A Multiscale Approach to Plant Disease Using the Metacommunity Concept

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Abstract

Plant disease arises from the interaction of processes occurring at multiple spatial and temporal scales. With new tools such as next-generation sequencing, we are learning about the diversity of microbes circulating within and among plant populations and often coinhabiting host individuals. The proliferation of pathogenic microbes depends on single-species dynamics and multispecies interactions occurring within and among host cells, the spatial organization and genetic landscape of hosts, the frequency and mode of transmission among hosts and host populations, and the abiotic environmental context. Here, we examine empirical evidence from these multiple scales to assess the utility of metacommunity theory, a theoretical framework developed for free-living organisms to further our understanding of and assist in predicting plant-pathogen infection and spread. We suggest that deeper understanding of disease dynamics can arise through the application of this conceptual framework at scales ranging from individual cells to landscapes. In addition, we use this multiscale theoretical perspective to synthesize existing knowledge, generate novel hypotheses, and point toward promising future opportunities for the study of plant pathogens in natural populations.

INTRODUCTION

Plant disease is controlled by processes acting at multiple spatial and temporal scales, and this interplay of processes across scales complicates predictions about pathogen diversity within hosts and within host populations. Recent work using next-generation sequencing and culture-based tools to quantify the substantial microbial diversity within plants underscores the likelihood that within-host microbial population growth and interactions play an important role in mediating among-host microbial transmission (29). Concomitant with our ability to quantify the diversity of plant microbiomes is a growing realization that community ecology, microbial ecology, the ecology of infectious disease, and plant pathology are tightly aligned fields (20, 50, 112). Here, we embrace this trend and examine patterns and data from multiple scales within a well-developed theoretical lineage in ecology, i.e., the metacommunity theory, to seek novel insights about processes maintaining diverse pathogen communities within hosts and host populations.

A metapopulation describes a population of populations (81) or, more specifically, a landscape made up of many small population patches that persist in a dynamic state of extinctions and colonizations via dispersal (e.g., 52, 81). Metapopulation theory demonstrates that the balance of extinction and colonization rates is central to persistence of species within a metapopulation, thus highlighting the key role of dispersal for metapopulation persistence (49). The relevance of spatial structure in host populations to disease dynamics has a long history in epidemiology (140) and effectively describes many properties of host-pathogen interactions. The ephemeral nature observed for many pathogens within host individuals and populations (27) is consistent with predictions of the metapopulation theory (52). This theoretical framework has proven useful for understanding the role of space in epidemiology and disease dynamics, e.g., in host-pathogen interactions (14, 26), plant disease resistance (75), evolution of pathogen-host specialization (97), and implications for disease and host conservation (55). Host individuals also have been conceived of as patches, with pathogen transmission among hosts providing another scale at which metapopulation theory has led to novel insights into host-pathogen interactions (e.g., 48, 73, 84). At the smallest scale, consideration of individual host cells as patches within the metapopulation framework has led to new insights into the role of pathogen movement among cells for pathogen transmission (e.g., 105, 135).

Despite the utility and insights gained from the metapopulation approach, the pervasiveness of diverse microbial communities coinfecting and moving among plant hosts is becoming clear with next-generation sequencing (e.g., 67, 126), suggesting that a predictive framework for plant disease dynamics may require a multispecies framework, such as metacommunity theory (see sidebar, Four Paradigms in Metacommunity Theory) (58, 78, 112). A metacommunity describes a community of communities, the multispecies analog to the metapopulation concept. In a metacommunity, groups of multiple species (a community) interact within patches, and patches are connected by dispersal (78). Although, like metapopulations, patch isolation or area can be important for the composition of species within metacommunity patches, the most important factors for metacommunities are those regulating the coexistence of multiple species (58). Thus, common responses examined for metapopulations are the presence or absence of the focal species (patch occupancy and global persistence), whereas the local diversity of species (alpha diversity) and compositional similarity among patches (beta diversity) are common metrics for metacommunity models. Although this framework was developed for populations and communities of free-living organisms (6, 78), it also may lead to new questions and insights into host-pathogen interactions and communities of microbes interacting within a host (e.g., 85, 112, 129).

