Chapter 10
Wildlife Disease Surveillance and Monitoring

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10.1   Introduction

Emerging diseases of human or veterinary importance are a major challenge to human society. As previously discussed, infectious diseases of wild mammal populations can have significant economic impact, may threaten human and livestock health (Artois et al. 2001), and can affect the welfare and conservation of game (Gortazar et al. 2006) and species of high conservation value (Cleaveland et al. 2002). Wild mammals are also implicated as sources of emerging diseases (Daszak et al. 2000a; Cleaveland 2003; Cunningham 2005). Comprehensive epidemiological investigations and disease surveillance of wild mammal populations will enhance our capacity to detect and control infectious diseases that may emerge in the future in human and domestic animal populations. Given that the majority of diseases that have emerged in the last couple of decades had a wildlife origin (see Chapter 1), surveillance for wildlife diseases may be seen as an essential tool for the protection of human health.

   For these reasons, the development of effective programmes for the surveillance of disease in wildlife populations is becoming increasingly important. Epidemiological investigations in wildlife are similar in many respects in terms of their objectives, concepts and methodology to those undertaken for domestic animal health surveillance and monitoring. However, there are also substantial differences, owing to the zoological, behavioural and ecological characteristics of wildlife populations. Consequently, definitions, methods and procedures must often be adapted to suit the unique conditions of wildlife disease surveillance.

10.1.1   Definitions

Several terms can be used to describe an investigation of disease in a population (see Table 10.1), but as they may refer to distinctly different concepts, or time frames, it is important to clarify their respective definitions. The main difference between surveillance or monitoring on the one hand and surveys on the other, is their duration. Surveillance and monitoring usually refer to an ongoing process, whereas surveys are more often limited in duration (i.e. a 'snapshot' in time). The term surveillance is commonly used to refer to the monitoring of behaviour or events from a distance. In an epidemiological sense however surveillance (sometimes called epidemiosurveillance) should be restricted to the ongoing recording of diseases in wildlife populations with a view to disease management (OIE 2006). It has been traditional to separate surveillance into scanning (or passive) surveillance (recording cases as they occur) or targeted (or active) surveillance (targeting individuals to detect the disease). An epidemiological survey on wildlife should not be considered as disease surveillance unless the survey is continuous and specifically designed to analyse and manage any associated health risks. In contrast, surveillance data are used to identify the areas to be targeted for control, and to anticipate spatial and temporal resurgences so that pre-emptive management interventions can be used to reduce disease risks.

Table 10.1 A comparison of definitions for terms referring to disease studies

Source	Investigation	Monitoring	Surveillance	Survey
Oxford Dictionary (OUP 2008)	"An inquiry into an incident or allegation so as to establish the truth"	"Keep under observation, especially so as to regulate, record, or control"	"Close observation, especially of a suspected spy or criminal"	"A general view, examination, or description"
Centre for Disease Control, (CDC)			"Systematic collection, of data to control and prevent disease"	
World Organisation for Animal Health, (OIE)			"Ongoing collection, of data to inform on the control and prevention of disease"	"Systematic collection of information on a sample within a defined time period"
Saunders Dictionary (Blood and Studdert 1999)		"Continuous measurement of a variable"	"Watching over a population with the aim of early detection …"	"Comprehensive examination of an area or population for a particular purpose"
Thrusfield (1995)		"The routine collection of information on disease, productivity and other characteristics possibly related to them in a population"	"An intensive form of monitoring, designed so that action can be taken to improve the health status of a population, and therefore frequently used in disease control campaigns. Appropriate action to control disease thus follows surveillance"	"An investigation involving the collection of information and in which a causal hypothesis usually is not tested …. It may suggest aspects worthy of study"
World Health Organisation, (WHO)			"Systematic ongoing collection, of data. So that action can be taken"	"Comprehensive compilation of baseline information on the health of populations"
Our definitions	Searching for the origins of disease events (in particular, outbreaks of infectious disease in humans and domestic animals which can originate in wildlife)	The systematic recording of epidemiological data, with no other specific purpose than detecting temporal trends. Ideally this should include or integrate with data on host abundance and distribution	A system for continuously collecting and analysing information on the health of wild species and associated risk factors, in order to meet the objectives of controlling or potentially eradicating disease in a population or community of wild animals	Collection of data on diseases or species, over a specific time frame (e.g. to analyse factors affecting disease distribution or to assess disease prevalence in a given population)

10.1.2 Importance of Monitoring and Surveillance

This chapter focuses largely on epidemiosurveillance and monitoring of disease in wildlife populations, and less on investigations and survey studies. Epidemio-surveillance and monitoring are important tools in public health, agricultural disease management and wildlife conservation. Surveillance and monitoring are both important for understanding and documenting emerging epidemiological situations and should be used not only in response to disease threats and outbreaks but also in association with high risk activities such as the translocation of wild animals from one geographic location to another.

Table 10.2 New pathogens identified in wild mammals in Italy (from 1995 to 2005) that were linked with previous wildlife translocation or other sources

Pathogen	Affected species	Suspected source of infection	Zoonosis	Source
Thelazia callipaeda (nematode)	Fox	Unknown	Yes	Rossi et al. (2002)
Physaloptera sibirica (nematode)	Fox, Badger	Unknown	No	Ferroglio and Ragagli (2008)
Setaria tundra (nematode)	Roe deer	Translocated wildlife	No	Favia et al. (2003)
Camelostrongylus mentulatus (nematode)	Roe deer	Camel from a circus	No	Rossi and Ferroglio (2001)
Brucella abortus (bacteria)	Chamois	Cattle	Yes	Ferroglio et al. (2003)
Brucella melitensis (bacteria)	Alpine ibex	Sheep	Yes	Ferroglio et al. (1998)
Hypoderma diana (diptera)	Roe deer	Translocated wildlife	No	Rambozzi et al. (2002)
Brucella suis (bacteria)	Wild boar	Translocated hares	Yes	Grattarola et al. (2006)
Ashworthius spp. *(nematode)*	Red deer	Translocated wildlife	No	Rossi unpub. data
Mycobacterium paratuberculosis (bacteria)	Red deer, roe deer, Alpine ibex	Unknown	Yes	Ferroglio et al. (2000); Nebbia et al. (2000)
Neospora caninum (protozoa)	Red deer, roe deer, chamois, Alpine ibex, European brown hare, field mouse	Unknown	No	Ferroglio et al. (2001); Ferroglio and Rossi (2001); Ferroglio and Trisciuoglio (2003); Ferroglio et al. (2007)
Mycobacterium bovis (bacteria)	Wild boar	Cattle	Yes	Bollo et al. (2000)
Mycobacterium bovis (bacteria)	Red deer	Translocated wildlife	Yes	Ferroglio unpub. data

Translocation is a commonly employed tool in wildlife management, with substantial health risks (Woodford and Kock 1991; Griffith et al. 1993; Viggers et al. 1993; Woodford and Rossiter 1993; Cunningham 1996; Daszak et al. 2000a). By way of illustration, Table 10.2 lists those pathogens which have probably spread as a result of wildlife translocations in northwest Italy during a ten-year period. The health risks associated with wildlife translocations, and other wildlife management practices, can be reduced by incorporating robust qualitative risk assessments into all levels of planning and implementation. These should ensure compliance with legislation covering these activities, and the relevant guidance from the World Organisation for Animal Health (OIE 2007). Such risk assessments require sufficient reliable information on the pathogens and host species present in both the source and destination ecosystems, so as to identify those to target for screening or treatment.

