 epidemic, no disease signs or disease-associated mortality was recorded during the 1981 outbreak. Many questions are thus raised about the determinants of CDV pathogenicity in lions and hypotheses are now being generated to explore links between CDV pathogenicity, host factors (e.g. nutritional status) and co-factors (e.g. climate, tick-borne diseases) (Kissui and Packer, 2004). The value of long-term data is in no doubt; with data from 1981 only, we might conclude that CDV is a totally benign pathogen of lions, whereas with data from 1994 alone we might conclude that

CDV is invariably highly pathogenic and poses a major threat. The true complexity of the situation is only now becoming apparent with the collection of data that span several outbreaks over many years.

Similar conclusions regarding long-term data sets can be drawn regarding interpretation of CDV age-seroprevalence data in domestic dog populations. As with lions, a cross-sectional survey conducted in a single year provides limited information. Age-seroprevalence data collected over several years (Figs 4a, b) have provided two important pieces of information: (a) an outbreak of CDV affected Maasai dogs in 1991, coincident with the time when African wild dogs disappeared from the Serengeti; (b) in the two years prior to the 1994 epidemic, CDV was present only in high-density dogs of Serengeti District, not Maasai dogs of Ngorongoro District. In combination with phylogenetic analyses, tempo-spatial patterns of incident cases and mortality data, these longitudinal data provided strong evidence that higher-density dogs to the west of the Serengeti were the source of CDV in the 1994 epidemic (Cleaveland et al., 2000). This conclusion could only be drawn with data from both wildlife (lion) and dog populations, demonstrating the importance of integrated and collaborative studies for understanding multi-host pathogens in the Serengeti.

These results have generated the hypothesis that higher-density dogs were the sole reservoirs of CDV in the Serengeti, and have led to large-scale field intervention studies involving mass vaccination of domestic dogs to test the hypothesis. Although studies are on-going, preliminary results suggest a pattern of increasing complexity in host-pathogen dynamics. Serological data indicate continued exposure of lions to CDV between 1995 and 1999, but an absence of infection in dogs in all but a very small number of villages bordering the national park. One interpretation is that reservoirs other than domestic dogs may now be established in the Serengeti ecosystem, a conclusion that is consistent with recent serological studies of CDV in Masai Mara spotted hyaenas {Harrison, Mazet, et al. 2004 11 /id}. As in the 1981 outbreak, CDV seropositivity in Serengeti lions between 1995 and 1999 was not associated with any recorded signs of clinical disease or mortality, emphasising the potential importance of co-factors as determinants of disease and disease threat in the Serengeti.

Clearly many questions remain about the persistence and management of CDV in the Serengeti. However, these studies demonstrate clearly that short-term data are

of limited value (and can be misleading) as they provide only a snapshot in time in a highly dynamic ecosystem. It is essential that epidemiological studies be sustained to collect the long-term data needed to recognise, explore, understand and respond to the complexities of infectious diseases in multi-host systems, such as the Serengeti.