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Editor's Note: Deanna Olson established the Diseases section in HR beginning in 2007 and has continued as the coordinating Associate Editor ever since.

A Decade of Herpetological Disease Papers: Puzzle Pieces of a Bigger Picture

DEANNA H. OLSON
US Forest Service, Pacific Northwest Research Station
3200 SW Jefferson Way, Corvallis, Oregon 97331, USA
e-mail: dedeolson@fs.fed.us

The Amphibian and Reptile Diseases section of *Herpetological Review* (*HR*) has experienced 10 years of tremendous participation and expansion since its initiation in the December issue of 2007. Through December 2017 there have been 185 disease articles by 594 authors, including reports on seven disease-causing agents and a geographic scope spanning 42 countries and 35 US states (Fig. 1). Considering the service contributed by local experts providing logistical support for field work, the laboratories that have analyzed samples, the organizations that funded the studies, an extensive international cadre of reviewers, and the addition of several Associate Editors to help with submission processing, this section represents a world community that has rallied to advance our understanding of infections that may threaten herpetofauna.

The inception of this section is tied to a larger strategic effort to accelerate the pace of science and its communication regarding potential threats of emerging infectious disease. In November 2007, an international amphibian chytrid fungus (*Batrachochytrium dendrobatidis*, or *Bd*) conference convened in Tempe, Arizona, USA. In preparation for the meeting, I initiated the Global *Bd* Mapping Project months earlier to compile existing knowledge of world *Bd* distribution to provide context at the conference and as possible, inform follow-up work. As national and regional data coordinators (the *Bd* Mapping Group: Olson et al. 2013) submitted their reports for synthesis, an astonishing number of unpublished sampling efforts were revealed. The science of *Bd* was rapidly expanding at that time (e.g., Berger et al. 2005; Lips et al. 2006; Rachowicz et al. 2006; Skerratt et al. 2007; Woodhams et al. 2007) and although descriptive reports of *Bd* prevalence in a species or location were being published, the number of unpublished reports highlighted a need for incentives for authors to pursue peer-reviewed products. In particular, an outlet facilitating dissemination of *Bd* prevalence studies was needed.

HR met this challenge by initiating the Diseases section. By asking reviewers for a 2-week turn-around on papers, an accelerated process unfolded. A truncated Introduction section has streamlined contributions, as almost all papers could begin by a general statement about the role of disease in population declines. Authors now take that as a given and get more directly to the gist of studies. By publishing reports that both detect and do not detect disease agents, data can be aggregated and larger patterns examined, with appropriate caveats about *ad hoc* sampling and different methods used in study designs and analyses. The publication of the no-detection data has been a particularly important contribution of *HR*. Continuing such aggregation of findings among studies after the 2007 *Bd* conference was anticipated from the inception of the *HR* Disease section, and led to inclusion of study details to facilitate later compilation across studies. In some ways, this has fostered use of standardized methodologies and terminologies as well. For example, at this time, due to concerns with false-positive or -negative findings from laboratory diagnostic tests, the use of the terms "detection or no-detection" of pathogens in samples tested is being favored, and methods sections are detailing how approaches have differed from previously published protocols.

After a decade, most (84%) *HR* Disease articles have addressed *Bd*. *Bd* sampling of amphibians, fish, birds, and water has been reported. These data as well as published accounts in other journals have been further compiled (largely through literature reviews by my office: data manager K. Ronnenberg, US Forest Service) into the world *Bd* data portal. This portal is currently in transition from the original repository at Bd-maps.net (D. Aanensen and M. Fisher; Imperial College, London, UK; Olson et al. 2013) that will soon be discontinued to an updated database at AmphibiaWeb (https://amphibiandisease.org; Michelle Koo, Museum of Vertebrate Zoology, University of California, Berkeley, CA, USA). The new portal has more nimble search and analysis options, and more efficient import and export capability (Bsal Task Force 2016). As part of an accessible world database, data from *HR* Disease contributions have been included in other studies, which have examined continental-to-world disease patterns (e.g., Xie et al. 2016; Grant et al. 2016; Gervasi et al. 2017). Results from such synthesis papers can then be used to generate hypotheses to explore local-to-regional host-pathogen dynamics. During our transition among portals, these data are available via direct request. Although *HR* Disease papers can be humble in reporting often fairly small-scope prevalence patterns, these papers are part of this larger strategic effort, feeding into additional cycles of scientific inquiry. In this way, the knowledge discovery reported in *HR* Disease papers that might be considered 'puzzle pieces' are contributing to larger advances and a bigger picture.