One fundamental but demanding aspect of wildlife disease surveillance is the early detection of outbreaks. In terms of public health (Hashimoto et al. 2000) and veterinary science (Doherr and Audigé 2001) 'early warning' can only be provided through adequate monitoring and surveillance (i.e. to find it you must first look for it).

10.2   Surveillance Targets and Cases

In this chapter we define wild mammal species as non-domesticated and free living. Any species legally exploited for recreational hunting can be termed 'game'; and may be divided into large (mostly ungulates) and small (mostly lagomorphs) game. The differing levels of management and husbandry to which game populations are subjected, categorise them into three broad groups: (1) unrestrained and self-sustaining, hunted populations, (2) fenced or managed game and (3) farm-reared game. In natural ecosystems, the practical and logistic aspects of disease and health monitoring of wildlife are challenging and require the development and implementation of novel techniques.

10.2.1   Targets

The most familiar method of recording the frequency of occurrence of a disease in a population is to record the number of individual cases, often expressed as a percentage of the total population size (see Section 10.3). This is usually sufficient to monitor a disease that is frequently encountered and easy to detect. However, wild mammals may inhabit remote areas and are often difficult to approach and examine. In addition, when an infection is acute, clinical expression in individuals may be brief, and hence the probability of detecting a diseased (or infected) animal is reduced. One option for dealing with this problem is to increase the size of the unit of sampling. For instance rather than targeting individuals, a group (e.g. herd, pack or social group) or a specific area (e.g. a forest, or pond) may become the sampling unit. To be considered as affected a herd or area would therefore need to contain at least one infected individual. The main advantage of this approach is that it allows epidemiologically useful

information to be derived from relatively poor data. An example is the definition of rabies-affected areas for treatment with vaccine baits, which could be made on the basis of only a handful of rabid foxes.

By definition, a pathogen imposes adverse effects on the health of susceptible individuals. Some pathogens have been intensively studied because they cause detectable harm to humans or domestic animals (and often have an economic impact). However many parasites may be harboured by wild mammals in the absence of any visible signs of clinical disease. Modern microbiological and immunological techniques may however allow epidemiologists to detect the presence of such organisms, or previous exposure of the host without the need to rely on clinical signs.

A syndrome is a collection of clinical signs, frequently observed in association and putatively linked with some aetiology or disease risk factors. Syndromes are of most value in helping us to recognise diseases that are incompletely defined. An example was rabbit haemorrhagic disease (RHD), now known to be a calicivirus infection of rabbits (see Box 10.1). In contrast to traditional surveillance, a syndromic approach (Henning 2004) does not attempt to detect known etiologic agents or diseases, rather

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Box 10.1 Monitoring in practice – rabbit haemorrhagic disease

Rabbit haemorrhagic disease (RHD) is an emerging viral disease of domestic and wild rabbits (*Oryctolagus cuniculus*), which rapidly spread around the world following its initial recognition in 1984. In farmed rabbits it caused high mortality and was not similar to any other disease previously reported in the species. Liver changes at the microscopic level were characteristic. As is usually the case, it was more difficult to be precise about the situation in free-living rabbits, although outbreaks resulting in high mortality were frequently observed in wild colonies and the clinical signs were again unlike those of any previously reported diseases. For example, nothing resembling the epidemic RHD outbreaks reported in wild rabbits in Britain in the mid and late 1990s had ever been reported before. In addition, the spatio-temporal distribution of outbreaks around the world, following the initial case in China in 1984, was typical of radiating disease, spreading first in Asia, followed by Europe, and subsequently to areas around ports throughout the world. Outbreaks of disease in wild rabbits were usually reported in these countries after disease in farmed animals. In Australia RHD was initially introduced by accidental escape from a field trial site in 1995, but subsequent deliberate releases occurred both there and in New Zealand.

We can be relatively confident that this was a new clinical disease spreading to farmed and wild rabbits around the world, primarily because it was readily observed and had not been recorded previously. The severe mortality observed in rabbit populations, and an initial lack of information on the causative agent, gave rise to concern over the potential risks to the health of humans,

livestock and other wild species, which made a compelling case for monitoring and risk assessment. As the causative agent was unknown, monitoring and surveillance was based on the characteristics of the syndrome, which allowed the detection of typical cases. RHD remained a syndrome for several years due to the length of time it took to definitively identify the pathogen (a novel calicivirus). Risk factor monitoring involved identifying areas with high populations of wild rabbits and monitoring for new patterns of mortality. Targeted surveillance for the pathogen itself proved difficult because of the limitations of the diagnostic tests. Furthermore, no single characteristic alone defines an RHD case. The early case definition was important because it allowed temporal and spatial tracking of disease incidents.

Rabbits affected with RHD died within 24 hours, usually underground, or were removed by predators, and therefore RHD morbidity monitoring was of limited practical use. Case mortality monitoring was important, however counting dead animals was problematic. Wherever spatial and longitudinal analyses of scanning surveillance data demonstrated mass mortality incidents in wild rabbits, then RHD was considered a possible cause together with other differential diagnoses including myxomatosis, juvenile coccidiosis and poisoning. As RHD was almost invariably fatal, carrier disease status occurred infrequently and so was not an important consideration for disease monitoring. In addition, other wild species were not identified as susceptible to RHD infection and were therefore thought unlikely to be virus carriers.

Until 1994, the diagnostic test of choice for detecting the agent was electron microscopy of the liver. This is a direct test in which the RHD virus is observed, however it required technical expertise, which made monitoring expensive and limited to specialised diagnostic laboratories. It was several years before RHD ELISA and PCR tests were developed. Detecting exposure by identifying antibodies was of little practical use in recognising new outbreaks of RHD in wild rabbits because the majority of animals died in a matter of days, before they had time to produce antibody.

In conclusion, monitoring for RHD is influenced by the characteristics of the pathogen, the host and the ecosystem they inhabit. In the case of RHD it was initially difficult to detect the disease agent. In some respects, the presence of the disease in nearby domesticated rabbits provided sentinel surveillance for RHD in wild populations. Syndromic surveillance was important for detection, where obtaining fresh carcasses was not possible. The spatial and temporal occurrence of RHD in wild rabbit populations is now seen as sporadic and difficult to model. This relates to the complicated epidemiological picture caused by the recognition of several different serotypes of varying pathogenicity (White et al. 2004). It is noteworthy that in Europe, monitoring in recent years was largely confined to Spain where the disease has caused prolonged depression of rabbit populations with significant consequences for biodiversity, in particular for threatened predators such as the Iberian lynx (*Lynx pardinus*) and the Spanish Imperial Eagle (*Aquila adalberti*).

it seeks to use the clinical or epidemiological characteristics of disease occurrences to provide evidence to establish whether they are likely to be linked.

