

Guidelines for Wildlife Disease Risk Analysis









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Fax: 33-(0)1 42 67 09 87 E-mail: oie@oie.int www.oie.int

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© Cover images from left to right:

- 1. Zebra and domestic animals share a grazing area near a local village in the buffer zone of Limpopo National Park, Mozambique. Photo courtesy of Michael Kock, 2010
- 2. From hunter to market table: animals throughout Asia and Africa are sought for human consumption. Photo courtesy of William B. Karesh, EcoHealth Alliance (right)
- 3. An elephant monitoring team patrols coastal forest in Gabon where elephants and other wildlife are prominent parts of the landscape. Photo courtesy of Michael Kock, 2004
- 4. Little red flying fox (*Pteropus scapulatus*). Photo courtesy of Mdk572 Wiki Creative Commons (http://creativecommons.org/licenses/by-sa/3.0/)
- 5. Collecting samples for avian influenza diagnostic testing from a gull during a HPAI H5N1 outbreak in Mongolia. Photo courtesy of William B. Karesh, EcoHealth Alliance
- 6. A gas flare at the Rabi Kounga oilfields located in the Ogooué-Maritime Province of Gabon attracts birds and other wildlife seeking warmth and insects. Photo courtesy of Michael Kock, 2004
- 7. Collecting samples for avian influenza diagnostic testing from a whooper swan during an HPAI H5N1 outbreak in Mongolia. Photos courtesy of William B. Karesh, EcoHealth Alliance
- 8. Gujarati cows: cows throughout India are often treated with diclofenac, a veterinary drug that reduces pain and inflammation. Photo courtesy of Richard Kock, Royal Veterinary College of London
- 9. Waterfowl on the Hakaluki Haor, a protected wetland in eastern Bangladesh. Photo courtesy of Parviez Hosseini, EcoHealth Alliance
- 10. Green-eyed tree frog (*Litoria genimaculata*). The green-eyed tree frog is one of several species threatened by chytridiomycosis, a disease that has been associated with declines in amphibian populations worldwide. Photo courtesy of Lee Skerratt, James Cook University, Townsville, Australia, 2005

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Contributors

The IUCN/OIE Guidelines for Wildlife Disease Risk Analysis (DRA) (hereafter 'Guidelines') was compiled by the IUCN Species Survival Commission's (SSC) Wildlife Health Specialist Group (WHSG), working in concert with the Conservation Breeding Specialist Group (CBSG), Reintroduction Specialist Group (RSG) and Invasive Species Specialist Group (ISSG). EcoHealth Alliance and the Royal Veterinary College (RVC) provided administrative support for the project and staff time.

The IUCN/OIE *Guidelines for Wildlife DRA* was primarily developed under the leadership of Richard Kock (Royal Veterinary College), William B. Karesh (EcoHealth Alliance), Lee Skerratt (James Cook University), Matt Hartley (Zoo and Wildlife Solutions Ltd) and Dominic Travis (Ecosystem Health Initiative, University of Minnesota College of Veterinary Medicine). Rosemary Barraclough and Katharina Stärk provided technical review, and Lisa Starr and Catherine Machalaba provided editorial support for the document. Richard Jakob-Hoff (New Zealand Centre for Conservation Medicine, Auckland Zoo) served as the Lead Editor for the overall project leading to these guidelines and a comprehensive toolkit, the *Manual of Procedures for Wildlife Disease Risk Analysis* (hereafter *Manual*). The IUCN SSC groups provided invaluable information about the needs related to wildlife DRA tools through a survey of the SSC membership.

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Initial plans were developed at the Disease Risk Analysis Tools Workshop at the Auckland Zoo, New Zealand, 4–7 April 2011, sponsored by the Auckland Zoo, Landcare Research, the New Zealand Department of Conservation and the IUCN-SSC Conservation Breeding Specialist Group. It was decided at this meeting that a policy promotion document (this *Guideline*), as a standalone, would best support the future global dissemination and use of the main *Manual*.

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Executive summary

In this document 'wildlife' refers to the World Organisation for Animal Health (OIE) definition of wild animal – an animal that has a phenotype unaffected by human selection and lives independent of direct human supervision or control. To further clarify the discussion, the term 'disease' in this text refers broadly to any impairment of the normal structural or physiological state of a living organism resulting from its physiological response to a hazard. In this case a 'hazard' is defined as: 'a biological, chemical or physical agent in, or a condition of, an animal or animal product with the potential to cause an adverse health effect'.

Disease risk analysis (DRA) is an important tool for analysing the risks of disease introduction or emergence in a population (we use emerging disease to describe those that are caused by newly identified species or strains (e.g. SARS (severe acute respiratory syndrome), HIV/AIDS (human immunodeficiency virus/acquired immune deficiency syndrome) that may have evolved from a known infection (e.g. influenza) or spread to a new population (e.g. West Nile virus) or geographic area or be re-emerging infections, such as drug-resistant tuberculosis. A DRA can also help to assess the risk of disease spill-over (when a disease moves from one species to another). Often DRA methods are used to assess a disease risk, which is precipitated by a new or potential action, such as movement (intentional or accidental) of a species into a new habitat. The end-goal of the DRA is to provide efficient and costeffective disease prevention and mitigation strategies.

