

FOCUSED TOPIC

Looking across Scales in Disease Ecology and Evolution*

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Submitted July 5, 2021; Accepted September 7, 2021; Electronically published December 3, 2021

ABSTRACT: Over the past few decades, it has become clear that ecological and evolutionary dynamics are influenced by processes operating across spatial and temporal scales. Processes that operate on small spatial scales have the potential to influence dynamics at much larger scales; for example, a change in the physiology of a primary producer can alter primary productivity in an ecosystem. Similarly, evolution—a process that historically was thought of as occurring at longer timescales—can influence ecological dynamics and vice versa. The importance of considering multiple scales is broadly true in ecology and evolution, and it is especially important for studies of disease ecology and evolution. Yet characterizing the scales at which individual studies operate is surprisingly challenging, as we (re)discovered while trying to characterize articles published in this journal over the past three decades. However, while it is difficult to determine where one scale ends and another begins, it is also clear that work that spans across a spectrum can yield insights that could not be gleaned from a narrower focus. To demonstrate this, we highlight studies previously published in this journal that show the value of working across scales. We then introduce the six articles that comprise this Focused Topic section. Together, these articles present systems, theory, and methods that provide important insights that could not have been obtained from studying a single scale in isolation.

Keywords: disease outbreaks, eco-evolutionary processes, multiple scales, spatial dynamics, temporal dynamics.

Introduction

While it was not the first article to address the importance of scale in ecology or evolutionary biology, the publication of Levin (1992) brought particular attention to issues related to scaling. As Levin stressed, to understand and predict patterns that we observe in ecological systems, we need to uncover the mechanisms that drive (often because of smaller scales) and constrain (often because of larger scales)

the processes responsible for our observations. The importance of working across scales continues to be recognized in ecology and evolutionary biology, including within the field of disease ecology and evolution (e.g., Tompkins et al. 2011; Borer et al. 2021; Tao et al. 2021). While certain topics in disease ecology and evolution may be addressed by studies at a single scale, many require looking across scales (Mideo et al. 2008; Alizon et al. 2011; Cressler et al. 2014). Processes at one scale (e.g., transmission rates between hosts or movement of disease between patches) can depend in subtle and nuanced ways on processes acting at a smaller scale (e.g., within-host interactions or between-host spread, respectively), so a full understanding of a system's dynamics requires considering multiple scales. This is even more essential when there is feedback from the larger back to the smaller scale (Mideo et al. 2008) or when there are nonlinearities in the system. For infectious diseases, nonlinearities arise, for example, when accounting for individual susceptibility (Dwyer et al. 1997) or when infected individuals differ in their ability to spread or limit the spread of a disease (e.g., superspreaders; Lloyd-Smith et al. 2005; VanderWaal and Ezenwa 2016). Such nonlinearities have the potential to scale up in unexpected ways to influence community-level patterns (e.g., Clay et al. 2021) and, thus, necessitate looking across scales.

To look across scales, we must first define what constitutes different scales. This, it turns out, is a surprisingly difficult task—where does one scale end and the next begin? While it is tempting to define discrete scales (e.g., within host, among host, across patches), assigning particular studies to specific bins is nontrivial. For example, a study that seeks to identify the mechanistic underpinnings of differences in virulence between two pathogen strains or species sounds decidedly “within host.” Yet predictions about virulence evolution (which may have motivated such a study) rely on between-host models, and/or the study may consider the implications of its results at this (or another) scale. In reality, studies of the ecology

* This contribution is the introduction to a Focused Topic organized by Bret Elderd, Nicole Mideo, and Meghan Duffy featuring studies bridging across scales in disease ecology and evolution.

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and evolution of infectious diseases fall along a spectrum from molecules through individuals, communities, ecosystems, biomes, and even the entire planet (as has become abundantly clear during the SARS-CoV-2 pandemic.)

Scale is often discussed with regard to levels of biological organization or space, but other scales are important as well. In particular, temporal scale has also gained prominence as we move from the split worldview of ecology and evolution happening on their own timescales to one that recognizes their concurrence (Hendry 2020). Indeed, in some cases we cannot explain the ecological dynamics of infectious diseases unless we explicitly consider the role of evolution on ecological timescales (e.g., Duffy and Hall 2008; Elder et al. 2008; Dwyer et al. 2022).

How do we know about the challenges associated with characterizing where disease ecology and evolution studies fall along the spectrum of scales of study? Because we tried to characterize studies in this journal from the past three decades (going back to 1992, when Levin's article on scales was published). We were entirely unable to characterize temporal scale—empirical studies often did not include the information we needed to determine whether they were on ecological or evolutionary timescales (or both). When attempting to characterize scales of biological organization, the three authors often disagreed with one another. Even after coming up with criteria and coming to a consensus via discussion, it was difficult to justify the boundaries we drew when challenged by a colleague who also has expertise in this area.