Studies of six other herpetofaunal disease agents have been reported in *HR* as well, reflective of the growing recognition of emerging infectious diseases in reptiles as well as amphibians. Single articles have addressed malaria, an oomycete water mold, and helminthes worms (submissions on gastrointestinal parasites such as helminthes should now be submitted as general Articles). Since 2009, Ranavirus in amphibians and turtles have been reported in 35 articles and 5 co-infection studies with *Bd*. Papers on snake fungal infection (4 *HR* articles) were first published in 2016. The recently described amphibian chytrid fungus from Europe and Asia, *B. salamandrivorans* (*Bsal*: Martel et al. 2013) is generating surveillance studies in North America with 4 *HR* articles in 2017, all of which are co-infection studies with *Bd*. *Bsal* has not been confirmed in North America at this time. In parallel efforts to the world *Bd* data portal, web portals have been established for Ranavirus (https://mantle.io/grrs; in cooperation with the Global Ranavirus Consortium, EcoHealth Alliance, and the US Forest Service) and *Bsal* (same portal as for *Bd*: amphibiandisease.org; a product of the 'Data Management Working Group' of the *Bsal* Task Team). At the amphibian chytrid portal for *Bd* and *Bsal*, in addition to reporting study results, projects can be established for communication of planned or ongoing work. Knowledge of other work that is in progress is especially important as it can increase the efficiency of disease science investigations to reduce overlap of objectives, aid networking among principal investigators, and yield an expanded scope of studies.

In addition to reports of prevalence studies of disease agents, several *HR* Disease articles have addressed other topics. For example, Muths et al. (2009) addressed the relevance of opportunistic versus systematic sampling efforts, and highlighted the need for sufficient sample sizes in reporting (see also Skerratt et al. 2008; Gray et al. 2017). White et al. (2016) published the *Bsal* case definition, and Iwanowicz et al. (2017) addressed *Bsal* diagnostic approaches. Also, two recent articles synthesize general disease sampling approaches and biosecurity issues (Gray et al. 2017), and necropsy methods (Duffus et al. 2017).

Disease organizations and their social networking are having an effect on herpetofaunal disease science and communication.