Disease risk is the probability of an occurrence (OIE 2006) and the use of the term denotes an intention to deal with the associated potentially negative impacts (e.g. threats to human health, economic losses). Risk surveillance often focuses on areas where the probability of occurrence or the seriousness of the consequence for target populations is high. Hence, it seeks to bias the collection of data in favour of species, areas, seasons or circumstances where risks are expected to be greatest.

10.2.2   Cases

A case is a unit for quantifying a health risk under epidemiological investigation. The science of epidemiology is largely concerned with quantifying and describing trends in data related to health events and so the definition of such events is at the root of any epidemiological study. As many of the pathogens of wild mammals are not routinely studied, accurate definition of a case is a fundamental challenge for wildlife disease surveillance. A positive case needs to be defined on the basis of the presence of a specific disease agent, a clearly described response to a diagnostic test, or in the case of a syndrome on a detailed description of lesions or clinical signs. In addition, it is important to accurately identify the host whenever possible, as this will help determine the epidemiological status of different species (e.g. are they reservoir or spillover hosts: see Box 3.4). This has often been a problem in the past when for instance on several occasions, European Bat Lyssavirus has been recorded as EBLV1a in 'a bat', and avian influenza cases as HPAI H5N1 in 'a duck'! The criteria that define positive cases need themselves to also be clearly defined, so that they can be routinely referred to as standards, compared, and challenged in the face of new data.

As mentioned above, a case may refer to an individual with a given disease, affected by a precisely described syndrome or carrying a specific pathogen. A case also may refer to a spatial or social unit (e.g. herd or region), when it may be described as an 'outbreak'; this term generally implies that several animals are affected (Thrusfield 2007). It is important that the units are clearly defined, in terms of geographical delineation (e.g. of an area or region) or composition (e.g. single cases or social groups of mammals).

10.2.2.1   Morbidity

Morbidity refers to the state of being diseased; from the Latin *morbidus*. Diseases causing macroscopic (visible) lesions such as infectious kerato-conjunctivitis in Alpine chamois (*Rupicapra rupicapra*) (Hars and Gauthier 1984) or obvious mortality like RHD (Villafuerte et al. 1994) may be relatively easily detected and monitored since the public (including hunters and gamekeepers) may provide useful epidemiological information. However, early stages of such disease are likely to be underreported. In reality, the expression of clinical signs in wild mammals may be difficult

to observe, and quantify, particularly when no comparative information is available on the infection in humans or domestic animals. Furthermore, even when such data is available, it may not always be useful because of the potential for wide inter-specific variation in the nature of the host-pathogen interaction. Clinical diagnosis has only been useful in a limited number of disease outbreaks where groups of free-ranging wild animals were subject to continuous monitoring by trained personnel. In such instances the observer must ensure that quantified clinical data on any sample of animals is reliable and representative. This may only be possible when dealing with health disorders affecting visible parts of the body or those that profoundly modify the behaviour of mammals which are habituated to the presence of humans.

10.2.2.2   Mortality

Accurate identification of a mortality event requires that a pathologist with particular expertise in examining wildlife carry out a detailed necropsy. This should be performed in accordance with a standardised procedure, regardless of the size and state of preservation of the carcass (Woodford et al. 2000). For the purposes of opportunistic surveillance, the carcasses of animals that have died from traumatic injury (e.g. road traffic casualties) may be used to screen for pathogens, even where they present no macroscopically visible signs. The spatial and longitudinal analysis of wildlife mortality statistics and the results of the associated systematic screening provides a useful resource for investigating health risks to, and emanating from, wildlife (provided the sampling is adequate). Again we must stress the importance of accurately recording the species, and where possible the sex, age and condition of hosts.

10.2.2.3   Pathogen Carriers

Clinical manifestations or lesions caused by many zoonotic or economically important pathogens that occur in wildlife can be difficult to observe. Hosts may for example be apparently healthy carriers. Therefore, disease surveillance for these pathogens must not be based on the collection of clinical data (i.e. mortality or morbidity). Below we describe approaches to detecting such pathogens, although there is little published information available to help investigators in the design of surveys for such conditions in wildlife populations (Kaandorp 2004).

10.2.2.4   Test Sensitivity and Specificity

Sensitivity and specificity are qualities of diagnostic tests that seek to distinguish individuals that are infected or have been previously exposed (see Section 10.2.2.6) to a pathogen from those which have not. When an animal is known to be affected, the sensitivity of a test is its ability to give a positive response. When an animal is known to be unaffected, specificity is the ability of the test to give a negative

response. The evaluation and interpretation of diagnostic tests is a complex issue. For the sake of simplicity, it is common practice to divide responses into positive or negative results. This often requires the identification of a cut-off value for test results. However it is important to understand that there is an inverse relationship between sensitivity and specificity, such that one characteristic is achieved at the expense of the other (Thrusfield 2007). Diagnostic test results should therefore always be interpreted with these limitations in mind.

Many diagnostic tests designed to screen for infectious diseases in domestic mammals do not have the same levels of sensitivity and specificity when used in wild mammals. However, as a general rule, tests aimed at directly detecting the pathogen tend to give similar results in both domestic and wild species. The same cannot be said for indirect tests, which are often based on detecting the immune response of the host to the pathogen, and so depend on recognising specific proteins associated with that response. Variations in host response amongst species means that indirect tests such as antibody ELISA tests or skin tests, may not be accurate indicators of exposure to the pathogen. For example, other pathogens may elicit antibodies that cross-react with the test, causing a false positive result. Validation of existing diagnostic tests in wild hosts can be difficult owing to the practical challenges of acquiring sufficient numbers of known positive and negative controls. Test sensitivity and specificity are also difficult to determine where there is no 'gold standard' test, for example when pathogen identification is difficult as can be the case in sub-clinical cases of bovine tuberculosis. Nevertheless, there may be opportunities to usefully employ insensitive tests to detect exposure at the group level (e.g. the herd). The OIE (Office International des Epizooties) Working Group on Wildlife Diseases maintains an updated list of recommended diagnostic tests for screening wildlife (OIE 2008a).

10.2.2.5   Detecting the Agent

Infectious agents can be directly detected using a wide variety of techniques including cultivation in laboratory animals, or preferably on cell culture or other media, identification of phenotypical characteristics (as identified by staining techniques for example), or genetic tests such as genomic amplification, PCR or RT-PCR and sequencing. Frequently, evidence of contact with the disease agent requires laboratory analyses based on agent isolation, PCR testing or serology.

For macroparasites (such as helminths and most arthropods), disease monitoring should ideally also include isolation of the relevant life stage of the parasite, such as larvae, nymphs etc. In many situations however, the mere presence of a parasite may be of less consequence if it is generally benign. Certain new technologies (e.g. PCR) are so sensitive that they can detect extremely small amounts of genetic material, such as the remnants of the pathogen, and so the results of these tests need to be interpreted with caution. Likewise, when a test fails to detect a pathogen this does not exclude the possibility that it is in fact present, because all tests have their limitations. Understanding and quantifying these limitations is essential and consideration of their influence should be central to the interpretation of epidemiological data.