DRA has increasingly been used to inform agricultural trade decisions and conservation-based species reintroduction or translocation efforts; however, especially as human-wildlife and domestic animal interactions increase, its potential use is much wider in the conservation field and beyond. Although international trade regulations for animals and animal products are already in place, a standard approach is still needed for assessing disease risks specific to conservation. The IUCN/OIE Guidelines for Wildlife DRA presents such an approach. The purpose of this document is to encourage readers to consider DRA as a planning tool and to direct readers to the technically comprehensive Manual of Procedures for Wildlife Disease Risk Analysis for implementation strategies.

These introductory Guidelines highlight the following key messages:

- Wildlife disease risks have immediate implications for species conservation, as well as wider relevance to other disciplines including human and livestock health, agriculture, economics, trade and ecosystems services.
- Wildlife DRA can and should be applied to a variety of situations and disciplines, including animal translocation or reintroduction scenarios but also in agricultural expansion, conservation planning and tourism, development of transport networks, urban and rural residential design, extractive industries, watershed and land-use planning, sanctuary planning, assessing bushmeat risks and even employee health.
- The main components of wildlife DRA are hazard identification, risk assessment, risk management and risk communication.
 Execution of these components is aided by the efforts of the technical team of wildlife managers and other stakeholders, the DRA tool selection, and data collection and analysis.
- Wildlife DRA allows for great flexibility around the level of available or devoted resources (i.e. financial, time or technical capabilities).
- Wildlife DRA provides an open, transparent process that can be easily followed for policy and risk management discussions.
- Importantly, rather than risk elimination, wildlife DRA promotes risk reduction. This allows for solutions that reduce risk while aiming to accommodate stakeholders' goals. This is predicated upon the fact that there is often no chance of obtaining 'zero' risk.

The IUCN/OIE *Guidelines for Wildlife DRA* intend to provide decision makers (e.g. wildlife managers, public and environmental health officials, government agencies, and industry representatives) with the information needed to integrate the wildlife DRA process into their work. It is hoped that the wildlife DRA process will be utilised on a wide scale to encourage risk mitigation strategies that are mutually beneficial to a variety of stakeholders.

Background and motivation

Disease plays an important role in the natural environment, serving as a regulator of the genetic fitness of wildlife through selective pressure in evolutionary processes. Conversely, it has been shown that the loss of certain microorganisms and parasites can be detrimental to the healthy functioning of ecosystems and species alike. Unfortunately, human-induced changes in our environment caused by habitat destruction or modification, industrial and urban development, population growth and global movement of people and animals have fundamentally changed the way disease affects not only wildlife but also entire ecosystems. These changes require a way of looking at disease that considers the biological, political and economic value of wildlife and the consequences of biodiversity loss. A process known as disease risk analysis (DRA) has been adopted by IUCN and other organisations to analyse and manage the possible outcomes of situations involving disease. These Guidelines demonstrate the importance of DRA specifically for wildlife and promote the use of the larger Manual of Procedures for Wildlife Disease Risk Analysis.

The most well recognised approaches to DRA are the processes set out in the World Organisation for Animal Health (OIE) *Terrestrial Animal Health Code* (www.oie.int/international-standard-setting/terrestrial-code/) and the Codex Alimentarius Commission (www.codexalimentarius.org). These documents focus primarily on import policy and food safety, respectively. Drawing on expertise across several disciplines, IUCN has built upon this existing OIE framework to address issues of biodiversity loss.

Wildlife DRA should be used in combination with other guidelines that promote evidence-based practices. For example, animal reintroduction planning should employ the use of the IUCN Reintroduction Guidelines as a source of practical information to supplement and guide DRA efforts (*Guidelines for Reintroductions and Other Conservation Translocations* (2013) can be found at http://www.issg.org/pdf/publications/RSG_ISSG-Reintroduction-Guidelines-2013.pdf).

Disease risk analysis – a means of conserving wildlife and biodiversity

Historically, DRA frameworks were applied ad hoc to situations involving wildlife often without a standardised approach. DRA for wildlife has been created to provide a consistent framework specifically targeted to situations that involve wildlife. The Manual, to which these Guidelines refer, describes the wide range of actions or events for which wildlife DRA might be appropriate.

When does DRA have value to decision makers?

A DRA has value to decision makers in all cases in which wildlife may be involved in, or affected by, disease occurrence. This can include the movement of animals or their products, exposure to toxins, investigations of wildlife population decline and analysis of risks associated with wildlife interactions with people or their domestic animals. DRA for wildlife is of value whenever wildlife, their products (e.g. hides, antlers, etc.) or their samples (e.g. blood, urine, etc.) are involved.

Who is affected in these cases?

- The animal or animals in question (exposure to a pathogen or toxin could cause disease outbreaks and/or decline in a population).
- Other animals exposed directly or indirectly during and after an event (the event could be animal movement, urban development, changing landuse).
- Other species of plants or animals that share the same habitat.
- Humans that come into contact with wildlife.

What type of organisation can benefit from using DRA?

- Public health agencies to help formulate policies and develop programmes focused primarily on human health.
- Conservation organisations to assist with designing wildlife protected areas, investigating wildlife population decline or guiding animal translocation or reintroduction efforts.
- Strategic planners for economic development (e.g. ecotourism projects), agricultural extension, development of transport networks, extractive industries, watershed and land-use planning, and urban and rural residential design (e.g. to analyse the risks of Lyme disease emerging in a new park).
- Government agencies to assist with the formulation of guidelines to be used at local, national or international levels.