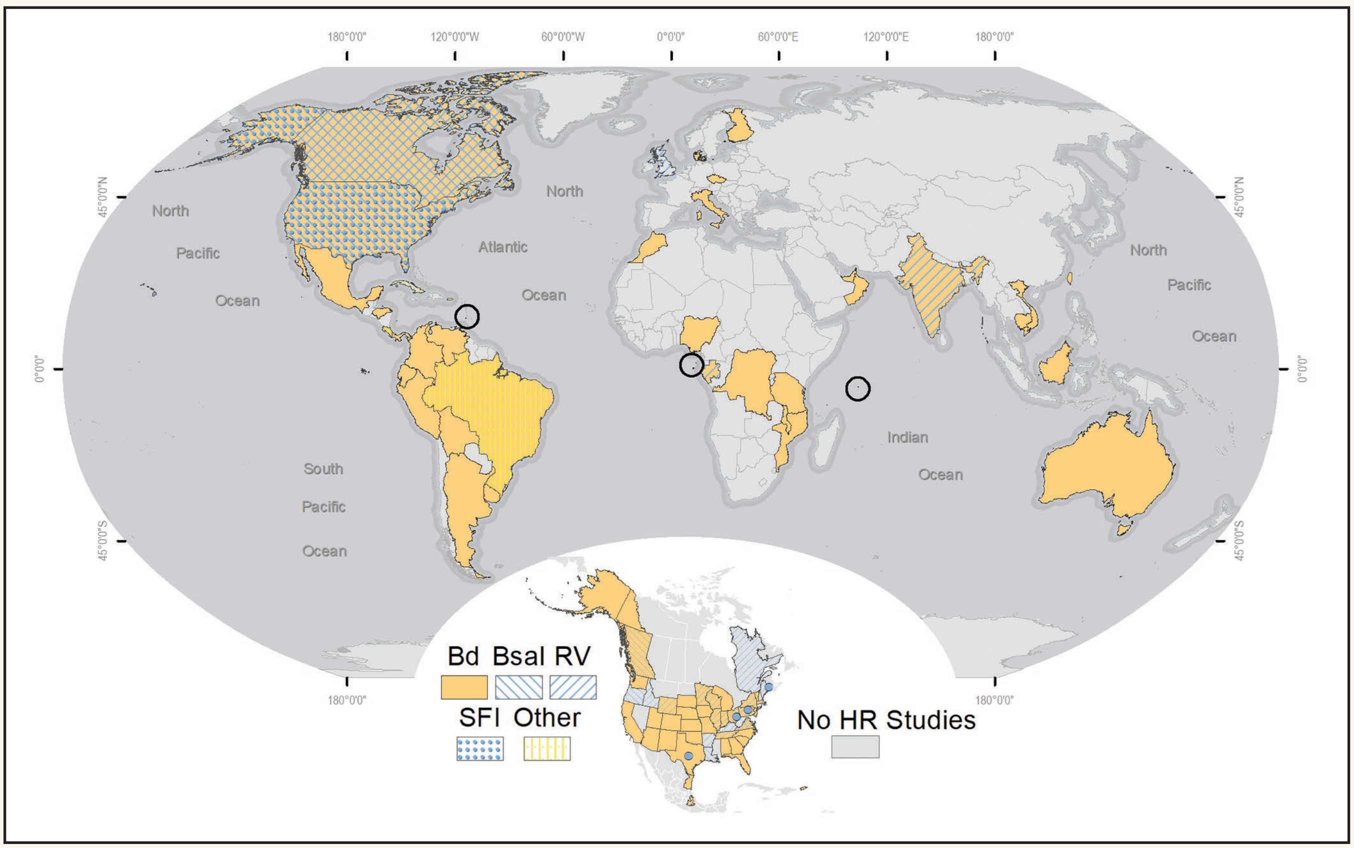

Fig. 1. Distribution of 185 studies reported in the Amphibian and Reptile Diseases section of *Herpetological Review* (*HR*) from December 2007 through December 2017 across 42 countries (upper figure), and states and provinces of North America (inset below). Studies include investigations of *Batrachochytrium dendrobatidis* (*Bd*), *B. salamandrivorans* (*Bsal*), ranavirus (RV), snake fungal infections (SFI), and others (malaria, oomycete, helminthes).

This effect is apparent as a common thread through these last few concept and synthesis papers in *HR*, and the establishment of disease web portals previously mentioned. In particular, the Gray et al. (2017) paper is a product of a coalition of herpetological disease specialists affiliated with the Partners in Amphibian and Reptile Conservation (PARC) Disease Task Team (http://parcplace.org/resources/parc-disease-task-team/). The Duffus et al. (2017) paper has its origins among a network of disease specialists who are aligned with PARC's Southeast working group (http://separc.org/task-teams/#/disease-team/). Early knowledge of the Iwanowicz et al. (2017) study findings informed the development of the *Bsal* Task Force and its seven working groups (Grant et al. 2015; Bsal Task Force 2016), and the White et al. (2016) paper is an outcome of the Bsal Task Force's Diagnostics Working Group. Members of these various organizations are collaborating on other products as well, endorsing a new social inertia of partnerships accelerating the pace and scope of disease advances.

The importance of the *people* part of herpetofaunal disease advances cannot be understated, and is integral to the *HR* Disease section. There is a growing tide of concerns about amphibian and reptile disease threats among experts, managers and the public, and this is broadly shared on social media, connecting people to these issues like never before. Mirroring this is a notable change in how contemporary science is being conducted: collaboration occurs early and often among colleagues and involves exchanges of initial findings and study designs; use of electronic journals for final reporting allows rapid and broad dissemination. This partnership approach is a change from the historical ivory-tower approach where papers with fewer authors made stepwise advances, which were revealed after the slower process of hard-copy publication. Additionally, new and strong partnerships have emerged as nature enthusiasts, biologists, and ecologists working with local fauna have interacted with others having complementary expertise to complete disease studies, which usually involve both field and laboratory components. A surge of students have been linked to mentors, with a flush of projects being linked to graduate education conducted at both smaller colleges and larger universities, in addition to a variety of state, provincial, and federal agencies and other organizations. In this way, diseases have increased interest in herpetofauna across a broad spectrum of land managers, scientists, and the public.