Thus, rather than presenting a review of the scales of focus for studies in this journal over the past three decades, we instead highlight three studies from three different decades that we all agreed spanned several scales, to the clear benefit of the science. However, in going through the process of attempting to characterize the scales of the different studies, we did notice other interesting patterns regarding where we choose to focus our research efforts, which we present briefly. After highlighting some earlier studies, we move on to introduce the six articles that are featured in this Focused Topic section. These articles answer a variety of questions about ecological and evolutionary processes associated with disease and disease transmission and serve as important illustrations that while working across scales can be challenging, it also leads to crucial insights that could not have been gained by focusing on a single scale alone. Overall, it is clear that scale—both spatial and temporal—matters to disease ecology and evolution.

Looking across Scales: A Brief Tour of Selected Articles from *The American Naturalist*

In exploring articles from the last three decades in *The American Naturalist*, we found that many studies explic-

itly or implicitly spanned several scales. Here, we describe three studies that span this time window, emphasizing their cross-scale nature and, where possible, identifying the benefits gained by working across scales.

Using a gene-for-gene model of host-pathogen interactions in trees, Stump et al. (2020) explore the conditions under which host resistance genes promote pathogen-mediated coexistence under the Janzen-Connell hypothesis (Janzen 1970; Connell 1971). The authors find that host species coexistence is promoted under two scenarios: when a host's resistance genes do not affect seedling susceptibility and survival (in other words, pathogens are species specific and not genotype specific, so rare species have an advantage) and when resistance genes are costly for the host. Under the latter scenario, nonresistance genes offer advantages to rare species, so their evolution can promote coexistence. In the absence of a cost to resistance genes, genetically diverse species harboring a number of different alleles have an advantage, and coexistence between species is not promoted. By combining a within-host evolutionary framework of genetic resistance with a model of community dynamics, Stump et al.'s (2020) work across scales enhances our understanding of a classic ecological explanation for tropical tree diversity arising from different assumptions about the molecular details of host-pathogen interactions.

Focusing on empirical data collected over a number of decades, Jaenike and Perlman (2002) present a comprehensive review of the ecological and evolutionary interactions between mycophagous *Drosophila* species and their nematode parasites. As such, the article builds from estimates of the costs of infection at the level of individual hosts, through to consequences of infection for host population dynamics and the structuring of *Drosophila* communities, and then to macroecological patterns of host susceptibility. On the evolutionary side, the study examines parasite genetic diversity, phylogenetic constraints on host range, and selective pressures on parasite virulence. This article is dramatically cross scale, and while it is explicit about considering both ecological and evolutionary timescales, it unassumingly spans at least three scales of biological organization—from individuals, to populations, to communities. Many of the articles cited in Jaenike and Perlman (2002) focus on a single scale—for example, quantifying temporal patterns of disease prevalence across host species or species-specific effects of infection—and there is clearly value in conducting such studies. The added value of bringing all this work together in one place is that patterns at one scale can be illuminated by considering processes at another. Here, individual-level measures of host behavior and its influence on survival and fecundity reveal species-level variation in the fitness effects of parasitism; combined with variation in parasitism across a geographic range, these data help to explain patterns of *Drosophila*

community composition and species coexistence. Given the empirical nature of the work, the need to draw on multiple studies necessitates that considerable time and effort is dedicated to understanding a system before being able to focus across scales.

Finally, Lively (1999) uses a combination of theory and data across multiple studies to understand empirical patterns of local adaptation by parasites. Lively begins with a description of previous observational and experimental work on a snail-trematode host-parasite system in New Zealand, explicitly tackling the issue of scale by describing evidence of local adaptation of parasites to their hosts collected from different lakes and then zooming in to the within-lake level to describe how differences in the biology of snails in shallow versus deep water influences the patterns of disease transmission and, hence, the potential for coevolution between host and parasite. Through a comprehensive discussion of the natural history of this system, Lively (1999) hypothesizes that high virulence of the trematode to snails may underlie the strong local adaptation observed. To test this and understand why local adaptation is not found in all host-parasite systems, Lively (1999) develops a simple mathematical model tracking the genotypes of hosts and parasites across two patches. He finds that virulence, a consequence of within-host interactions (and in this model determined by the pairing of host and parasite genotypes), and migration, which determines between-patch movement, jointly determine whether parasite local adaptation occurs, what the evolutionary dynamics look like, and hence whether local adaptation can be measured. At its core, studying local adaptation consists of estimating the infectivity of parasites to local host populations compared with more “distant” host populations within a number of different patches. However, understanding the patterns that emerge across the landscape and why they differ across systems benefited from a mathematical model that captures processes happening within and between populations and implicitly at the within-individual level.