In addition to its use prior to planned or intentional movement of wild animals or animal products, the wildlife DRA process is increasingly being applied to situations in which public health, domestic animal health or wildlife population health is at risk. In some cases, a thorough DRA will reveal that current risk reduction or risk management practices are either already adequate or could be easily adapted from other existing sources. These practices may include disease testing, quarantine, containment, disinfection or vaccination. In other cases, the DRA will reveal information or procedural gaps that need to be addressed prior to implementing actions involving the animals, people or habitat.

Steps in the disease risk analysis process

The DRA framework we propose is based on the one developed by the World Organisation for Animal Health (OIE), which is used to identify, assess and manage the risks posed by animal diseases with a focus on economic and human health impacts.

The term 'risk analysis' refers to the overall process regardless of the format used or how individual

components are defined. The risk analysis begins with problem description (the process of describing and justifying the problem or question) and then consists of five interconnected components (Fig. 1): risk communication; hazard identification; risk assessment; risk management; and implementation and review. Each component of the risk analysis is focused on answering basic question(s).

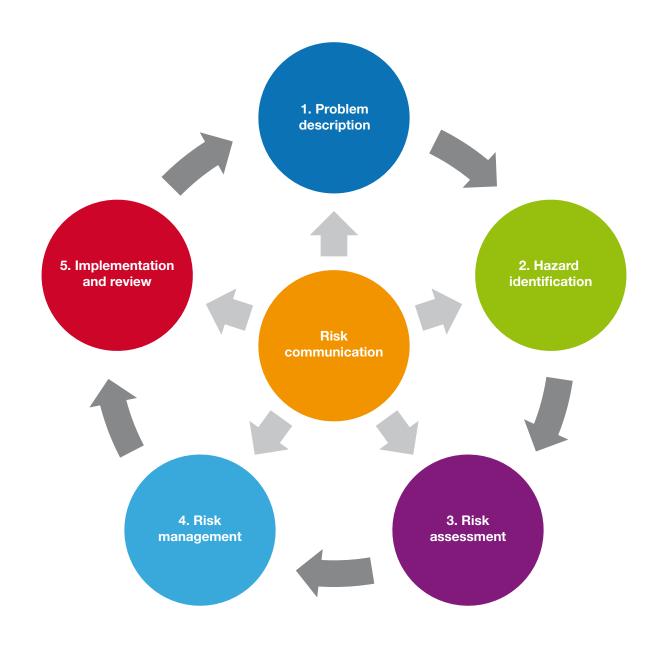


Fig. 1 Steps in the disease risk analysis process

Risk communication (applies throughout all disease risk analysis steps)

Purpose: Engage with a wide group of technical experts, scientists and stakeholders to maximise the quality of analysis and probability that recommendations arising will be implemented.

Questions: 'Who has an interest, who has knowledge or expertise to contribute and who can influence the implementation of recommendations arising from the DRA?'

Problem description

Purpose: Outline the background and context of the problem, identify the goal, scope and focus of the DRA, formulate the DRA question(s), state assumptions and limitations and specify the acceptable level of risk.

Questions: 'What is the specific question for this DRA, and what kind of *risk analysis* is needed?'

Hazard identification

Purpose: Identify all possible health hazards of concern and categorise into 'infectious' and 'non-infectious' hazards. Establish criteria for ranking the importance of each hazard within the bounds of the defined problem. Consider the potential direct and indirect consequences of each hazard to help decide which hazards should be subjected to a full risk assessment. Exclude hazards with zero or negligible probability of release or exposure, and construct a scenario tree for remaining, higher priority hazards of concern, which must be more fully assessed (Step 3).

Questions: 'What can cause disease in the population of concern?', 'How can this happen?' and 'What is the potential range of consequences?'

Risk assessment

Purpose: To assess for each hazard of concern:

- a) the likelihood of release (introduction) into the area of concern;
- b) the likelihood that the species of interest will be exposed to the hazard once released;
- c) the consequences of exposure.

On this basis the hazards can be prioritised in descending order of importance.

Questions: 'What is the likelihood and what are the consequences of an identified hazard occurring within an identified pathway or event?'

4 Risk management

Purpose: Review potential risk reduction or management options and evaluate their likely outcomes. On this basis decisions and recommendations can be made to mitigate the risks associated with the identified hazards.

Questions: 'What can be done to decrease the likelihood of a hazardous event?' and 'What can be done to reduce the implications once a hazardous event has happened?'

5 Implementation and review

Purpose: To formulate an action and contingency plan and establish a process and timeline for the monitoring, evaluation and review of risk management actions. The review may result in a clearer understanding of the problem and enable refinement of the DRA.

Questions: 'How will the selected risk management options be implemented?' and, once implemented, 'Are the risk management actions having the desired effect?' and, if not, 'How can they be improved?'