Here, we evaluate empirical evidence that a metacommunity framework could be appropriately applied to pathogens in natural plant communities and outline ways in which this theoretical framework may contribute to advancing our predictive understanding of pathogen dynamics that

FOUR PARADIGMS IN METACOMMUNITY THEORY

Leibold et al. (78) describe four paradigms of metacommunities. The simplest is the neutral paradigm, in which patches are identical and species' dispersal rates, competitive abilities, and fitness are equal; thus, patch occupancy and community composition are primarily due to stochastic dispersal and demographic events (60). In this paradigm, spatial patterns are created by dispersal limitation, community composition is in a state of near-constant flux, and communities are "largely accidental collections of species" (60, p. 15). In the patch-dynamic paradigm, patches are still identical; however, coexistence is maintained via trade-offs between species' competitive and colonization abilities. The species sorting paradigm adds realism in the form of among-patch heterogeneity. In the species sorting paradigm, competition and exclusion following colonization can lead to differing patch composition, depending on the patch environment. Thus, habitat suitability and within-patch interactions are more important in this paradigm than in the patch-dynamic model. Finally, the mass effects paradigm combines among-patch heterogeneity with very high colonization rates. In the mass effects paradigm, the outcome of species interactions varies among patches, as in the species sorting paradigm. However, populations can persist in habitats from which they would otherwise be excluded because their populations are subsidized by immigrants and propagules from other patches.

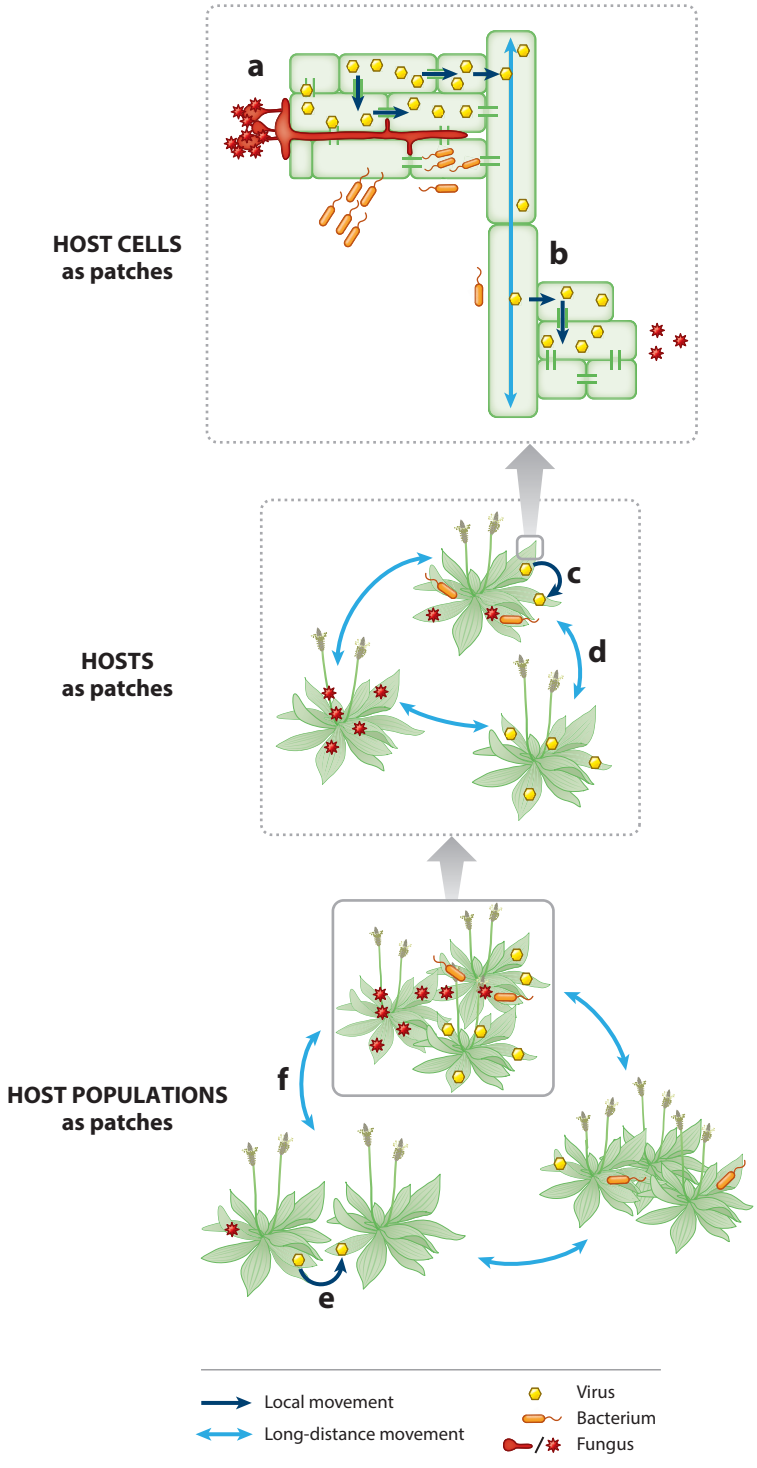
are not effectively captured with more traditional disease modeling approaches. Although our primary focus is on evidence from natural plant communities, the processes and conceptual framework we describe are also relevant for plants in agricultural and other human-dominated landscapes. Further, while our focus is on plant pathogens, pathogenic microbes represent only a small subset of the microbial diversity that composes the plant microbiome (106, 110). The framework we evaluate here holds equal promise for understanding the full community of pathogenic and nonpathogenic plant microbes (35, 85, 112).