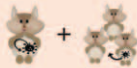

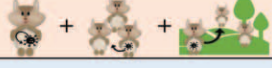


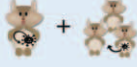
As each of these studies demonstrate, whether using theory, empiricism, or a combination of both, understanding host-pathogen interactions and their ecological and evolutionary implications requires thinking about these processes across multiple temporal and/or spatial scales. The empirical focus of Lively (1999) and Jaenike and Perlman (2002) required that the individual articles brought together a large body of work. This pinpoints the need for long-term studies not just to understand the ecology and evolution of infectious disease but to understand ecology and evolution in general. Stump et al. (2020) built a multiscale mechanistic model that seeks to explain empirical observations regarding species diversity. Together, these highlighted *American Naturalist* articles (and there are many more we could have highlighted here) show that empirical systems need to be

developed over multiple years and, perhaps, the course of an investigator’s career. They also show how theoretical approaches allow one to bridge time and space to point toward areas ripe for exploration, whether from a theoretical and/or empirical standpoint.

Looking across Scales: The Articles in This Focused Topic Section

The articles that are part of this Focused Topic section similarly demonstrate how and why thinking across scales is important (fig. 1). From an empirical perspective, Eck et al. (2022) show how a within-host process, priority effects, dictates which pathogen strains of a powdery mildew fungus infects patches of *Plantago lanceolata* and, in turn, how this plays out across the landscape among multiple patches. By estimating strain fitness from epidemiological data, their analyses suggest that even high-fitness strains are not able to overcome the disadvantage of late arrival in a host population. Penczykowski et al. (2022) take a blended approach by combining empirical results from a *Daphnia dentifera*-based system with theory to demonstrate that a within-host process (reduced feeding rates of infected hosts) can cause host density to increase via a foraging-mediated hydra effect (Abrams 2009). In Greek mythology, the many-headed Hydra of Lerna would sprout two new heads when a single one was cut off. In ecology, the hydra effect describes when a source of mortality leads, counterintuitively, to increased population size (Abrams 2009). In the *Daphnia*-parasite system, the hydra effect arises from a reduction in host feeding rates, which allows resource levels to increase and, indirectly, host densities to increase—a surprising outcome given that without this trait-mediated effect, one would expect this virulent parasite to dramatically reduce host densities during severe outbreaks. Without considering the connection among within-host (i.e., feeding rates), between-host (i.e., pathogen transmission), and food web-level (i.e., consumer-resource dynamics) processes, we might incorrectly assume that this virulent parasite was a mutualist or turn to other similarly incorrect explanations to explain patterns observed in natural lakes. Only by considering cross-scale processes do the true mechanisms become revealed.

As the previously published articles we highlighted show, host-parasite interactions can influence host species competition and coexistence (Jaenike and Perlman 2002; Stump et al. 2020). In this issue, Rovenolt and Tate (2022) shine a further light on the complexities present within hosts by asking how competition between parasite species (i.e., coinfection) impact these dynamics. Combining a within-host competition model with a classic susceptible-infected-recovered (SIR) transmission model (Kermack and McKendrick 1927),

Study	Spatial scales	Temporal scale(s)	System	Summary
Dewald-Wang et al.		Seasons to decades	Phyllosphere: host-pathogen	Coevolutionary dynamics between bacteria and phage are asymmetrical, challenging classic theories
Dwyer et al.		Weeks to decades	Insect host-viral pathogen	Eco-evolutionary dynamics better explain insect population cycles than eco-only models
Eck et al.		Season	Plant-fungal pathogen	For multiple pathogen strains, priority effects rule the day
Pandey et al.		Multiple generations	<i>In silico</i> : pathogens that also grow in environmental reservoirs	Life in an environmental reservoir generates many constraints on pathogen virulence, leading to diverse evolutionary trajectories
Penczykowski et al.		Season	Invertebrate host-fungal pathogen	The hydra effect, counterintuitively, increases host density during a disease outbreak
Rovenolt & Tate		Multiple generations	<i>In silico</i> : competing insect hosts and their coinfecting parasites	Coinfection may lead to coexistence or competitive exclusion between competing host species




 = within host,  = between host,  = between patches

Figure 1: List of the individual articles in alphabetical order (by first author) appearing in this Focused Topic section examining disease dynamics across multiple scales. Colors of rows correspond to the type of study (orange = empirical; blue = theory; green = both). Spatial scales examined are represented as within host, between host, and between patches.