Wildlife disease case studies – disease risk analysis put into practice

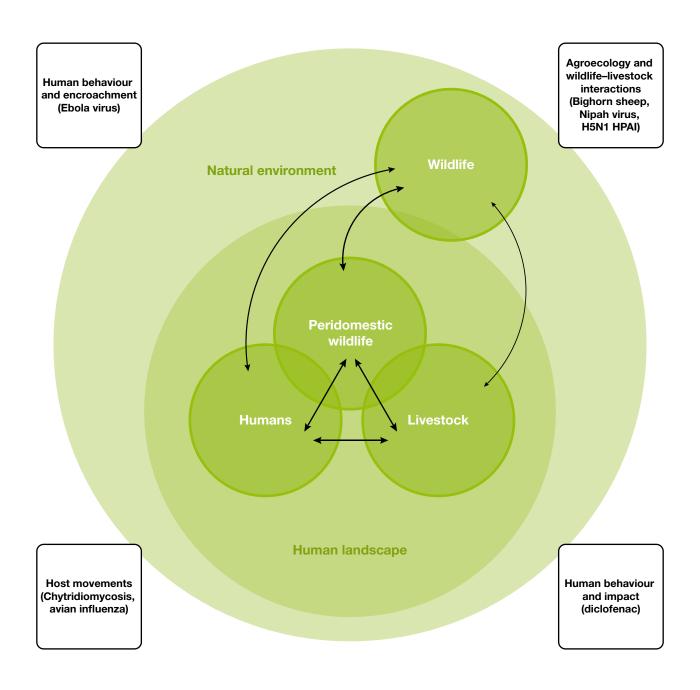


Fig. 2
Pathogen flow and drivers at the human–livestock–wildlife interface
The arrows in Figure 2 indicate direct, indirect or vector-borne pathogen flow
Each box represents a driver for which a case study is provided in the text

The case of the bighorn sheep reintroduction: not as easy as it seems

- Bighorn sheep (Ovis canadensis), a free-ranging species that was once very abundant throughout North America, has experienced population decline from over two million individuals at the turn of the century to only several thousand individuals decades later (Goodson 1982).
- Scientific studies have indicated that their populations have declined in large part as a result of diseases transmitted from domestic sheep that increasingly have shared the same grazing territory.
- Free-ranging bighorn sheep are susceptible to many diseases that domestic sheep can carry, including scabies, lungworm and pneumonia (Callan et al. 1991).

- Outbreaks of pneumonia, in particular, have been shown to influence the distribution of bighorn populations throughout North America, and there have been several large-scale die-offs due to pneumonia in both the United States and Canada (Shannon et al. 1995; Hobbs and Miller, 1992; Jorgenson et al. 1997; Valdez and Krusman, 1999).
- Disease has also been shown to compound the effects of other stressors that already threaten bighorn survival such as development on, or near, bighorn sheep habitat, internal and external parasites acquired from domestic animals, and overcrowding on rangeland (Garde et al. 2005).
- Reintroduction attempts for bighorn sheep have had mixed results owing to infectious diseases.
- Disease risk analyses are now being used by wildlife agencies to help guide future planning and to improve conservation outcomes for the reintroduction of bighorn sheep (USDA 2006).



Desert bighorn sheep being released in Southern California with a tracking collar
Bighorn sheep are at risk from diseases carried by domestic sheep that share the same grazing areas, so knowing where bighorn are and where they interface with domestic sheep is very valuable in developing management plans
Photo courtesy of Michael D. Kock

Amphibian population decline

- Chytridiomycosis (caused by the fungus Batrachochytrium dendrobatidis) has been associated with the extinction of approximately 100 amphibian species and the severe decline of many more from the late 1970s onwards (Skerratt et al. 2007).
- Amphibian species in protected, relatively pristine habitats have been particularly affected, showing that traditionally 'protected' areas are not immune to introduced diseases (Skerratt et al. 2007).
- Spread of the fungus may be related to increased international movement of amphibian species for use as laboratory animals, food or pets (Weldon et al. 2004).
- Large population sizes that are distributed through a range of climates and habitats are more resilient to infection and decline owing to environmental constraints on the pathogen. This is a good

- example of the positive correlation between high biodiversity and increased resilience to threats and change (Murray and Skerratt 2012).
- The global community is now responding to the threat of chytridiomycosis through improving the biosecurity of free-ranging amphibian populations, ex situ conservation (including captive breeding), and researching ways of mitigating disease transmission in situ (Australian Government 2006; Gagliardo et al. 2008; OIE 2011).
- A DRA could contribute to the success of both ex situ and in situ programmes for amphibians by identifying the most important risk factors for disease exposure and transmission and approaches to prevention and control.



Green-eyed tree frog (Litoria genimaculata)
The green-eyed tree frog is one of several species threatened by the chytrid fungus, a malady that may be responsible for declines in amphibian populations worldwide
Photo courtesy of Lee Skerratt, James Cook University, Townsville, Australia

Fatal consequences from changing land use: Nipah virus's deadly cycle

- The Nipah virus outbreak among pigs and pig farmers in Malaysia in 1998 and 1999 demonstrated that human-driven intensification of contact among wildlife, livestock and people can have deadly consequences.
- Nipah virus is carried by pteropid fruit bats, which do not show signs of the disease when infected (Field 2009).
- Swine production expanded rapidly in the 1990s in Malaysia, resulting in clearing of forest in pteropid bat habitat (Chua et al. 2002; Pulliam et al. 2012).
- Some swine producers maintained mature fruit trees over open pigsties, resulting in nighttime feeding by pteropid bats and subsequent infection of pigs via bat urine and faecal or salivary ground (Luby et al. 2009).
- contamination of partially eaten fruits that fell to the

Little red flying fox (Pteropus scapulatus) These little red flying foxes are one of many species of fruit bats affected by the deadly Nipah virus Photo courtesy of Mdk572 Wiki Creative Commons (http://creativecommons.org/licenses/by-sa/3.0/)

- It is suggested that pigs, their semen and infected farm workers moving between pig farms have facilitated the movement of the virus among pig farms (CFSPH 2007; Goh et al. 2000).
- The World Health Organization (WHO) has estimated the number of people infected with Nipah virus that die (the case fatality rate for humans) at 40% to 75%. In addition to the effect on human health, agriculture in the region was severely affected as these outbreaks led to the culling of more than one million swine and the implementation of strict quarantine measures to prevent further human to human transmission (Ahmad 2000).
- Analysis of risk factors identified the removal of fruit trees from pig farms as a mechanism for preventing the future introduction of the disease, and this has become standard protocol in Malaysia (Nahar et al. 2010; Siembieda et al. 2011).
- The addition of wildlife DRA to agricultural and industrial development planning could help to identify potential disease risks, such as Nipah virus, and in turn guide appropriate risk mitigation strategies to prevent an outbreak.

