

*Special Issue: Wildlife Parasitology*

# Emerging infectious diseases of wildlife: a critical perspective

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**We review the literature to distinguish reports of vertebrate wildlife disease emergence with sufficient evidence, enabling a robust assessment of emergence drivers. For potentially emerging agents that cannot be confirmed, sufficient data on prior absence (or a prior difference in disease dynamics) are frequently lacking. Improved surveillance, particularly for neglected host taxa, geographical regions and infectious agents, would enable more effective management should emergence occur. Exposure to domestic sources of infection and human-assisted exposure to wild sources were identified as the two main drivers of emergence across host taxa; the domestic source was primary for fish while the wild source was primary for other taxa. There was generally insufficient evidence for major roles of other hypothesized drivers of emergence.**

## Introduction

Be they impacting people, agriculture, or wildlife, emerging infectious diseases (disease-causing agents that rapidly increase in geographical range, host range, or prevalence) are acknowledged to be occurring at an increased rate globally [1–3]. Management to successfully mitigate these threats requires identifying and understanding their drivers. However, it is increasingly recognized that many reports of currently and recently emerging disease-causing agents may have insufficient supporting evidence to substantiate their status as such [4,5]. In such cases, frequently limited resources for research and management may be misallocated with respect to where they could make the most valuable impact. In addition, the ‘noise’ generated by spurious cases may obscure accurate assessments of emergence drivers and thus be misleading in considerations of suitable and effective management actions to decrease risk of emergence.

Here we conduct to the best of our knowledge the most critical review and assessment to date of the current and recent vertebrate wildlife emerging infectious disease lit-

erature (see [Box 1](#) for the methodology used). Our aim is threefold. First, we separate agents for which there is sufficient evidence of emergence from those for which there is insufficient evidence to support such a conclusion and interrogate the patterns observed with respect to host and agent taxa and the timing and geography of emergence. Second, based on only those agents with sufficient evidence, we objectively identify and rank in terms of importance the causes and drivers of disease emergence in vertebrate wildlife, to provide robust guidelines for management to mitigate such threats to wild populations (see [Box 2](#) for all of the potential drivers of disease emergence indicated by the full review). Third, we provide direction to researchers regarding where efforts would be best focused to further increase our understanding of, and thus our ability to prevent, such disease emergence.

## Amphibians and reptiles

Nine disease-causing infectious agents of amphibians and reptiles were identified with evidence of potential emergence from 2000 onward (Table S1 in the supplementary material online). Amphibians were the most affected group (with six potential agents) followed by turtles (with three). Almost half of the potential emergences are ongoing from the past century and there is no obvious temporal bias in those reported this century ([Figure 1](#)). There is also no strong evidence of any agent taxon bias, microparasite versus macroparasite bias, or geographical region bias within this set.

Of the nine agents identified, only three (all microparasites) were considered to have sufficient evidence of their current emergence ([Figure 1](#) and [Table 1](#)): *Batrachochytrium dendrobatidis* causing the disease chytridiomycosis in adult amphibians [6,7]; the related *Batrachochytrium salamandrivorans* in fire salamanders in The Netherlands [8]; and ranavirus causing mass mortalities of larval amphibians [9,10] (Table S1 in the supplementary material online). Both *B. dendrobatidis* and ranavirus are ongoing emergences from the past century, with the spread of ranavirus both within North America and to England and the continued global spread of *B. dendrobatidis*. *B. salamandrivorans* is a recent emergence.

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1471-4922/

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### Box 1. Literature review methodology

To provide an initial set of candidate disease-causing infectious agents that are potentially emerging or continuing to emerge, we applied a consistent set of search terms to the Web of Science and Google Scholar databases and the Google search engine. This set comprised all combinations of pathogen\*, parasite\*, or disease\* with each of the following in turn: emergence, emergent, emerging, resurgent, new, novel, expanding range, change\*, shift\*, switch\*, expansion\*, introduction\*. Searches were run separately for different host taxon sets (amphibians and reptiles, birds, eutherian mammals, fish, marsupials and monotremes) and the findings interrogated to generate a list of disease-causing agents for which there is some evidence of emergence from 2000 onward in wild host populations. Reports of newly discovered agents, expanding host or geographical ranges, increasing disease impacts, or increasing prevalence of known disease-causing agents were all considered indicators of potential emergence. However, cases where the evidence presented was entirely speculative or was (without other supporting evidence) the first host record for a known generalist parasite, the first geographical record for a known widespread parasite, reported in a single individual, or a new species or strain in a group known for its diversity across hosts were excluded. Agents with no known disease impacts were also excluded, as were agents with evidence for emergence in domestic populations only and reported diseases with putative but not yet confirmed causative agents.