Rovenolt and Tate demonstrate that parasite-mediated apparent competition due to coinfection may lead to multiple steady states in the system that include both coexistence and competitive exclusion among host species. This model is motivated by competition between two flour beetle species, *Tribolium castaneum* and *T. confusum*, that are infected by a number of different parasites.

These studies clearly show that within-host interactions can drive processes at the between-host and among-patch levels and have nonintuitive influences on host population dynamics. This, in turn, can result in a feedback that influences outcomes at the individual level. Together, these three studies demonstrate how looking across multiple spatial scales leads to greater insight into the ecology of disease transmission and, in turn, how it influences population dynamics.

While the above-described studies focused on ecological processes, the impacts of scale can also be readily seen when asking questions from an evolutionary perspective. While ecologically based consumer-resource models are often used for understanding population cycles seen in field data, evolutionary explanations based on fluctuating host resistance due to selection are often invoked when analyzing laboratory-based studies. To address whether the same laboratory arguments hold for field data, Dwyer et al. (2022) needed to collect field and lab data along with developing transmission models across multiple spatial

scales and over a relatively long-term period. In doing so, Dwyer and colleagues look across the eco-evolutionary divide using both empirical data and theory to examine pathogen-driven boom and bust cycles, which are observed in a number of insect host-pathogen systems. Combining data from several spatial and temporal scales, the authors conclude that the eco-evolutionary models, which account for within-host and between-individual processes, better explain the long-term dynamics of *Lymantria dispar*, an invasive lepidopteran pest, compared with the strictly ecological models.

Two different explanations of coevolutionary dynamics between a host and a pathogen are often called on to explain changing resistance of a host to its pathogen—arms race dynamics and fluctuating selection. However, as Lively (1999) pointed out, coevolutionary dynamics are, in fact, dynamic; thus, if only short-term data are used, it is not easy to distinguish between these two processes. Using a series of time-shift experiments, Dewald-Wang et al. (2022) sought to disentangle these potential drivers of host-pathogen coevolutionary dynamics in the horse chestnut (*Aesculus hippocastanum*) bacteria-phage system. Prior work had suggested an asymmetry in host-pathogen coevolution in this system—a finding that was intriguing but that might have simply reflected the relatively short window previously investigated (i.e., months; Koskella 2014; Koskella and Parr 2015). In the study in this Focused Topic section,

Dewald-Wang and colleagues show that the previously observed asymmetries still exist even over long timescales (i.e., years): hosts evolve durable resistance (suggestive of an arms race), whereas phages are most infective on hosts from the recent past, losing their ability to infect host types from further back in time (suggestive of fluctuating selection). Thus, this finding was not simply an artifact of the timescale used in earlier experiments but rather suggests that the dominant models used to explain host-pathogen coevolution are too simplistic. Thus, work from this more complicated system—with longer timescales and in “messier” natural communities instead of laboratory conditions—points to an important gap in our existing theories of host-pathogen coevolution.

Gaps similarly exist in theory for pathogen evolution. A number of pathogens facultatively infect their hosts and are also able to readily grow in environmental reservoirs, yet models of virulence evolution that include environmental transmission have invariably focused on pathogens that experience net decay outside the host (e.g., Boldin and Kisdi 2012). Growth in the environment makes defining fitness for a pathogen nonintuitive and opens up possibilities for pathogen evolution to be shaped by trade-offs operating across habitats—within the host and in the environment. Pandey et al. (2022) take up this challenge and develop a model that is grounded in the biology of a number of important diseases of humans to explore the evolution of virulence. Depending on the trade-offs at play, the pathogen may exhibit evolutionary bistability, evolving either low or high levels of virulence, or evolutionary branching, where low- and high-virulent strains coexist.

As was seen in the studies focused on ecological processes, these articles highlight the insights gained from examining questions across multiple scales, whether spatial or temporal, to answer questions focused on evolutionary processes. These studies also point to the importance of additional scales and sources of complexity that might be considered and are not fully captured in our categorization of spatial scales (fig. 1). For example, the Pandey et al. (2022) study considers dynamics within and between two qualitatively different types of habitats (i.e., hosts and environmental reservoirs), while the Dewald-Wang et al. (2022) study investigates two “levels” of hosts (i.e., trees and bacteria) and their respective associated pathogens (i.e., bacteria and phage). In short, it is clear that disease ecology and evolution occur across scales and that we miss important processes and insights if we do not consider those scales.

Moving Forward

As the articles in this Focused Topic section show (fig. 1), one often needs to look across multiple scales to under-

stand disease dynamics and the impacts of disease on ecological and evolutionary processes. Articles in this feature demonstrate a number of different approaches to take when examining processes across scales—for instance, modeling the dynamics at multiple levels (e.g., Penczykowski et al. 2022) and using experimental results from a smaller spatial scale as Bayesian priors for larger-scale models (e.g., Dwyer et al. 2022). While the examples given above focus on spatial dynamics, the same ideas hold for temporal dynamics as well.