Handling and consumption of wildlife: prevention is better than cure

- Human populations are increasingly encroaching into wildlife habitats and facilitating an increased trade in bushmeat and other wildlife products.
 This increases human contact with a diversity of wildlife and their pathogens.
- Annual bushmeat consumption in Central Africa alone has been estimated to be a billion kilograms, comprising millions of individual wild animals (Karesh et al. 2005).
- Diseases such as HIV infection/AIDS, Ebola haemorrhagic fever virus, monkeypox, and SARS have all been linked to the handling of wild animals for the purpose of human consumption (Greger 2007).
- Disease transmission can also occur from humans or domestic animals to wildlife, as documented for endangered mountain gorillas, which have experienced deadly respiratory infections from human metapneumovirus and human measles.
 Human-facilitated introduction of domestic species to an area may bring in diseases such as rabies or bovine tuberculosis (Bengis et al. 2002).
- DRA in this situation would be similar to the approaches used for determining risks from foodborne infections, including value chain analysis, i.e. determining all the steps from food source to consumption and identifying appropriate monitoring and intervention points.
- A full DRA for bushmeat and other wildlife products intended for trade would include the risk of acquiring animals, handling and transport, consumption and/or use, the implementation of disease prevention strategies, and identification of the relative risks of various products and uses.



From hunter to market table

Animals throughout Asia and Africa are sought for human consumption. This hunter pictured here (in Sudan) represents a common beginning of the wildlife trade cycle and the bushmeat on the market table in Asia a familiar end. As hunters reach deeper into the forest, seeking wildlife for food, both humans and wildlife can be exposed to disease

Photos courtesy of Richard Kock (left) and William B. Karesh, EcoHealth Alliance (right)

• 'Bird flu': disease risk analysis helping to direct resources

Local newspapers hypothesise that wild bird migration may contribute to the spread of avian influenza. Partially in response to popular media and some scientific reports, the culling of wild birds was proposed in some parts of the world as a solution to control the spread of the disease.

- For over a decade, wild birds have been implicated as a source or a vector of highly pathogenic avian influenza (HPAI) H5N1.
- While HPAI H5N1 has been found in wild birds, to date no long-term reservoir of HPAI H5N1 has been identified in wild bird populations, despite over a million samples tested from a wide range

- of species and habitats across the globe. It is rarely found in live wild birds, limiting its potential for spread through migration and contact with other animals (Scientific Task Force on Avian Influenza, 2008).
- Follow-up research has shown that domestic poultry and related trade and production and inadequate disease control methods were a primary driver of the HPAI H5N1 outbreaks (Hogerwerf et al. 2010).
- A DRA conducted after the initial outbreaks would have prompted research to quantify the risk that wild birds posed in terms of HPAI H5N1 transmission to other wild birds, humans and poultry. A retrospective DRA can still use information gathered from field research conducted to date to guide current control methods.



Collecting samples for avian influenza diagnostic testing from a whooper swan during an HPAI H5N1 outbreak in Mongolia Photo courtesy of William B. Karesh, EcoHealth Alliance

Vulture mortality in India: an ecotoxicology case study

- Vultures serve a highly valuable ecological role through the removal of dead animal carcases and thereby contribute to the maintenance of public health (preventing the spread of disease agents) and the health of the ecosystem.
- From 1992 to 2007 several species of vultures, including the Oriental white-rumped vulture (*Gyps bengalensis*), Indian Vulture (*G. indicus*) and the slender-billed vulture (*G. tenuirostris*) experienced serious and rapid declines throughout Asia (Gilbert et al. 2002; Prakash et al. 2003).
- It was found experimentally that vultures ingesting cattle carcases recently treated with diclofenac, a popular non-steroidal anti-inflammatory drug, needed very little of the drug to succumb to kidney failure and eventually death (Oaks et al. 2004). Diclofenac residues in the tissues of dead cattle are highly toxic to vultures, resulting in up to 99% mortality in these birds (Prakash et al. 2005).
- This near extinction of *Gyps* species vultures was met with a resounding response from both governments and drug manufacturing companies. The national and local governments banned the veterinary use of diclofenac in 2006 and pharmaceutical companies have increased production of the alternative anti-inflammatory drug meloxicam (Cuthbert *et al.* 2011).

- Unfortunately, continued use of diclofenac in humans and animals has persisted.
- A DRA conducted now could help determine the potential impact of diclofenac in other species (particularly other scavengers) and help guide future production and licensing of similar compounds.



