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Response to Comment on “Amphibian fungal panzootic causes catastrophic and ongoing loss of biodiversity”

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Lambert *et al.* question our retrospective and holistic epidemiological assessment of the role of chytridiomycosis in amphibian declines. Their alternative assessment is narrow and provides an incomplete evaluation of evidence. Adopting this approach limits understanding of infectious disease impacts and hampers conservation efforts. We reaffirm that our study provides unambiguous evidence that chytridiomycosis has affected at least 501 amphibian species.

In Scheele *et al.* (1), we quantified the impact of chytridiomycosis—a disease first described in 1998—on the world’s amphibians. Our contribution builds on previous work that inextricably links chytridiomycosis and global amphibian

declines (2) and is underpinned by extensive research on two fungal species that cause chytridiomycosis, *Batrachochytrium dendrobatidis* (*Bd*) and *B. salamandrivorans* (*Bsal*). Our assessment concluded that the disease has con-

tributed to the decline of at least 501 species, including 90 presumed extinctions. Our estimate is likely conservative, as the disease has caused declines in undescribed species (3). Lambert *et al.* (4) challenge our methodology, focusing on the evidence we used to assign “strength of evidence scores” that implicate chytridiomycosis in declines.

Lambert *et al.* claim that our strength of evidence scores were not adequately justified, and reassigned species from higher scores to the lowest score of “expert opinion of the assessor only” (1). The fundamental difference between our approach and that of Lambert *et al.* is that we incorporated expert knowledge of amphibian species and integrated a comprehensive epidemiological framework to evaluate all available evidence. In contrast, the Lambert *et al.* approach lacked species expertise, applied a limited evidence framework, and used only easily accessible sources. They claim that their approach is more replicable and hence more rigorous. However, on the contrary, their exclusion of expertise, evidence, and data is neither comprehensive, nor is it best practice. For example, using a less comprehensive assessment led Lambert *et al.* to question some of the most well-documented chytridiomycosis-driven declines [e.g., *Bsal*-driven salamander collapses in northern Europe and *Atelopus chiriquiensis* declines in Mesoamerica (5, 6)]. Thus, adopting a restricted approach may seriously limit understanding of disease impacts and hamper conservation efforts in the face of the current mass extinction crisis (7).

The narrow approach adopted by Lambert *et al.* ignores information we provided justifying species categorization as either “single line of correlative evidence” or “multiple lines of correlative evidence.” Lambert *et al.* assumed the data provided in columns J to M of data S1 (1) to be the only information justifying the assigned strength of evidence scores, and hence misrepresent our methodology. However, we used multiple lines of evidence that were not all captured in these four columns [supplementary materials of (1)]. We included columns J to M to show what published reports were available for these common and easy-to-categorize lines of evidence. However, our strength of evidence scores were informed by integrating evidence from 454 cited references, which was supplemented in some cases with expert judgment (see below). This holistic assessment, considering all available evidence, was only possible by drawing together information regarding specific species and locations, amphibian biology, disease ecology, epidemiology, and pathology.

Lambert *et al.* critique our use of expert opinion. Expert judgment is commonly used in many scientific fields and is necessary to critically evaluate multiple lines of evidence. Following best practices in expert elicitation (8), we assembled a large, diverse, and global group that combined disease and amphibian expertise with a first-hand

understanding of the broader amphibian conservation challenges in the assessed countries. Furthermore, our assessments were accomplished via iterative group processes, using well-defined, structured, quantitative questions, with assessments cross-checked by the group of experts (8). For transparency, and to help readers understand our methodology, we included eight “worked examples” in our original paper [see data S1 (1)], but these were overlooked by Lambert *et al.* Thus, our study provides the best-vetted and comprehensive dataset on amphibian declines at a global scale, and is underpinned by a substantial body of empirical research.

Lambert *et al.* make an unsubstantiated claim that our referencing is inaccurate. Our assessment included evidence of species declines that occurred before *Bd* was described but are now linked to chytridiomycosis [figure 3, A and B, in (1)]. The fact that many declines subsequently attributed to chytridiomycosis are described in publications predating the description of *Bd*, and that many of those publications tentatively suggested other drivers of decline, neither invalidates data contained in those sources nor contradicts more recent findings implicating chytridiomycosis. In fact, pre-*Bd* sources provide invaluable information regarding the spatio-temporal patterns and processes of species declines that are fundamental components of holistic epidemiological assessments (9). For example, research published in 1989 documented the decline of Australia’s iconic corroboree frogs (*Pseudophryne corroboree*) and noted that declines occurred during a drought (10). However, subsequent research has clearly demonstrated the role of chytridiomycosis in corroboree frog declines (11).

Lambert *et al.*’s critique raises several deeper issues for the study of infectious disease and conservation. Lambert *et al.* treat expert knowledge and retrospective evidence as unreliable (at best) and suspicious (at worst) sources of information. Used rigorously, such forms of evidence are fundamental epidemiological tools routinely applied to diagnose the role of pathogens in disease outbreaks (12), particularly for declines that occurred before a causative agent is identified, as with chytridiomycosis. More broadly, omitting evidence compromises the ability to achieve a global overview by biasing assessments to regions that have more resources, infrastructure, and funding for wildlife research. Heterogeneity of evidence is a common challenge in conservation (13, 14). Such challenges are amplified when integrating data at a global scale. For conservation information to be applicable to as many regions as possible, we need to rigorously consider all evidence available.

We are in an era of unprecedented biodiversity loss (7). The scientific community has a great responsibility to be both rigorous and holistic in providing data that are unbiased and inclusive of all the information available. Our re-

search demonstrates that chytridiomycosis has irrefutably devastated amphibians and remains a global threat. Our timely assessment documents the current state of knowledge, which researchers can augment as new information becomes available. Under the scenario of ongoing amphibian declines, the scientific community has five important tasks: (i) to describe and quantify threats to biodiversity, (ii) to help prevent further declines and extinctions due to chytridiomycosis, (iii) to facilitate the recovery of affected species, (iv) to build on the lessons learned from chytridiomycosis to prevent further wildlife panzootics, and (v) to document current species distributions and abundances (with appropriate metadata) to provide baseline data against which to assess the impacts of future emerging diseases (15). In accomplishing these goals, we can confront the global conservation challenge.

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