We begin our review with the pathogens, focusing on the evidence for pathogen-dispersal pathways and limitations across the hierarchy of transmission scales, spanning among-cell movement all the way to transmission among populations of hosts (**Figure 1**). Ultimately, pathogen dynamics are likely linked across many spatial scales from the intercellular to the biogeographic (21), but for simplicity we structure this review on the interactions across pairs of transmission scales (e.g., the effects of among-cell transmission on the distribution of a pathogen within a host). We also consider differences in perceptions of scale by pathogens with different transmission modes (e.g., vectored or directly transmitted).

We focus next on heterogeneity among patches of habitat created by hosts and their environment and experienced by pathogens, and we examine how environmental heterogeneity can alter pathogen interactions within and among individual hosts as well as among populations of hosts. We also examine the interactions between heterogeneity in nutrient supply and among-host transmission of single and multiple pathogens. Unlike traditional metacommunity theory, infection of host patches by a pathogen can lead to host death, thereby removing patches from the global population. Thus, we turn our attention to ways in which pathogen infection can feed back to alter the spatial structure of host-pathogen interactions. In each section and at the end of this review, we use the metacommunity theoretical framework to highlight research directions that would benefit from further empirical or theoretical exploration.

HIERARCHY OF SPATIAL SCALES FOR PATHOGENS

The concept of a metacommunity provides a framework for considering the linkages among multiple spatial scales that may affect predictions about the distribution, abundance, and interactions


HOST CELLS
as patches
a
b
HOSTS
as patches
c
d
HOST POPULATIONS
as patches
f
e
Local movement
Long-distance movement
Virus
Bacterium
Fungus

among species (78). For our examination of plant pathogens within this conceptual framework, we consider a patch as a discrete habitat that can hold a community of pathogenic microbes, and a metacommunity as a collection of habitat patches. Pathogen individuals, e.g., individual virions or bacterial cells, can colonize and proliferate at one spatial scale—a host cell, for example—then move to nearby or distant cells. Interspecific and intraspecific interactions, such as competition for host-derived resources, occur within a patch, whereas movement occurs among patches (**Figure 1**). Similarly, a host can be conceived of as a patch, potentially hosting many pathogens that interact directly or indirectly (e.g., compete for host resources), and individuals in a population or community of host plants represent the metacommunity. Metacommunity theory provides a single conceptual framework that can be applied across the full range of scales, from cells to landscapes, thereby generating an integrated understanding of the processes that govern pathogen dynamics.

A decade of development and empirical testing of metacommunity theory demonstrates that the interplay of local and regional processes can control the abundance and diversity of species (78). Here, we explore the empirical evidence that viewing the interplay among scales through a metacommunity lens could further inform our understanding of the likelihood of host infection and the diversity of pathogens coinfecting a host (85, 112). Thus, we use the metacommunity abstraction to help us organize our thinking about processes spanning multiple spatial scales that may control pathogen infection and diversity in plant communities.