Oriental white-rumped vultures, Gyps bengalensis, feeding on a domestic water buffalo, Bubalus bubalis, in India
Photo courtesy of Munir Virani – The Peregrine Fund



Gujarati cows: cows throughout India are often treated with diclofenac, a veterinary drug that reduces pain and inflammation This drug is lethal to vultures that ingest the bovine carcases after death

Photo courtesy of Richard Kock, Royal Veterinary College of London

Overview of disease risk analysis methodologies and tools

Selecting the most appropriate tool for your situation

Many tools are available to support the DRA process, ranging from simple to complex, and these are presented in detail in the Manual. They may employ a simple paper and pencil, widely available software packages or highly sophisticated quantitative modelling programmes. Tool selection for a given scenario varies according to the team's expertise, the quantity and type of data that exist, and the time and resources available to collect additional information. Figure 3 hereafter highlights some common tools used to address the different phases of the risk analysis process. This figure reflects experience and is not meant to provide an exclusive list of tools, nor is it an endorsement of any specific software programme or company. The following section provides some initial guidelines for tool selection, including circumstances that favour qualitative or quantitative tools for risk assessment and management.

A note on the use of the term 'model'

A 'model', in the context of DRA, is a simplified representation of something that exists in the real world. This is an especially valuable process when trying to understand and/or assess relationships between dynamic systems such as the ecosystem, individual or populations of animals and microbiological disease-causing agents. A simple model may consist of a picture or diagram to help a discussion of how a biological system works. Complex models often consist of quantitative and/or spatial analyses using complex layers of data. The point is that models are an attempt to simplify the real world into something both understandable and representative.

The risk analysis process creates a logical model that helps to work systematically through the different aspects of the overall analysis from a science-based policy perspective (Fig. 2).

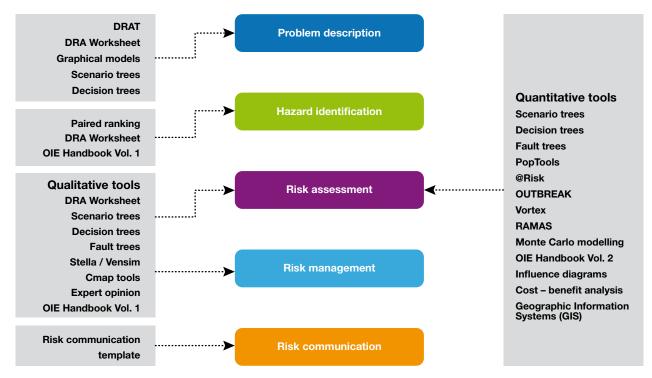


Fig. 3 Various tool types to assist the disease risk analysis process

The hazard identification step of the process involves the creation of scientifically explicit models of the disease hazards using qualitative or quantitative data. The risk assessment step results in an estimation of risk based upon the specific policy question while the analysis as a whole provides a scientific basis for the most appropriate policy response to minimisation of the identified risks. It is an iterative process and can be revisited at any time with new data or tools to improve the accuracy of the modelling and risk definition and quantification. Approaches for post hoc attention to risk assessment include the use of a Bayesian updating framework to identify both when and where new data are to be taken and how to incorporate these in updated assessments - this is part of SADA (spatial analysis for decision assistance) www.tiem.utk.edu/~sada/index.shtml.

Amount and quality of available data

Generally an insufficient amount or quality of data is available on wildlife to make meaningful *quantitative* risk assessments or precise estimates during the first iteration of the process. Therefore, the application of a structured qualitative approach is usually preferred as it readily incorporates lack of precision and it is the best way to use available information to analyse risks and generate the insights needed to make informed decisions about where to focus risk management actions.

Limited resources

Much can be accomplished with basic, easy to use tools such as pre-packaged programmes. Often qualitative tools are recommended for the first iteration of the process as they require fewer specialised resources (such as mathematical or programming skills and equipment) and can be conducted with the available information during group workshops.

Qualitative versus quantitative tools

Both qualitative and quantitative processes will highlight information gaps, which can be used to generate research priorities that can provide the quantitative data needed to further refine risk assessments.

In qualitative risk assessments the likelihood of the outcome, or the magnitude of the consequences, is expressed in pre-defined terms such as 'high', 'medium' or 'low'. In quantitative risk assessments the likelihood is expressed in terms such as 'one disease outbreak per 100 animal introductions' or 'failure to correctly identify one diseased animal out of 100'. Both qualitative and quantitative approaches to risk assessment are valid and, in practice, all risk assessment are usually first conducted qualitatively. Only if further insight is required is it necessary to attempt to quantify the risk. As North (1995) explains, quantitative '... risk analysis is best used to develop insights, and not to develop numerical results which might mistakenly be considered to be highly precise. The discipline of numerical calculation can help to sharpen thinking about risks involving high levels of complexity and uncertainty, and thereby enable conclusions to be drawn which could not have been reached solely on the basis of qualitative reasoning.'

Scale issues

Given the extensive impact that scale (temporal and spatial) has in ecological decision-making this needs to be addressed early on in DRA: not only increasing use of geographical information system (GIS) tools as decision support but also a broader context of conceptualising responses potentially occurring at different spatial scales, depending upon the species/communities/ecosystems of concern, is needed (Fuller et al. 2008). An example might be a DRA around the

development of fencing options for animal movement control that have broad ecological impacts and which can positively and negatively impact disease occurrence depending on the species and system considered. It is the broadening of the scope in DRA that wildlife DRA requires and which is very different from the conventional veterinary DRA, which is focused on the host and pathogen in the context of trade or animal movement.