While we failed at our initial goal of characterizing scales for close to 300 articles on host-parasite interactions published in this journal over the past 30 years, we did uncover some patterns of interest over that time span. Most of the articles we reviewed focused on terrestrial systems, with many fewer focused on aquatic habitats (fig. 2*a*). In contrast, there was balance between studies of microparasites and macroparasites (and those more generally about parasites; fig. 2*b*). The types of parasites studied has shifted over time (fig. 2*c*); most notably, recent studies encompass a greater diversity of parasite groups. In the first 5-year window of study, more than half (55.6%) of all studies in our data set focused on invertebrate parasites (i.e., parasitoids), and there were only six parasite groups. In the most recent time interval analyzed, there was much greater diversity: studies of invertebrate parasites were still relatively common but accounted for only 16.7% of studies; this time interval contained 14 parasite groups. In terms of hosts, vertebrate-focused studies have increased, while few studies have focused on bacteria or fungi (fig. 2*d*). While we can only speculate about the reasons behind some of the patterns we uncover, the reduction in the number of studies of parasitoids might reflect advances in technology that allows identifying the presence and quantifying the abundance of microscopic organisms (fig. 2*c*). In addition, an increasing appreciation of the risk of zoonoses for human health (e.g., Jones et al. 2008) may be (partially) responsible for the increased focus on vertebrate hosts (fig. 2*d*).

Thus, in terms of where we choose to conduct research and on what species, there is a considerable bias in empirical studies toward terrestrial habitats (fig. 2*a*). This raises the possibility that aquatic habitats offer unexplored opportunities for generating new insight. The question remains whether there are habitat types that lend themselves to asking questions across scale. Most likely, this is both system and question dependent. When considering aquatic systems for future research, it would also be helpful to consider the core processes that are of interest in disease ecology and evolution; a recent analysis found that commonly used model systems for studying the ecology and evolution of infectious diseases tend to focus only on transmission and disease but not recovery, which reflects another important gap (Wale and Duffy 2021).