10.2.2.6   Detecting Exposure

Many techniques are now available for detecting prior exposure of an individual to a specific pathogen. One approach is to use physiological or biochemical changes, such as the level of chemical compounds in the blood or tissues which act as markers for previous exposure. Exposure to most infectious agents can provoke the appearance of antibodies in blood, excreta or secretions. These antibodies are not necessarily linked with immune resistance, but can be used to evaluate what fraction of a population has been exposed. However, antibody responses can wane with time after exposure, thus decreasing the sensitivity of detection. This can vary between individuals, so the amount of antibodies present does not tell you how long ago the animal was exposed to the agent. It also does not tell you if the animal had been diseased, or infectious, only that it was exposed to the agent. Many studies use blood serum samples to detect antibodies, and their results are often referred to as seroprevalence. In a UK study of European Bat Lyssavirus 2 in the Daubenton's bat (*Myotis daubentonii*) the observed seroprevalence was approximately 5%, but the virus itself was not identified in a single case, and hence disease prevalence was zero (Harris et al. 2006).

10.2.2.7   Non-Invasive Tools

Animal welfare concerns and the need to limit manipulation of highly endangered species have prompted the development of non-invasive disease monitoring techniques. Available tools include faecal sampling for parasitological or bacteriological surveys, and feather and hair sampling for genetic and toxicological analysis. Non-invasive approaches are currently rarely adequate substitutes for traditional sampling techniques. Nevertheless, this is an area of much recent research activity which may yield valuable surveillance tools for wildlife diseases in the future.

10.3   Indicators and Statistics

The most useful parameters to quantify disease presence and describe patterns in space and time are prevalence and incidence (Thrusfield 1995). In practice, however it is difficult to accurately determine the number of cases and the size of the target wild mammal population. This difficulty may be compounded by the influences of the spatial and social structure of mammal populations on the distribution of cases (see Chapter 2) and the probability of their detection.

10.3.1   Prevalence and Incidence

Prevalence is the total number of cases (expressed as a proportion or percentage) in an exposed population over a given sampling period. Incidence is the number of new cases (expressed as a proportion or percentage) that arise in a population per

unit of time. Both are usually given as proportions of the total sub-population sampled, and this is often assumed to be an unbiased estimator of the true population prevalence or incidence.

In practice, it is unlikely that the absolute size of a population of free-living wild mammals is known. The size and social organisation of wild mammal populations can often only be crudely estimated, and the development of improved methods for estimating animal abundance is a fundamental challenge for wildlife disease management. Hence, the proportion of cases in a sample of wild animals can only be considered as an indication of the probability of infection or exposure to the pathogen. However, the more representative the sample is of the wider population, the more accurate the final estimate is likely to be.

10.3.2   Issues of Host Abundance

The denominator for prevalence and incidence estimates is the size of the 'local' population from which the sample was derived, rather than the national population. Since disease is often aggregated, and most populations are continuous, defining the extent of this sample population is difficult. Diseases are often expected (not always correctly) to increase in prevalence as host density increases, so an estimate of population density would also be useful in many circumstances. Estimates of mammal population size can be performed by capture-mark-recapture studies, but these are expensive and time consuming, since they involve the repeated capture of animals, and ideally estimates of population turnover and emigration. A population census (i.e. a complete count) can be performed in limited circumstances, where the species is large and distinct. Alternatively, population size can be estimated from survey data using methods that correct for the probability of detection, as have been developed for rabbits (Poole et al. 2003), and badgers (Hounsome et al. 2005) in the UK. For many mammalian species, field signs such as footprints and droppings can be used as crude estimators of abundance but such methods often have serious limitations (Wilson and Delahay 2001). Genetic methods, such as the non-invasive: sampling of faeces or hair, are becoming more reliable (e.g. Wilson et al. 2003). Quantitative comparisons of the various techniques for estimating abundance are urgently required for many species, as different approaches all have their advantages and disadvantages (Wilson and Delahay 2001; Acevedo et al. 2008).

10.3.3   Spatial and Temporal Trends

Recording cases of morbidity and mortality in a given area can provide information on spatial and temporal trends of infection in wildlife. However, the distribution of hosts in space and time will influence the temporal and spatial distribution of morbidity.

It is important to be able to describe 'background noise' in morbidity and mortality rates, in order that any significant deviations indicative of emerging disease events or new diseases can be identified. A variety of statistical techniques have been developed for the explicit purpose of identifying clusters of cases that cannot be explained by chance occurrence (Lawson and Kleinman 2005).

Pathogens can survive and propagate in populations in different spatial and temporal patterns (Begon 1995), for example the invasion of pathogens into susceptible areas can lead to spectacular waves of new cases. Mathematical modelling allows epidemiologists to describe the most significant factors that are likely to contribute to the spatio-temporal trends observed. These trends are often categorised into a few basic types (forms) that are used to describe disease events (see Thrusfield 1995; Toma et al. 2001). Morbidity or mortality events that oscillate above and below an average over time are indicative of an endemic situation (the term enzootic is used to specify that the population is composed of animals). An outbreak suddenly appearing in a place where it was previously unrecorded is called an epidemic (or epizootic for animal populations). Morbidity events, which occur in an unpredictable manner in time and space, are called sporadic.

Another important concept in epidemiological investigation is whether a morbidity event is propagating from individual to individual (direct or indirect transmission), or if the event is clustered around focal point sources (e.g. a water-borne source in an arid environment). At an early stage of the event, it can be difficult to distinguish which disease pattern one is dealing with, but analysis of the distribution of cases in time and space will give some indication of the potential transmission dynamics.

10.3.4   Detection of New Diseases

Detection of new diseases is a challenging task. The definition of 'new disease' should include the occurrence of known disease agents in novel host species, in addition to completely new agents. Detection probability will depend on disease prevalence, patterns of transmission and disease-induced mortality. Sampling effort will therefore be crucial and the resources available for this are likely to be greater for disease agents that could spill over to humans or have a potentially substantial economic impact.

For new diseases to be confidently identified, a sound baseline knowledge of the pre-existing disease status of a range of hosts in a given area is required. This is not always available for wild hosts, but at the very least the detection of new pathogens will require systematic investigation of those clinical cases where the aetiology is unclear or potentially novel. This can be achieved through careful scanning (or passive) surveillance focused on specific syndromes or areas perceived to be at greater risk (see Box 10.2). This flexible capability should be possible as part of any existing programme for the surveillance of disease in wildlife.

Box 10.2 Early disease detection in wildlife: European brown hare syndrome

European brown hare syndrome (EBHS) is caused by a calicivirus that is related to, but distinct from, the rabbit haemorrhagic disease (RHD) calicivirus. The detection of EBHS in the UK illustrates several principles and problems in the early detection of new diseases in wildlife.

Unexplained mass mortality incidents in brown hares (*Lepus europaeus*) had been observed in England for many years by the *ad-hoc* and non-systematic surveillance schemes employed at the time. A toxicological aetiology was suspected but assay results were consistently negative. Tissues from some of these mortality incidents were archived by freezing. A syndromic description was not produced for EBHS at the time, and in retrospect this significantly delayed the detection of the disease. Instead, the description of 'large numbers of dead hares found at one location' was sufficient to alert workers to the possibility of a new disease, and to archive incident reports and tissues, but was too vague to provide any indication of aetiology.