Conclusion: wildlife disease risk analysis working in concert with other agencies

Varying DRA formats are currently being used by a diverse array of organisations. These separate guidelines originate from sectors including public health, agriculture, trade, the pharmaceutical industry and wildlife conservation. With a common theme in mind, the specific goals of each DRA may vary depending on the objectives of the individual organisation. IUCN's vision in presenting this approach to DRA is that it will be applied across all sectors concerned with wildlife disease and

in doing so reinforce the 'One Health' principle that recognises that the health of people, animals (domestic and wild) and the environment are interconnected. IUCN further hopes that the application of these *Guidelines* will help to promote a standardised and consistent approach to the use of DRA and assist in effective, evidence-based decision making with respect to wildlife interventions and management of wildlife species.

Useful links

IUCN/SSC – Wildlife Health Specialist Group (WHSG). Available at: www.iucn-whsg.org/

IUCN/SSC – Conservation Breeding Specialist Group (CBSG). Available at: www.cbsg.org/cbsg/

IUCN/SSC – Reintroduction Specialist Group (RSG). Available at: www.iucnsscrsg.org/

IUCN/SSC – Invasive Species Specialist Group (ISSG). Available at: www.issg.org/

OIE *Terrestrial Animal Heath Code.* Available at: www.oie.int/international-standard-setting/terrestrial-code/

FAO/WHO Health Standards – Codex Alimentarius. Available at: www.codexalimentarius.net/web/index_en.jsp

Guidelines for the In Situ Reintroduction and Translocation of African and Asian Rhinoceros (IUCN AfRSG/AsRSG publication). Available at: www.rhinoresourcecenter. com/index.php?s=1&act=refs&CODE=ref_ detail&id=1236875944 Conservation and Development Interventions at the Wildlife/Livestock Interface – Implications for Wildlife, Livestock and Human Health (IUCN/SSC Occasional Paper from the Animal and Human Health for the Environment and Development [AHEAD] Program). Available at: www.wcs-ahead.org/wpc_launch.html

Health Risk Analysis in Wildlife Translocations (OIE – Wildlife Disease Working Group). Available at: www.ccwhc.ca/wildlife_health_topics/risk_analysis/rskguidintro.php

FAO – EMPRES. Available at: www.fao.org/ag/againfo/programmes/en/empres/home.asp

IUCN/SSC AfESG Guidelines for the in situ Translocation of the African Elephant for Conservation Purposes. Available at: www.african-elephant.org/tools/trnsgden.html

IUCN Policy Paper: Enhancing the Science and Policy Interface on Biodiversity and Ecosystem Services. Available at: http://cmsdata.iucn.org/downloads/ipbes_position_paper_for_3rd_ipbes_meeting_may_2010_final_web.pdf

Centre for Evidence Based Medicine. Available at: www.cebm.net/

References

Ahmad K. (2000). – Malaysia culls pigs as Nipah virus strikes again. *Lancet*, **356** (9225), 230.

Australian Government (2006). – Threat abatement plan: infection of amphibians with chytrid fungus resulting in chytridiomycosis. Department of the Environment and Heritage, Canberra, Australia.

Bengis R.G., Kock R.A. & Fisher J. (2002). – Infectious animal diseases: the wildlife/livestock interface. *In* Infectious diseases of wildlife: detection, diagnosis and management (Part One) (R.G. Bengis, ed.). *Rev. sci. tech. Off. int. Epiz.*, **21** (1), 53–65.

Callan R., Bunch T.D., Workman G.W. & Mock R.E. (1991). – Development of pneumonia in desert bighorn sheep after exposure to a flock of exotic wild and domestic sheep. *J. Am. vet. med. Assoc.*, **198**, 1052–1056.

Chua K.B., Chua B.H. & Wang C.W. (2002). – Anthropogenic deforestation, El Niño and the emergence of Nipah virus in Malaysia. *Malays. J. Pathol,* **24** (1), 15–21.

Cuthbert R., Taggart M.A., et al. (2011). – Effectiveness of action in India to reduce exposure of *Gyps* vultures to the toxic veterinary drug diclofenac. *PLoS One*, **6** (5).

Field H.E. (2009). – Bats and emerging zoonoses: henipaviruses and SARS. *Zoonoses Public Health*, **56** (6–7), 278–284.

Fuller M.M., Gross L.J., Duke-Sylvester S.M. & Palmer M. (2008). – Testing the robustness of management decisions to uncertainty: everglades restoration scenarios. *Ecol. Appl.*, **18**, 711–723.

Gagliardo R., Crump P., Griffith E., Mendelson III J.R., Ross H. & Zippel K.C. (2008). – The principles of rapid response for amphibian conservation, using the programmes in Panama as an example. *Int. Zoo. Yb.*, **42**, 125–135.

Garde E., Kutz S., Schwantje H., Veitch A., Jenkins E. & Elkin B. (2005). – Examining the risk of disease: transmission between wild Dall's sheep and mountain goats, and introduced domestic sheep, goats, and llamas in the Northwest Territories. *Other Publ. Zoonotics wildl. Dis.* Paper 29.

Gilbert M., Virani M.Z., et al. (2002). – Breeding and mortality of Oriental white-backed vulture *Gyps bengalensis* in Punjab Province, Pakistan. *Bird Cons. Int.*, **12** (4), 311–326

Goh K.J., Tan C.T., et al. (2000). – Clinical features of Nipah virus encephalitis among pig farmers in Malaysia. *N. Engl. J. Med.*, **342** (17), 1229–1235.