Furthermore, these liaisons have cross-pollinated the study of herpetological diseases with expertise from multiple disciplines. This is an intellectual and creative infusion which includes herpetological, ecological, and epidemiological sectors, as well as a host of additional -ologists. For example, knowledge from the study of herpetological disease (in particular, *Bd*) accrued over the years has informed mammalogists and wildlife specialists faced with the emergence of white-nose syndrome (WNS; caused by the fungal pathogen *Pseudogymnoascus destructans*) in bats. In turn, advances in understanding WNS has informed the *Bsal* science and management response, and both WNS and *Bsal* lessons-learned are now informing experts addressing sea star wasting disease. Alignment of these efforts is facilitated by amphibian disease organizations (above) in cooperation with the Association of Fish and Wildlife Agencies (Novarro et al. 2017), among others. Further interdisciplinary connections are being forged as well—for example, the world *Bd* map, which includes *HR* studies, has appeared in a microbiology text book (Wessner et al. 2013) and a mycology exhibit in a museum (Hesse Museum, Germany; fig. 1 from Xie et al. 2016). Hence, these diverse disciplines are being informed by *HR* Disease studies in aggregation with others. The scope of this collective work has gone beyond the original amphibian and reptile population decline context and is touching upon a more integral understanding of microbiota and their interplay with macrobiota.

In all, *HR* Disease studies are contributing to a bigger picture, indeed, the outcome of which is perhaps yet to be realized. In Aldo Leopold's words, "*To keep every cog and wheel is the first precaution of intelligent tinkering.*" In this light, expanded efforts to describe our natural heritage today, inclusive of host-pathogen occurrence patterns, can aid in understanding the scope and extent of changes that may come in the future. More importantly, increased understanding of the host-pathogen *processes* are much needed, such as the contexts of when infection is seemingly benign and when it leads to disease and population decline. As surveillance studies can expand to address the *how* and *why* of herpetofaunal disease, greater strides can be made in understanding pathogens as integral component parts of biological communities and diseases as potential threats.

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Literature Cited

Berger, L., G. Marantelli, L. F. Skerratt, and R. Speare. 2005. Virulence of the amphibian chytrid fungus *Batrachochytrium dendrobatidis* varies with the strain. Dis. Aquat. Org. 68:47–50.

Bsal Task Force. 2016. 2016 Annual Report. Accessed 30 January 2018: http://www.salamanderfungus.org/wp-content/uploads/2016/11/Bsal-Report_1610_4-0v.pdf.

Duffus, A. L. J., H. M. A. Fenton, M. J. Gray, and D. L. Miller. 2017. Investigating amphibian and reptile mortalities: A practical guide for wildlife professionals. Herpetol. Rev. 48:550–557.

Gervasi, S. S., P. R. Stephens, J. Hua, C. L. Searle, J. Urbina, D. H. Olson, B. A. Bancroft, V. Weis, J. I. Hammond, and R. A. Relyea. 2017. Linking ecology and epidemiology to understand predictors of multi-host responses to an emerging pathogen, the amphibian chytrid fungus. PLoS ONE 12(1):e0167882.

Grant, E. C. H., D. A. W. Miller, B. R. Schmidt, M. J. Adams, S. M. Amburgey, T. Chambert, S. S. Cruickshank, R. N. Fisher, D. M. Green, B. R. Hossack, P. T. J. Johnson, M. B. Joseph, T. A. G. Rittenhouse, M. E. Ryan, J. H. Waddle, S. C. Walls, L. L. Bailey, G. M. Fellers, T. A. Gorman, A. M. Ray, D. S. Pilliod, S. J. Price, D. Saenz, W. Sadinski, and E. Muths. 2016. Quantitative evidence for the effects of multiple drivers on continental-scale amphibian declines. Nature 6: 25625. 9 pp. Accessed 29 January 2018: https://www.nature.com/articles/srep25625.pdf.

———, E. Muths, R. A. Katz, S. Canessa, M. J. Adams, J. R. Ballard, L. Berger, C. J. Briggs, J. Coleman, M. J. Gray, M. C. Harris, R. N. Harris, B. Hossack, K. P. Huyvaert, J. E. Kolby, K. R. Lips, R. E. Lovich, H. I. McCallum, J. R. Mendelson, III, P. Nanjappa, D. H. Olson, J. G. Powers, K. L. D. Richgels, R. E. Russell, B. R. Schmidt, A. Spitzen-van der Sluijs,

M. K. Watry, D. C. Woodhams, and C. L. White. 2015. Salamander chytrid fungus (*Batrachochytrium salamandrivorans*) in the United States—Developing research, monitoring, and management strategies. U.S. Geological Survey Open-File Report 2015–1233 http://dx.doi.org/10.3133/ofr20151233.