Identification of the first case of EBHS in England in 1989 occurred when a live but non-responsive hare, exhibiting no fear of humans, was submitted for veterinary examination. This focused on central nervous disease and the brain was examined. However, the investigator had read a surveillance report on hare deaths in Germany where liver disease was suspected, and as a consequence electron microscopy revealed many calicivirus particles in the liver. This first case of EBHS exhibited hepatic encephalopathy in which impaired brain function occurred secondarily to severe liver dysfunction. Retrospective examinations of the archived hare livers and their associated reports showed that the disease had been present in England since at least 1982. Archived reports hinted at suspicious incidents from the mid-1970s and archived sera showed a high seroprevalence to EBHS in hares sampled as far back as 1963 (Duff et al. 1996).

This example illustrates how difficult it can be to detect a novel disease in wildlife, even when the condition is an acute infectious disease such as EBHS. In retrospect, we can identify several reasons why this syndrome was not identified earlier. Firstly, at this time in England there was no systematic scanning surveillance scheme for diseases in wildlife, which would have detected unusual hare mortality incidents and then targeted carcass submissions. Also, the gross pathology of EBHS is usually unremarkable, there was no systematic approach to laboratory investigation for wild mammals, and there was no routine microscopic examination of tissues (histopathology). Finally, EBHS incidents frequently lasted only a few days and by the time investigators received negative laboratory results they rarely had access to more dead animals. Critically, a clearer and more detailed syndromic description at the time of the outbreaks would undoubtedly have allowed earlier detection of the condition.

10.3.5 *Precision, Bias and Accuracy*

Precision, bias and accuracy are characteristics of any sampling design, and it is important to understand their respective meanings and the way they may influence results.

10.3.5.1 Precision

The term precision refers to the repeatability of a result. Confidence intervals provide a measure of the precision associated with a prevalence estimate (p) and can be calculated from the sample size (n). A frequently used formula for estimating the confidence interval associated with an estimate of microparasite infection prevalence is

$$\text{S.E.95\%C.I.} = 1.96[p(1\text{–}p)/n]^{1/2} \text{ (Martin et al. 1987).}$$

Prevalence and similarly proportions can be compared using a variety of statistical tests (Siegel and Castellan 1988). Macroparasites usually exist in aggregated distributions, whereby a relatively small number of hosts carry many parasites, but more hosts carry fewer or even none. This left-biased frequency distribution is best described by the negative binomial distribution, and specific approaches have been developed for the calculation of prevalence estimates (Rózsa et al. 2000; Rózsa 2005). As a general rule for both micro and macro-parasites, increasing the sample size will increase the precision of any prevalence estimate.

10.3.5.2 Bias

The bias of an estimator is a reflection of the extent to which it (e.g. observed prevalence in the sample) differs from the true value of the parameter being estimated (e.g. actual prevalence in the exposed population). Wildlife sampling using carcasses from hunting bags, road casualties or cetacean strandings for example, may include bias that could lead to either over or under-estimation of disease prevalence. If bias is likely, then sampling should be random or preferably stratified (e.g. split into sub-samples) relative to those factors of concern, such as habitat, region, date, age and gender. This will allow comparison between different sub-samples, although small sample sizes can become an issue. Also, there may be additional logistic or economic reasons why it is not possible to adopt such a systematic approach.

The design of any sampling strategy should generally seek to minimise potential sources of bias. In most situations, stratified random sampling is the most advisable design for investigating wildlife populations. This is likely to require some basic knowledge of host population structure and distribution. Larger sample sizes however, will not necessarily reduce or remove the influence of bias. For example,

increasing the size of a survey based on the collection of trapped animals will not reduce bias resulting from diseased hosts being more or less likely to be captured. Furthermore, the trappability of some categories of individuals may change over time and hence could modify the perception of the temporal trend in cases (Courchamp et al. 2000). Unlike precision, bias cannot generally be quantitatively estimated.

Bias can nevertheless also be beneficial, for example when trying to detect a novel disease, or where the aim is to establish that a disease is absent. The submission of suspect carcases for rabies surveillance is for example highly biased because it concentrates on those animals displaying aberrant behaviour, and is consequently more effective at detecting cases than random sampling would be. However, this approach does require that the direction of bias is known.

10.3.5.3 Accuracy

The term accuracy relates to how close a given result is to the true value. Hence a prevalence estimate, based on a given sample size, is more accurate the closer it reflects the true prevalence in the whole population. This can only be determined by sampling a sufficiently large and representative proportion of the total population. It is however, often difficult in studies of wild mammals, to achieve adequate sample sizes. Nevertheless, even if the entire population were able to be sampled (i.e. a census) then the observed prevalence would still be subject to the limitations of test sensitivity and specificity.

10.3.6 Disease Absence and Limits of Detection

The likelihood of being able to detect the presence of a pathogen increases with prevalence and sampling effort. Hence it is relatively easy to obtain prevalence estimates for diseases that affect a large proportion of the population such as tuberculosis lesion prevalence in wild boar in Spain (Vicente et al. 2006). But this becomes increasingly difficult when prevalence is below 1%, such as for transmissible spongiform encephalopathies in European cervids (Schettler et al. 2006). It follows that confirmation of the absence of a disease is a difficult task. For example, in order to be 99% confident that disease is absent or below 1%, a sample size of 448 undiseased individuals would be required from an estimated total population size of 10,000. This calculation is derived from the formula:

$$n = [1-(1-a)^{1/D}][N-(D-1)/2],$$

where n is the required sample size, a is the probability of observing at least one diseased animal in a sample when the disease affects at least D/N, and D is the number of diseased animals in a population of size N (see Martin et al. 1987). In fact, practical constraints mean that most wildlife disease surveys can only provide information on sample prevalence, with difficulties in extrapolating accurately to population prevalence.

10.4 Data Collection, Storage and Interpretation

Surveillance and monitoring may be carried out by the 'passive' collection of samples or alternatively by an 'active' process of collecting material for diagnostic testing. When animals are routinely submitted for investigation on an *ad hoc* basis, for example as a result of road casualties, 'pest' control, abnormal individuals in a game bag or mortality during rehabilitation, and this information is collated, then this constitutes scanning (or passive) surveillance. Alternatively, we use the term targeted (or active) surveillance when animals are proactively sampled (either dead or alive), by various means (e.g. by dedicated capture or sub-sampling of game bags) specifically for the purpose of examining and testing them for evidence of exposure to pathogens. Such studies can provide data in the form of the number of cases or outbreaks observed during a given time period. These data can then be centralised and (where necessary) cases may be notified to local, regional or national authorities. However, notification may also be based on continuous (real-time) reporting of results as they arise (as part of mandatory activities involving results of laboratory diagnoses or examination of game and game meat at inspection points), in which case it is referred to as *ad hoc* or routine sampling.

Scanning surveillance based on official notification, is not sensitive and is inevitably biased towards species and diseases of priority interest. Nevertheless, this provides a non-representative indicator of events and trends, which may be of interest for public health, veterinary and wildlife management purposes, and may be particularly useful for the initial detection of exotic diseases.

10.4.1 Recording and Storage of Data

Before data are recorded, they must be coded in order to standardise case definitions and to allow comparisons in time and space. Such standards are rarely used in surveillance of disease in wild mammals. There is currently no internationally agreed standard, although in 2002 the American Veterinary Medical Association approved support of a Systematized Nomenclature of Medicine (SNOMED) as a standard for veterinary data recording and management (Anon 2002). Across Europe, harmonised standards are either absent or are inadequately implemented (Klein 2002).