Goodson N.J. (1982). – Effects of domestic sheep grazing on bighorn sheep populations: a review. *Proceedings of the Biennial Symposium of the Northern Wild Sheep and Goat Council*, **3**, 287–313.

Greger M. (2007). – The human/animal interface: emergence and resurgence of zoonotic infectious diseases. *Crit. Rev. Microbiol.*, **33** (4), 243–299.

Hobbs N.T. & Miller M.W. (1992). – Interactions between pathogens and hosts: simulation of pasteurellosis epizootics in bighorn sheep populations. *In* Wildlife 2001: Populations (D.R. McCullough & R.H. Barnett, eds). Elsevier Science Publishers, London, UK, 997–1007.

Hogerwerf L., Wallace R.G., Ottaviani D., Slingenbergh J., Prosser D., Bergmann L. & Gilbert M. (2010). – Persistence of highly pathogenic avian influenza H5N1 virus defined by agro-ecological niche. *Ecohealth*, **7** (2), 213–225.

Jorgenson J.T., Festa-Bianchet M., *et al.* (1997). – Effects of age, sex, disease, and density on survival of bighorn sheep. *Ecology*, **78**, 1019–1032.

Karesh W.B., Cook R.A., Bennett E.L. & Newcomb J. (2005). – Wildlife trade and global disease emergence. *Emerg. Infect. Dis.*, **11** (7), 1000–1002.

Luby S.P., Gurley E.S. & Jaghangir Hossain M. (2009). – Transmission of human infection with Nipah virus. *Clin Infect. Dis.*, **49** (11). 1743-1748. doi: 10.1086/647951.

Murray K.A. & Skerratt L.F. (2012). – Predicting wild hosts for amphibian chytridiomycosis: integrating host life-history traits with pathogen environmental requirements. *Hum. Ecol. Risk Assess.*, **18** (1), 200–224.

Nahar N., Sultana R., Gurley E.S., Jahangir Hossain M. & Luby S.P. (2010). – Date palm sap collection: exploring opportunities to prevent Nipah transmission. *Ecohealth*, **7** (2), 196–203.

Oaks J.L., Gilbert M., *et al.* (2004). – Diclofenac residues as the cause of vulture population decline in Pakistan. *Nature*, **427** (6975), 630–633.

Prakash V., Pain D.J., et al. (2005). – Catastrophic collapse of Indian white-backed *Gyps bengalensis* and long-billed *Gyps indicus* vulture populations. *Biol. Cons.*, **124** (4), 561–561.

Pulliam J.R., Epstein J.H., *et al.* (2012). – Agricultural intensification, priming for persistence and the emergence of Nipah virus: a lethal bat-borne zoonosis. *J. R. Soc. Interface*, **9** (66), 89–101.

Shannon N.H., Hudson R.J., Brink V.C. & Kitts W.D. (1975). – Determinants of spatial distribution of Rocky Mountain bighorn sheep. *J. Wildl. Manag.*, **39**, 387–401.

Siembieda J.L., Kock R.A., McCracken T.A. & Newman S.H. (2011). – The role of wildlife in transboundary animal diseases. *Anim. Health Res. Rev.*, **12**, 95–111.

Skerratt L.F., Berger L., Speare R., Cashins S., McDonald K.R., Phillott A.D., Hines H.B. & Kenyon N. (2007). – Spread of chytridiomycosis has caused the rapid global decline and extinction of frogs. *Ecohealth*, **4** (2), 125–134.

Scientific Task Force on Avian Influenza (STOAI) (2008). – What is the role of wild birds in the spread of HPAI H5N1? Available at: www.unep-aewa.org/publications/avian_influenza/ai_brochure_english.pdf.

United States Department of Agriculture (USDA) (2006). – A risk analysis of disease transmission between domestic sheep and bighorn sheep on the Payette National Forest. USDA, Washington, District of Columbia.

Valdez R. & Krausman P.R. (1999). – Mountain sheep of North America. University of Arizona Press, Tucson, Arizona.

Weldon C., du Preez L.H., Hyatt A.D., Muller R. & Speare R. (2004). – Origin of the amphibian chytrid fungus. *Emerg. Infect. Dis.*, **10** (12), 2100–2105.

World Organisation for Animal Health (OIE) (2011). – Chapter 8.1: Infection with *Batrachochytrium dendrobatidis*. *In* Terrestrial Animal Health Code, 14th Ed. OIE, Paris.

Guidelines for Wildlife Disease Risk Analysis

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The IUCN–OIE *Guidelines for Wildlife Disease Risk Analysis* will be of value to those policy-makers and decision-makers faced with the social, political and technical complexities involved in wildlife-disease-associated scenarios. It provides an overview of the science-based processes and tools available for wildlife disease risk analysis and their application to a broad range of contemporary issues, including human–wildlife interactions, domestic animal–wildlife interactions and the impacts of massive ecological change on biodiversity conservation. This is a companion volume to the *Manual of Procedures for Wildlife Disease Risk Analysis*.



INTERNATIONAL UNION FOR CONSERVATION OF NATURE

WORLD HEADQUARTERS Rue Mauverney 28 1196 Gland, Switzerland mail@iucn.org Tel +41 22 999 0000 Fax +41 22 999 0002 www.iucn.org