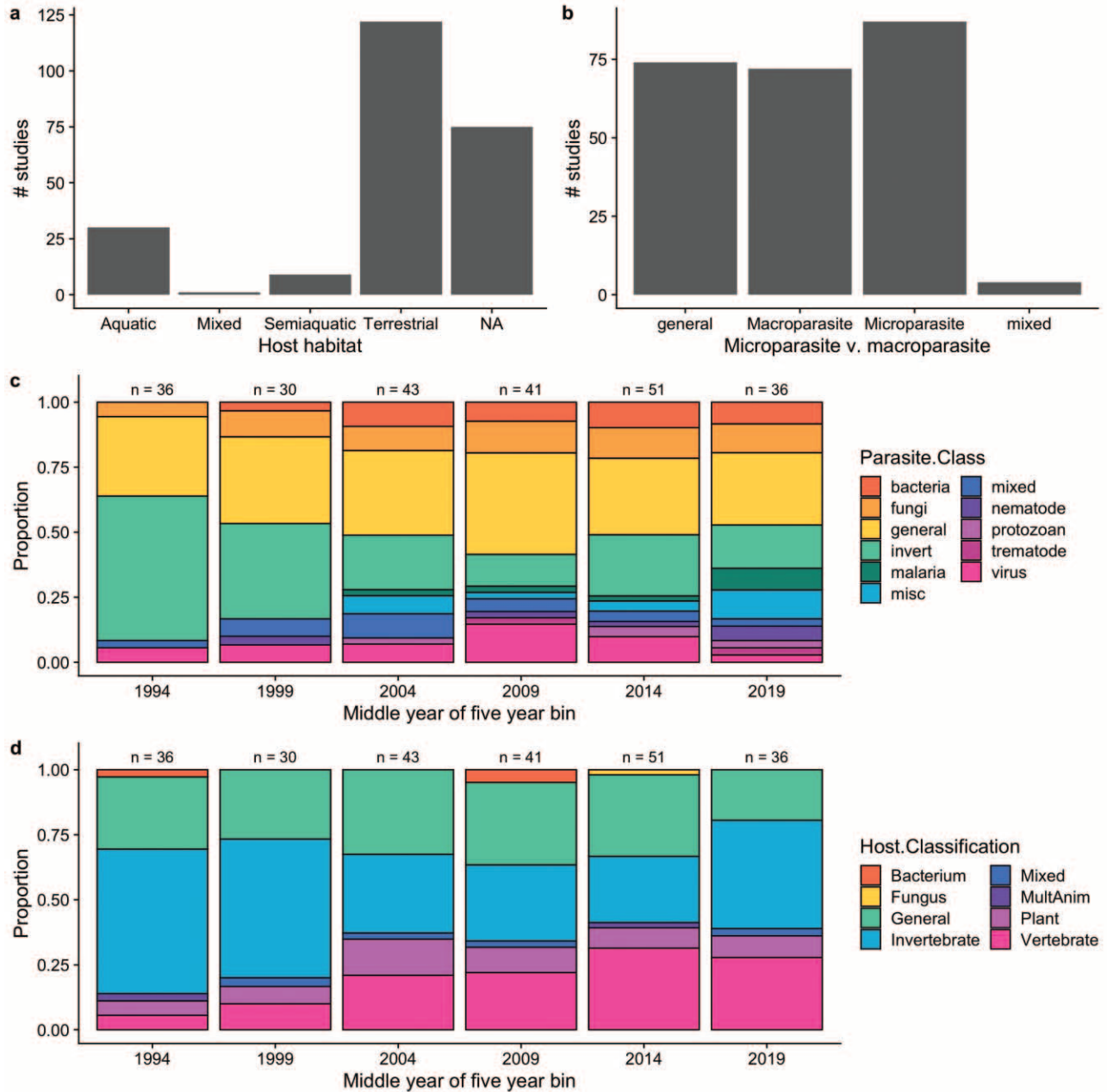


Figure 2: Characteristics of all of the articles published in *The American Naturalist* since 1992 that contained “disease,” “parasit*,” or “pathogen” in the article title, excluding those on brood parasites. Shown are the number of pathogen/disease-focused studies across host habitat types (a), the number of studies of microparasites versus macroparasites (b), the proportion of studies grouped by parasite in 5-year bins (c), and the proportion of studies grouped by host in 5-year bins (d) in *The American Naturalist* since the publication of Levin (1992). Notably, groups of parasites and hosts that have been the focus of disease ecology and evolution studies have shifted over time. For d, “MultAnim” was used for two studies that were focused broadly on animal hosts. For the full data set, see the CSV file at <https://doi.org/10.5281/zenodo.5504012> (Elder et al. 2021).

Undoubtedly, we have the tools and understanding to move beyond a single scale, and we are continuing to develop new methods and ideas to do so. The articles in this Focused Topic section provide further examples of how to

examine processes across multiple scales along with the resulting benefits. When looking across spatial scales, our research focus often bridges the within-host and between-host scales (fig. 1), and we tend to exclude even larger

spatial scales beyond between-host processes. Studies like Ezenwa and Jolles (2015), where the authors examined the spread of bovine tuberculosis in wild buffalo, show the value of work at these larger scales. Similarly, longer temporal scales also can provide crucial insights into the drivers of disease dynamics (e.g., McDonald et al. 2018, where the authors looked at bovine tuberculosis in European badgers). The dearth of large-spatial-scale and/or long-term studies may be constrained by the logistics encountered when asking large-scale questions and may be reflected in the fact that we tend to study small things on short timescales (Duffy et al. 2021). For large-scale questions, these logistical constraints often lead to reliance on observational studies rather than experimental studies at larger spatial and temporal scales (e.g., Farnsworth et al. 2006; Elder et al. 2013). From a temporal and empirical perspective, the ability to collect and use long-term data are key (Lively 1999; Jaenike and Perlman 2002). Given the time that these types of data take to collect (i.e., decades), we have only recently been able take advantage of long-term data sets in both disease ecology and evolution (McDonald et al. 2018). The ability to draw on new studies will depend on a combination of investigator perseverance and long-term research funding. The latter, unfortunately, may be more of an issue. On the spatial side of the coin, we can start to examine disease dynamics at much larger scales by taking advantage of new technologies. For example, the spread of plant pathogens across a landscape may be effectively captured by aerial drone surveys (e.g., Sandino et al. 2018) or LiDAR (e.g., Husin et al. 2020). Additionally, there appears to be an opportunity for community science initiatives (e.g., conjunctivitis in house finches; Altizer et al. 2004) to collect data at both larger spatial and longer temporal scales, which can also help fill this void. Perhaps an *in silico* approach to large-scale questions can serve as a preliminary way to explore processes across space and time. From there, the *in silico* analysis could lead to designing experiments at multiple scales. This would lend itself to the much-needed and much-called-for back and forth between empirical and theoretical approaches to understanding ecological and evolutionary dynamics (Barraquand et al. 2017). We therefore join the chorus calling for more research across scales and hope the six articles in this Focused Topic section provide inspiration to do so.