10.4.2 Effects of Management on Disease Prevalence and Distribution

The most obvious effects of successful wildlife disease management are reductions in disease prevalence (in either the wildlife, domestic or human population) and in the spatial and temporal range of infection. The monitoring of disease prevalence

in a given area allows one to distinguish between endemic situations (e.g. rabbit myxomatosis) and emerging or epidemic situations (e.g. the arrival of rabbit haemorrhagic disease). This distinction is important for establishing the appropriate management actions (if any), and the optimal design of surveillance to detect new cases. When calculating disease prevalence, the relevant confidence interval, or level of uncertainty associated with the result should also be known. Where trends are being examined it is important to remember that a change in the prevalence estimate for a given sample does not necessarily equate to a measurable change in the population prevalence, particularly if the sample size is small. When looking at local disease prevalence, sub-dividing the total sample quickly reduces sample sizes and levels of confidence in the results.

10.4.3 Effects on Disease Intensity and Transmission Risks

In some cases, wildlife disease management can target disease intensity and transmission risks rather than disease prevalence. In the case of most parasitic diseases for example, hosts in good body condition may have lower parasite burdens than undernourished or stressed individuals. The body condition of red deer (*Cervus elaphus*) was improved by supplementary feeding, at the cost of increased host contact rates. Deer in good condition carried lower nematode burdens possibly related to the nutritional costs of improved immune function. However, supplementary feeding encouraged the aggregation of individuals and enhanced the potential risks of bovine tuberculosis (bTB) transmission (Vicente et al. 2007b). In such cases risk surveillance (focused on clinically affected animals, or intensively managed populations) would be advisable for management purposes.

10.4.4 Effects on Other Species that Share Disease

Disease control in an abundant wild host may reduce risks to less abundant and more valuable wildlife species. For example, in Spain the endangered Iberian lynx (*Lynx pardinus*), is threatened with spillover of viral infections from feral cats (*Felis catus*) and bTB from their wild ungulate prey (Delibes et al. 2000). Disease surveillance is almost certain to be more straightforward if focused on the more abundant feral cats and ungulate prey, which are likely to be the subject of management actions. A different situation exists where wild boar are implicated as potential sources of several notifiable diseases in domestic pigs. In this instance, surveillance data on disease incidence in domestic pigs can be used to monitor the success of the management actions that target the wildlife species (e.g. control of CSF by vaccination, see Box 6.3). Both examples illustrate how disease surveillance carried out on hosts that are not necessarily either the species of most concern or the direct target of management efforts can be useful in assessing the impact of interventions.

10.5 Existing Monitoring and Surveillance Systems (MoSS)

The Internet and the World-Wide Web have introduced major changes in the way we observe and record events, and share data. New sites and information networks are constantly appearing and provide opportunities to continuously update information in 'real-time'. Perhaps the oldest global surveillance network for wildlife health and diseases is that organised by the OIE, which has been collecting data since 1993, particularly on diseases of importance to international trade and agriculture. These pathogens are described as 'listed diseases'. Initially, data was only collected on listed diseases in domestic species, but following the creation of a Working Group on Wildlife Diseases in 1993, the surveillance system began to expand to include wild animals (OIE 2008b). Data are collated from notifications submitted by each member country's designated wildlife disease reporter (or 'focal point').

Among the earliest general surveillance programmes for wildlife diseases in Europe were those established in the 1930s in Scandinavian countries (Mörner et al. 2002). Another comprehensive wildlife disease surveillance programme is the SAGIR network in France, which started in 1986 (Terrier et al. 2006). The World Health Organization (WHO) created a rabies-specific centre for surveillance and research which has published a quarterly bulletin since 1977 (WHO 2008b). At the scale of the European Union, although there is informal coordination of organisations conducting disease surveillance in wildlife populations, this is not yet formalised. Most EU countries have appointed a focal point to notify the OIE annually of significant wildlife disease events, and this informal network is coordinated under the auspices of the European Section of the Wildlife Disease Association (EWDA 2008). In addition, EU funding allows groups to formalise surveillance for important or notifiable diseases (e.g. EDEN 2008; MedVetNet 2008).

In European countries, the organisation of these systems for surveillance and monitoring follows one of two basic models. In the first, one or more laboratories with relevant skills and facilities gathers samples from all over the country (or region, province etc.), conducts analyses, processes data and disseminates the results. This approach operates in Austria, Scandinavian countries and Switzerland (and, at a regional scale, in Italy, Germany and Spain). In the second system, one organisation, or in some instances, a person appointed for this duty, collects results from various laboratories or sources and publishes a synthesis. This system has been employed for many years in France, the UK, Italy and the Netherlands.

Various other types of surveillance systems have been implemented elsewhere in the world. In Canada, for example, a multi-centre organisation deals with scanning and targeted surveillance (see Box 10.3). In South Africa, most surveillance is based in conservation areas such as Kruger National Park, where scanning surveillance is ongoing and coupled with campaigns of active detection of specific diseases (see Box 10.4). The variety of surveillance systems is therefore broad, from active to scanning, from general to targeted. The future challenge will be to find effective ways to share and exchange data on a global scale so as to improve our capacity to identify new health risks in wildlife populations and enhance our capability to manage them when necessary.

Box 10.3 Wildlife disease surveillance in Canada

In Canada, a national programme of monitoring and surveillance of pathogens and diseases in wild animals has been carried out since 1992 by the Canadian Cooperative Wildlife Health Centre (CCWHC 2008), a partnership among Canada's five veterinary colleges and federal, provincial and territorial government agencies (Leighton et al. 1997). The central pillar of this programme is scanning disease surveillance based on *post mortem* examination of wild animals found dead or diseased. Data and knowledge developed by this core program have given rise to numerous additional projects and programmes in targeted disease surveillance and other research. This national programme now plays a key role in developing, testing and improving Canada's overall capacity for disease detection and responses, and management of animal and human health.

The primary objectives of the surveillance programme are to develop a complete national inventory of pathogens, their vertebrate hosts and their geographic ranges, to assess changes in these over time, to detect diseases of socio-economic and zoonotic importance as early as possible, and to inform decisions by government agencies responsible for public health, domestic animal health and wildlife conservation and management. Secondary objectives are to use the material generated by the programme to educate the wildlife health personnel who will be needed by Canada in the future, and to identify priorities for research related to wild animal health and disease.

The core disease surveillance programme of the CCWHC integrates four separate activities: (1) detection of dead or diseased wildlife, (2) identification (diagnosis) of pathogens and disease processes in those specimens, (3) management of the information derived from these two activities through a national wildlife disease database, and (4) communication of relevant information to government decision makers and the public.

The CCWHC model has proven highly effective and cost efficient. The CCWHC provides wildlife health services to the nation and, thereby, generates knowledge, specimens and infrastructure for scientific research and education in the wildlife health field. The veterinary colleges provide the CCWHC with much of its professional expertise and all of its physical space, laboratory and information facilities. Government investment in the operation of the CCWHC assures access to expert wildlife health services for government agency programmes, and the education and training of a much-needed pool of potential future employees. As an organisation outside of government, the CCWHC is particularly well-positioned to coordinate complex national disease surveillance and management programmes among a wide range of government agencies at all levels, and with non-government agency partners.