To consider the drivers of emergence, a more conservative set of agents was derived from the 'potentially emerging' list. Specifically, we considered only those agents with sufficient evidence of emergence. This refinement was necessary since including cases that are not actually emerging (which considering the full list of

potentially emerging agents would likely do) would obscure our assessment of the relative importance of various drivers. By contrast, the potential loss of one or two actually emerging agents, while minimizing 'false positives' in this way, would not obscure our assessment as long as any potential biases generated by this approach are considered. We used the following criteria: evidence (not solely correlational) that the agent causes disease impacts at either the individual or the population scale, together with either: (i) evidence of a consistent trend of increase (or a maintained increase) in disease impact, host species range, or geographical range; or (ii), for epizootic outbreaks, evidence that the outbreaks observed are likely not snapshots of natural long-term variation in disease dynamics. For this second criterion, where agents have undergone monotonic increases in host or geographical range (or disease incidence or impact), we considered at least one survey of relevant host, spatial, and temporal extent prior to the potential emergence that shows a significantly lower level of infection to be sufficient. Where agents have sporadic outbreak dynamics, we required enough evidence of prior absence or difference to be confident that such outbreaks have not occurred previously (dependent on the size and duration of those currently/recently observed) for sufficiency.

Note that under our criteria the documentation of a new species or strain of infectious agent that is known to be variable in ecological timeframes is not considered emerging, unless such variation allows that agent to infect a novel host species or hosts in a new geographical region or at a novel level of infection or impact. Every time a new strain of the common cold appears, we do not consider the cold to be emerging; rather, it is part of the natural dynamics that characterizes this disease.

### Birds

Eight disease-causing infectious agents of birds were identified with evidence of potential emergence from 2000 onward (Table S2 in the supplementary material online), counting Lineages 1 and 2 of West Nile virus as distinct emergences. Six of these agents solely or mainly impact passerine birds while two impact waterfowl. A large proportion were initially reported from North America or Europe, also with a temporal bias in reporting; while two are ongoing from the past century, the other six were all first reported during 2000–2004 (Figure 1). All of the agents in this set are microparasites (with over half of them being viruses).

Of the eight agents identified, five (four viruses and one bacterium) were considered to have sufficient evidence of their current emergence (Figure 1 and Table 1): the ongoing spread of West Nile virus Lineage 1 [11,12] and *Mycoplasma gallisepticum* [13,14] in North America; the emergence and spread of avian influenza A (H5N1) across Asia, Europe, and Africa [15] [World Health Organization (2011) *H5N1 Avian Influenza: Timeline of Major Events* ([http://www.who.int/influenza/human\\_animal\\_interface/en/](http://www.who.int/influenza/human_animal_interface/en/))]; and the emergence and spread of both West Nile virus Lineage 2 [16,17] and Usutu virus [18,19] in Europe.

### Eutherian mammals

Eighteen disease-causing infectious agents of eutherian mammals were identified with evidence of potential emergence from 2000 onward (Table S3 in the supplementary material online). While the most common host orders were the Carnivora (both terrestrial and aquatic) and Cetacea, potential emergences were reported from a wide host range. As with birds, a large proportion of potential emergences were initially reported from North America or

Europe, again with a temporal bias in reporting; while four potential emergences are ongoing from the past century, ten were first noted during 2000–2004 compared with only three during 2005–2009 and one during 2010–2014 (Figure 1). The potentially emerging agents are strongly biased toward microparasites (particularly viruses and bacteria). Note that H5N1 is considered emerging in birds (with occasional spillover to eutherian mammals [20–23]) and thus is not counted here.

Of the 18 agents identified, only five (four microparasites and one macroparasite) were considered to have sufficient evidence of their current emergence (Figure 1

### Box 2. Potential drivers of disease emergence indicated by the full review

- Host species or population exposure to an infectious agent from other wild populations. Such exposure can occur through movement of the exposed host, or agent movement. It can be human-assisted or natural, and may be facilitated by agent adaptation to new hosts or vectors after initial emergence.
- Host species or population exposure to an infectious agent from domestic populations. Agents in domestic populations to which wildlife can be exposed may be the result of agent movement into and among populations, high host densities, transmission among species, and agent evolution in domestic populations.
- Host clustering/overcrowding/stress due to habitat modification.
- Host poor nutrition/food supply variation/dietary shifts.
- Host thermal stress/climate change.
- Waning host immunity/immune variation/immune system modulators.
- Host genetic instability/low genetic diversity/inbreeding.
- Favorable climate for vectors/other drivers of increasing vector numbers.
- Note that several of these drivers are not necessarily independent (e.g., waning host immunity may be caused by stress, poor nutrition, or genetic issues).

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