Acknowledgments

B.D.E. acknowledges support from the National Science Foundation (1316334) and the US Department of Agriculture (20196701429919) as part of the joint NSF-NIH-USDA Ecology and Evolution of Infectious Diseases program. N.M. acknowledges support from the Natural Sciences and Engineering Research Council of Canada (RGPIN-2018-

06017). M.A.D. acknowledges support from the National Science Foundation (DEB-1748729) and the Moore Foundation (GBMF9202; <https://doi.org/10.37807/GBMF9202>). We thank all of the authors of the articles in this Focused Topic section as well as Luis Zaman for providing Chippie for use in figure 1.

Data and Code Availability

A file containing the studies from the literature and how they were classified as well as code for generating figure 2 are available in Zenodo (<https://doi.org/10.5281/zenodo.5504012>; Elder et al. 2021).

Literature Cited

- Abrams, P. A. 2009. When does greater mortality increase population size? the long history and diverse mechanisms underlying the hydra effect. *Ecology Letters* 12:462–474.
- Alizon, S., F. Luciani, and R. R. Regoes. 2011. Epidemiological and clinical consequences of within-host evolution. *Trends in Microbiology* 19:24–32.
- Altizer, S., W. M. Hochachka, and A. A. Dhondt. 2004. Seasonal dynamics of mycoplasma conjunctivitis in eastern North American house finches. *Journal of Animal Ecology* 73:309–322.
- Barraquand, F., S. Louca, K. C. Abbott, C. A. Cobbold, F. Cordoleani, D. L. DeAngelis, B. D. Elder, et al. 2017. Moving forward in circles: challenges and opportunities in modelling population cycles. *Ecology Letters* 20:1074–1092.
- Borer, E. T., L. Asik, R. A. Everett, T. Frenken, A. L. Gonzalez, R. E. Paseka, A. Peace, et al. 2021. Elements of disease in a changing world: modelling feedbacks between infectious disease and ecosystems. *Ecology Letters* 24:6–19.
- Clay, P. A., M. H. Cortez, and M. A. Duffy. 2021. Dose relationships can exacerbate, mute, or reverse the impact of heterospecific host density on infection prevalence. *Ecology* 102:e03422.
- Connell, J. H. 1971. On the role of natural enemies in preventing competitive exclusion in some marine animals and rainforest trees. Pages 298–312 *in* P. J. den Boer and G. G. R., eds. *Dynamics of populations*. Centre for Agricultural Publishing and Documentation, Wageningen.
- Cressler, C. E., W. A. Nelson, T. Day, and E. McCauley. 2014. Disentangling the interaction among host resources, the immune system and pathogens. *Ecology Letters* 17:284–293.
- Dewald-Wang, E. A., N. Parr, K. Tiley, A. Lee, and B. Koskella. 2022. Multiyear time-shift study of bacteria and phage dynamics in the phyllosphere. *American Naturalist* 199:126–140.
- Duffy, M. A., C. García-Robledo, S. P. Gordon, N. A. Grant, D. A. Green, A. Kamath, R. M. Penczykowski, M. Rebolledo-Gómez, N. Wale, and L. Zaman. 2021. Model systems in ecology, evolution, and behavior: a call for diversity in our model systems and discipline. *American Naturalist* 198:53–68.
- Duffy, M. A., and S. R. Hall. 2008. Selective predation and rapid evolution can jointly dampen effects of virulent parasites on *Daphnia* populations. *American Naturalist* 171:499–510.
- Dwyer, G., J. S. Elkinton, and J. P. Buonaccorsi. 1997. Host heterogeneity in susceptibility and disease dynamics: tests of a mathematical model. *American Naturalist* 150:685–707.