Box 10.4   Disease surveillance and monitoring in free-ranging African wildlife

Disease surveillance in wild mammals is generally weakly structured and usually passive in approach, because free-ranging wildlife are not visited and observed on a regular basis, frequently do not have owners, and are not easily manipulated for 'hands on' examination or specimen collection. For these reasons, surveillance techniques for wildlife should be structured so as to maximise the information gained from the limited availability of captured animals and carcasses. Opportunities for investigations into causes of morbidity and mortality are infrequent because carcasses are either not found or have been scavenged. Hence, one must make full use of every opportunity to monitor animal and environmental health indicators in extensive free-range ecosystems

Here we describe the surveillance and monitoring techniques currently in use for four common infectious diseases and one possibly eradicated disease of African wild mammals.

Anthrax

In sub-Saharan Africa, anthrax outbreaks are generally driven by dry climatic conditions with hydrological stagnation, coupled to relative or absolute over-abundance of preferred hosts. Outbreaks are generally short lived and are dramatically terminated by the onset of the rainy season. Anthrax is an acute multi-species disease caused by a bacterium (*Bacillus anthracis*), and its preferred hosts vary amongst habitats and ecosystems. Scanning surveillance for anthrax is mainly executed by trained field staff, including rangers, game guards, biologists and veterinary technicians. Suspect carcasses of most mammal species that die of anthrax, are usually in good body condition, and frequently have no signs of predation, when found soon after death.

In the Kruger National Park (KNP) field personnel are issued with blood smear collection kits, which include two glass slides wrapped in a small data sheet and a waterproof pouch. Blood smears are taken from all suspect carcasses, data sheets are completed and the samples are dispatched for staining and microscopic examination, or for culture when necessary. Once an outbreak has been detected, surveillance and monitoring moves into a targeted mode, involving moderate-scale deployment of staff, vehicles, a mobile laboratory and a helicopter. A central command centre is established at the nearest rest camp, and collected data is collated, stored and mapped on a daily basis to identify spatio-temporal trends (De Vos and Bryden 1996). Circling and descending vultures are one of the most important indicators for pinpointing carcass locations. GPS co-ordinates are collected for every carcass. The use of GPS technology facilitates data management and mapping using GIS imaging and layering.

Box 10.4 (continued)

Foot and mouth disease

In sub-Saharan Africa, the endemic cycle of foot and mouth disease (FMD) is maintained in buffalo (*Syncerus caffer*) herds with virus cycling between adult carriers and the annual cohort of calves (Thomson et al. 1992). Most buffalo calves are born in the rainy summer season, and receive colostral antibodies against FMD from their dams. As this passive immunity wanes at between 5 and 9 months of age, most juvenile buffalo become susceptible to infection during the dry season of mid-winter and early spring, a time when many species are congregating around the remaining permanent sources of surface water. During primary infection, buffalo calves shed large amounts of virus, and the infection (usually sub-clinical) rapidly spreads to the other buffalo calves in the herd, and may spill over into other sympatric cloven-hoofed species, resulting in an epidemic cycle.

In the KNP, impala (*Aepyceros melampus*) are the most abundant wild cloven-hoofed ungulates, are highly susceptible to FMD and develop clinical disease when infected. Hence, to detect FMD epidemic outbreaks, impala are targeted through surveillance of herds (Bengis et al. 1994). Clinical signs of FMD in impala include pilo-erection (febrile response), "walking on eggs" (weight shifting from one limb to another), overt lameness, lagging behind the herd and lying down. Animals with clinical signs are sampled (non-lethally or lethally) to obtain blood and tissue samples for virus isolation and serology. During epidemic outbreaks, clinical disease may also be diagnosed in kudu (*Tragelaphus strepsiceros*), and less frequently in giraffe (*Giraffa camelopardalis)*, bushbuck (*Tragelaphus scriptus*), nyala (*Tragelaphus angasii*) and warthog (*Phacochoerus aethiopicus*). More recently, active sero-surveillance for FMD in impala has been employed, whereby 30–40 animals are randomly selected, chemically immobilized, examined and blood sampled on a monthly basis. This sampling is applied to three geographically distinct populations of impala in the Kruger National Park, on a three monthly rotation cycle.

Bovine tuberculosis

This bacterial disease has a wide host spectrum, and has entered several free-ranging buffalo populations (Guilbride et al. 1963; Woodford 1982; Bengis et al. 1996; De Vos et al. 2001), as well as kudu (Thorburn and Thomas 1940; Keet et al. 2001a) and lechwe (*Kobus leche*) (Gallagher et al. 1972). These species all appear to be efficient maintenance hosts, with aerosol transmission predominating. Infection spills over into predators and scavengers that ingest infected material, and frequently involves the mesenteric lymph nodes, with secondary haemotogenous spread to distal sites, including lungs, bones, joints, spleen, kidneys and serosal surfaces (Keet et al. 1996; Keet et al. 2001b). Aerosol and percutaneous infection are also important transmission modes in lions (*Panthero leo*).

Bovine tuberculosis (bTB) is a slow progressive disease with a long sub-clinical phase, lasting months to years. In buffalo, lechwe, baboons (*Papio spp*.) and warthogs, only animals with disseminated or advanced disease show any clinical signs, which may include coughing, emaciation, staring hair-coat, non-healing skin lesions, depression and lameness. Therefore scanning surveillance generally only detects the tip of the iceberg. Kudu, however, frequently develop overt swellings of one or more of the lymph nodes of the head, at a relatively early stage. The parotid lymph nodes, in particular, tend to enlarge massively due to abscess formation, and sinus tracts draining muco-purulent material are commonly seen below the ears.

Lions frequently present with emaciation, swellings of bones and synovial structures, and non-healing bite wounds with underlying granulomatous infection of the subcutaneous and muscular tissue.

In most species necropsies, or non-lethal sampling with *ante mortem* testing using the intradermal tuberculin or blood-based tests (if validated for the species), are necessary for bTB detection and monitoring. There are unfortunately no sensitive or specific *ante mortem* diagnostic tests currently available for pachyderms.

Rabies

On the African continent, rabies has been diagnosed in 33 carnivorous and 23 herbivorous species, with regional variation in the dominant role-players (Swanepoel 1994). Scanning surveillance for rabies involves the sampling of individuals of any species that display abnormal behaviour such as extreme aggression, dumbness, tameness, aimless wandering, paralysis, hypersexuality and excessive vocalisation. Salivation and an inability to drink or swallow may also be seen. For diagnostic reasons, suspect animals should not be shot in the brain.