Gray, M. J., A. L. J. Duffus, K. H. Haman, R. N. Harris, M. C. Allender, T. A. Thompson, M. R. Christman, A. Sacerdote-Velat, L. A. Sprague, J. M. Williams, and D. L. Miller. 2017. Pathogen surveillance in herpetofaunal populations: guidance on study design, sample collection, biosecurity, and intervention strategies. Herpetol. Rev. 48:334–351.

Iwanowicz, D. D., W. B. Schill, D. H. Olson, M. J. Adams, C. Densmore, R. S. Cornman, C. Adams, C. Figiel, Jr., C. W. Anderson, A. R. Blaustein, and T. Chestnut. 2017. Potential concerns with analytical methods used for the detection of *Batrachochytrium salamandrivorans* from archived DNA of amphibian swab samples, Oregon, USA. Herpetol. Rev. 48:352–355.

Lips, K. R., F. Brem, R. Brenes, J. D. Reeve, R. A. Alford, J. Voyles, C. Carey, L. Livo, A. P. Pessier, and J. C. Collins. 2006. Emerging infectious disease and the loss of biodiversity in a Neotropical amphibian community. Proc. Nat. Acad. Sci. USA 103:3165–3170.

Martel, A., A. Spitzen-van der Sluijs, M. Blooi, W. Bert, R. Ducatelle, M. C. Fisher, A. Woeltjes, W. Bosman, K. Chiers, F. Bossuyt, and F. Pasmans. 2013. *Batrachochytrium salamandrivorans* sp. nov. causes lethal chytridiomycosis in amphibians. Proc. Nat. Acad. Sci. USA 110:15325–15329.

Muths, E., B. S. Pedersen, and F. S. Pedersen. 2009. How relevant is opportunistic *Bd* sampling: Are we ready for the big picture? Herpetol. Rev. 40:183–184.

Novarro, A. J., P. Nanjappa, and J. Williams (Eds.). 2017. Annual Report: 2016. Partners in Amphibian and Reptile Conservation (PARC), Annual Report No. 6. Hagerstown, Maryland. 20 pp. Accessed 29 January 2018: http://parcplace.org/wp-content/uploads/2017/07/2016-PARC-Annual-Report.pdf

Olson, D. H., D. M. Aanensen, K. L. Ronnenberg, C. I. Powell, S. F. Walker, J. Bielby, T. W. J. Garner, G. Weaver, the Bd Mapping Group, and M.C. Fisher. 2013. Mapping the global emergence of *Batrachochytrium dendrobatidis*, the amphibian chytrid fungus. PLoS ONE 8(2):e56802.

Rachowicz, L. J., R. A. Knapp, J. A. T. Morgan, M. J. Stice, V. T. Vredenburg, J. M. Parker, and C. J. Briggs. 2006. Emerging infectious disease as a proximate cause of amphibian mass mortality. Ecology 87(7):1671–1683.

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

———, ———, H. B. Hines, K. R. McDonald, D. Mendez, and R. Speare. 2008. Survey protocol for detecting chytridiomycosis in all Australian frog populations. Dis. Aquat. Org. 80:85–94.

Wessner, D., C. Dupont, and T. Charles. 2013. Microbiology. John Wiley & Sons. New York, New York.

White, C. L., M. J. Forzan, A. P. Pessier, M. C. Allender, J. R. Ballard, A. Catenazzi, H. Fenton, A. Martel, F. Pasmans, D.L. Miller, R. J. Ossiboff, K. L. D. Richgels, and J. L. Kerby. 2016. Amphibian: A case definition and diagnostic criteria for *Batrachochytrium salamandrivorans* chytridiomycosis. Herpetol. Rev. 47:207–209.

Woodhams, D. C., V. T. Vredenburg, M. A. Simon, D. Billheimer, B. Shakhtour, Y. Shyr, C. J. Briggs, L. A. Rollins-Smith, and R. N. Harris. 2007. Symbiotic bacteria contribute to innate immune defenses of the threatened mountain yellow-legged frog, *Rana muscosa*. Biol. Conserv. 138:390–398.

Xie, G. Y., D. H. Olson, and A. R. Blaustein. 2016. Projecting the global distribution of the emerging amphibian fungal pathogen, *Batrachochytrium dendrobatidis*, based on IPCC climate futures. PLoS ONE 11:e0160746.