- Dwyer, G., J. R. Mihaljevic, and V. Dukic. 2022. Can eco-evo theory explain population cycles in the field? *American Naturalist* 199:108–125.
- Eck, J. L., B. Barrès, S. Soubeyrand, J. Sirén, E. Numminen, and A.-L. Laine. 2022. Strain diversity and spatial distribution are linked to epidemic dynamics in host populations. *American Naturalist* 199:59–74.
- Elder, B. D., J. Dushoff, and G. Dwyer. 2008. Host-pathogen dynamics, natural selection for disease resistance, and forest-defoliator outbreaks. *American Naturalist* 172:829–842.
- Elder, B. D., N. Mideo, and M. A. Duffy. 2021. Data from: Looking across scales in disease ecology and evolution. *American Naturalist*, Zenodo, <https://doi.org/10.5281/zenodo.5504012>.
- Elder, B. D., B. J. Rehill, K. J. Haynes, and G. Dwyer. 2013. Induced plant defenses, host–pathogen interactions, and forest insect outbreaks. *Proceedings of the National Academy of Sciences of the USA* 110:14978–14983.
- Ezenwa, V. O., and A. E. Jolles. 2015. Opposite effects of anthelmintic treatment on microbial infection at individual versus population scales. *Science* 347:175–177.
- Farnsworth, M. L., J. A. Hoeting, N. T. Hobbs, and M. W. Miller. 2006. Linking chronic wasting disease to mule deer movement scales: a hierarchical Bayesian approach. *Ecological Applications* 16:1026–1036.
- Hendry, A. P. 2020. *Eco-evolutionary dynamics*. Princeton University Press, Princeton, NJ.
- Husin, N. A., S. Khairunniza-Bejo, A. F. Abdullah, M. S. M. Kassim, D. Ahmad, and A. N. N. Azmi. 2020. Application of ground-based LiDAR for analysing oil palm canopy properties on the occurrence of basal stem rot (BSR) disease. *Scientific Reports* 10:6464.
- Jaenike, J., and S. J. Perlman. 2002. Ecology and evolution of host-parasite associations: mycophagous *Drosophila* and their parasitic nematodes. *American Naturalist* 160(suppl.):S23–S39.
- Janzen, D. H. 1970. Herbivores and the number of tree species in tropical forests. *American Naturalist* 104:501–528.
- Jones, K. E., N. G. Patel, M. A. Levy, A. Storeygard, D. Balk, J. L. Gittleman, and P. Daszak. 2008. Global trends in emerging infectious diseases. *Nature* 451:990–993.
- Kermack, W. O., and A. G. McKendrick. 1927. A contribution to the mathematical theory of epidemics. *Proceedings of the Royal Society of A* 115:700–721.
- Koskella, B. 2014. Bacteria-phage interactions across time and space: merging local adaptation and time-shift experiments to understand phage evolution. *American Naturalist* 184(suppl.):S9–S21.
- Koskella, B., and N. Parr. 2015. The evolution of bacterial resistance against bacteriophages in the horse chestnut phyllosphere is general across both space and time. *Philosophical Transactions of the Royal Society B* 370:20140297.
- Levin, S. A. 1992. The problem of pattern and scale in ecology: the Robert H. MacArthur Award lecture. *Ecology* 73:1943–1967.
- Lively, C. 1999. Migration, virulence, and the geographic mosaic of adaptation by parasites. *American Naturalist* 153(suppl.):S34–S47.
- Lloyd-Smith, J. O., S. J. Schreiber, P. E. Kopp, and W. M. Getz. 2005. Superspreading and the effect of individual variation on disease emergence. *Nature* 438:355–359.
- McDonald, J. L., A. Robertson, and M. J. Silk. 2018. Wildlife disease ecology from the individual to the population: insights from a long-term study of a naturally infected European badger population. *Journal of Animal Ecology* 87:101–112.
- Mideo, N., S. Alizon, and T. Day. 2008. Linking within- and between-host dynamics in the evolutionary epidemiology of infectious diseases. *Trends in Ecology and Evolution* 23:511–517.
- Pandey, A., N. Mideo, and T. G. Platt. 2022. Virulence evolution of pathogens that can grow in reservoir environments. *American Naturalist* 199:141–158.
- Penczykowski, R. M., M. S. Shocket, J. Housley Ochs, B. C. P. Lemanski, H. Sundar, M. A. Duffy, and S. R. Hall. 2022. Virulent disease epidemics can increase host density by depressing foraging of hosts. *American Naturalist* 199:75–90.
- Rovenolt, F. H., and A. T. Tate. 2022. The impact of coinfection dynamics on host competition and coexistence. *American Naturalist* 199:91–107.
- Sandino, J., G. Pegg, F. Gonzalez, and G. Smith. 2018. Aerial mapping of forests affected by pathogens using UAVs, hyperspectral sensors and artificial intelligence. *Sensors* 18:944.
- Stump, S. M., J. H. Marden, N. G. Beckman, S. A. Mangan, and L. S. Comita. 2020. Resistance genes affect how pathogens maintain plant abundance and diversity. *American Naturalist* 196:472–486.
- Tao, Y., J. L. Hite, K. D. Lafferty, D. J. Earn, and N. Bharti. 2021. Transient disease dynamics across ecological scales. *Theoretical Ecology*, <https://doi.org/10.1007/s12080-021-00514-w>.
- Tompkins, D. M., A. M. Dunn, M. J. Smith, and S. Telfer. 2011. Wildlife diseases: from individuals to ecosystems. *Journal of Animal Ecology* 80:19–38.
- VanderWaal, K. L., and V. O. Ezenwa. 2016. Heterogeneity in pathogen transmission: mechanisms and methodology. *Functional Ecology* 30:1606–1622.
- Wale, N., and M. A. Duffy. 2021. The use and underuse of model systems in infectious disease ecology and evolutionary biology. *American Naturalist* 198:69–92.