Rinderpest

Rinderpest was possibly the most serious infection ever to affect mammals on the African continent, causing the devastation of populations of susceptible species from the late 19th to the 21st Century. Over this period, several strains affected a wide range of artiodactyls with particular virulence expressed in buffalo, tragelaphine antelope, giraffe and warthog. The disease significantly reduced populations, with mortalities anecdotally quoted at 90% during the early pandemic and confirmed at 60% amongst buffalo in Kenya in the mid 1990s (Kock et al. 1999a). Such was its impact that it may have influenced the current distribution of some species (Rossiter 2003). Intermittent *ad hoc* surveillance of wildlife populations was undertaken, but the apparent persistence of the virus in wild mammals at the end of the Pan African Rinderpest campaign, resulted in the launch of a major epidemiosurveillance initiative. This has involved over 30 African countries, and employed passive and active

Box 10.4 (continued)

methods of surveillance, focusing on buffalo but also including a wide range of other species (Kock et al. 2006; Kock 2008). Epidemiological evidence from buffalo and some other species showed that wildlife were not able to act as a long-term reservoir but that they could prolong epizootics, and that the current strategy for eradication remains valid. There has been no confirmed infection in wildlife since 2001 (in Meru National Park, Kenya), and it is hoped that the disease is now eradicated. During the campaign it was also possible to monitor for peste des petite ruminants (PPR) as part of differential diagnosis and evidence for circulation was established in some species (particularly buffalo). The invasion of old rinderpest strongholds with PPR is perhaps not surprising given that vaccination is cross protective between these two diseases.

Summary

These examples illustrate the multi-faceted approaches that are required to establish a meaningful disease surveillance system for free-ranging populations of wild African mammals. The sampling opportunities presented during any wildlife management activities need to be maximised and followed by intensive diagnostic screening and detailed necropsies, where appropriate. Efficient data collection, storage and management are essential, and the value of serum and tissue storage banks for retrospective studies and analysis cannot be over stated.

10.6 Conclusions

Traditional wildlife epidemiosurveillance based on passive and active ongoing reporting should be expanded to all countries and areas where sufficient resources are available. The results need to be collected by international organisations such as the OIE and then shared at a global scale. Once such a system is available, efficient early warning of emerging risks will require further development of approaches in three fields in particular.

10.6.1 Sentinel Surveillance

Wild animals can be used for the detection of emerging infectious diseases (EID) or pathogens, because they are often more at risk of infection than humans or domestic animals. The use of wildlife sentinels may be a particularly valuable approach to surveillance for emerging zoonotic infections, many of which have their origins in wild hosts. For example, wild lagomorphs (Lane et al. 1991) and deer (Gallivan et al. 1998) are exposed to ticks

carrying the bacterium (*Borrelia burgdorferi*) that causes Lyme disease in humans and so may be used as sentinels during disease surveillance. Certain taxa may be relatively more efficient at concentrating some pathogens, for instance predators at the top of food chains or scavengers that may be exposed to infectious carcasses (Smith 1994; Leighton et al. 1995). Plans for animal based surveillance of human infections have been considered in the field of public health, such as using the model of animal rabies surveillance (Childs et al. 2007), but as yet there are few practical projects that make use of animal sentinels for human health decision making (Rabinowitz et al. 2005). In addition, once a disease control campaign is underway, monitoring wildlife may be the only way to check whether pathogens are still circulating (Couacy-Hymann et al. 2005).

10.6.2   Risk Surveillance

As discussed earlier, surveillance can focus on critical transmission routes or on specific sites where the local ecology favours the probability of outbreaks. Risk-assessment methods can be used to inform the design of the surveillance approach such that it is optimised for the early detection and management of diseases (Stärk et al. 2006). This may involve targeting of wild animal populations that have a high probability of exposure to diseases or hazards. McKenzie et al. (2007) developed a methodology to prioritise pathogens for a wildlife disease surveillance strategy in New Zealand. The risk evaluation was based on the probability of importing pathogens using the framework recommended by the OIE (Murray 2004). The relative risks of different pathogens were represented by ranked scores for each of several taxonomic groups of hosts, allowing the priorities for surveillance to be clearly identified.

Observations of abnormal behaviour in terrestrial mammals have been used for decades in Europe to monitor rabies (WHO 2008b). This is an example of efficient risk-based surveillance. Surveillance of wild animals at rescue centres, or in sites at risk (as adopted for Highly Pathogenic Avian Influenza H5N1 in Europe: Pittman et al. 2007) are other examples of risk-based surveillance.

10.6.3   Syndromic Surveillance

Syndromic surveillance is designed to improve early detection of outbreaks by using existing data monitored in real time (Henning 2004). Efficient syndromic surveillance has to be based on clear definitions of cases, which could be recognised by computer programmes (medical informatics). As the data processing must be optimised to be efficient (standardisation of cases, data extraction and analysis), only well-established wildlife surveillance systems are likely to be able to operate such 'epidemio-surveillance'. Syndromic surveillance is an established approach in human epidemiology, but is still in its infancy as a tool for wildlife disease detection. Since

clinical signs and lesions are difficult to observe in wildlife, syndromic surveillance may often be difficult to achieve in practice (Vourc'h et al. 2006). Also, the use of this approach to provide early identification of a potential risk to human or domestic animal health from diseases in wild hosts, assumes that the pathogen will have similar clinical effects in all these hosts. However, this of course could not be assessed until the causative agent was identified and described. Despite these potential limitations, syndromic surveillance holds much promise, especially where data from long term wildlife disease monitoring is already available (Zeng et al. 2005).

10.6.4   Future Challenges

The above approaches to disease surveillance are by no means mutually exclusive, and could be used in combination to improve detection and the prediction of future risks. New high throughput approaches such as microarray technology will enable more wildlife samples to be screened for more pathogens, and as this technology improves so more sophisticated surveillance systems may be developed. However, ultimately the reliable prediction of future outbreaks rests largely on our ability to understand the origins and drivers of disease emergence.

During the preparation of this chapter, the director general of OIE stated "*surveillance of wildlife diseases must be considered equally important as surveillance and control of diseases in domestic animals. Wildlife often acts as sentinels for animal diseases thus allowing an effective management and control of the diseases in domestic animals*" (Vallat 2008). The majority of human emerging infectious diseases (72%) originate in wildlife (e.g. SARS, Ebola), a trend which has increased significantly in recent times (Jones et al. 2008). In addition to these "*practical reasons*" it is the duty of humanity "*to maintain biological diversity, have better knowledge of animal sanitary statuses and prevent species at risk from disappearing while protecting the human and domestic animal populations from the introduction of diseases*" (Vallat 2008). Thus the road forward is laid out: scientists, veterinarians, game managers and wildlife conservationists, all have to build a new paradigm in the field of health and disease surveillance in wildlife.

With a few notable exceptions, wildlife disease monitoring or surveillance systems across the globe are largely in their infancy. New concepts are constantly being developed or adapted from experiences gained in public health. Novel technologies are emerging that can be applied to wildlife disease diagnostics, and these will require new approaches to collecting and processing data. Such developments will undoubtedly improve the efficiency of monitoring and surveillance of disease in wild mammals in the near future. Nevertheless, the costs of implementing such systems can be a major impediment, particularly in developing countries. The cooperation of the wealthier nations is therefore necessary to enlarge surveillance at a global scale. As most EIDs originated in the Southern hemisphere (Jones et al.

2008), the money spent there will represent a wise investment in the preservation of health in the more affluent nations of the North. If we are to successfully antici-pate and manage the risks emanating from disease in wildlife in the future, then we must view the financial investment required to develop effective surveillance sys-tems in relation to the potential costs of doing nothing.