Host Cells and Tissues as Patches

The processes that govern the spread of pathogens from cell to cell and among tissues within a host effectively map onto the metacommunity framework (112) (**Figure 1**); however, there are few examples where this approach has been explicitly used to understand the dynamics of pathogens within a single host (but see 135). Nevertheless, it is likely that employing the metacommunity framework to better understand the spatial dynamics of pathogens within hosts would yield novel insights. For example, infection of individual cells and pathogen movement among local and distant cells are key spatial scales for understanding the process and progression of host infection because the transition from initial inoculation to systemic infection is a key factor for predicting disease severity and pathogen transmission and epidemiology (105).

At the smallest spatial scale, cells may be considered to be habitat patches where resource acquisition occurs, and the collection of cells making up a host individual represents the complete metacommunity (**Figure 1*a*,*b***). For example, plant viruses require the host's cellular machinery for replication and must infect host cells and proliferate before individual virions colonize adjacent cells (**Figure 1*a***) (32, 109). Although plant viruses can spread between adjacent host cells, a virus must interact with the host's cytoskeletal elements and cell wall proteins to move among cells (103) and can colonize only a small area of host tissue via cell-to-cell movement (56, 146), leading to strong intraspecific competition and self-limitation, in addition to inducing localized host immune

Figure 1

Multiple spatial scales of plant-pathogen metacommunities. When host cells are conceived of as patches, (*a*) local movement involves inoculation, replication, among-cell transport, or hyphal growth, whereas (*b*) long-distance movement involves movement to distant cells and tissues via the phloem, xylem, or intercellular space, or via sporulation. When hosts are conceived of as patches, (*c*) local inoculation and replication occur within hosts, and (*d*) long-distance dispersal occurs among hosts. At the largest spatial scale, (*e*) host populations locally harbor one or multiple pathogen species, whereas (*f*) long-distance transmission occurs among patches of hosts.

defenses (57). A metapopulation model of pathogen transmission among individual host cells demonstrates that the spatial aggregation of infected cells near the initial point of infection is of central importance for limiting infection spread (135). However, the likelihood of transmission among hosts increases when an infection becomes systemic; thus, rapid movement outside of the point of infection, a patch in the metacommunity framework, is highly beneficial to the persistence of a pathogen (105).

Systemic infections can occur when pathogens are transported in the vascular tissues of plant hosts; a diversity of viruses, fungi, and bacteria colonize and move through the xylem or phloem of their host (**Figure 1*b***). Colonization of vascular cells is an effective mechanism for pathogens to disperse to distant regions of a host. This key pathway of pathogen movement among cells in a host allows exploitation of uninfected cellular resources and reduces intraspecific competition among pathogens, increasing pathogen population size (e.g., viral titer), which, in turn, increases the likelihood of successful transmission to a new host (56). For example, *Agrobacterium* sp., the causal agent of crown gall, colonizes xylem vessels, allowing it to move long distances through a plant host and garner resources from cells and tissues distant from the original point of entry (28, 39). Similarly, pathogenic fungi such as *Ophiostoma* spp., including the causal agent of Dutch elm disease, and *Fusarium oxysporum*, which causes vascular wilt or root rot in more than 100 different host species, colonize xylem vessels and move through the plant via both passive transport and mycelial growth through the xylem (143). Most pathogenic plant viruses are transported throughout hosts via phloem, following the transportation pathway of plant carbohydrates (32, 56).

Although host cells are a relevant patch scale for many pathogens, localized regions of host tissues, such as a single leaf or stem, also can be conceived of as a patch for many pathogens. For example, different stems of the same plant can be infected by different genotypes of anther smut (59), and two cryptic species of powdery mildew can co-occur on the same host individuals (*Erysiphe alphitoides* and *Erysiphe quercicola*) in natural oak stands (42). Thus, cells or localized collections of cells within a tissue may be appropriately considered a patch within the metacommunity framework, whereas systemic transport and infection distant from the point of pathogen entry represent among-patch movement (**Figure 1*a*,*b***).

This balance between acquisition of host resources from single cells or small, localized clusters of cells and dispersal throughout a host—the patch-dynamic paradigm of metacommunities, for example—raises the question of whether pathogen competitive ability for host resources and pathogen among-cell dispersal are negatively correlated within and among different pathogen species. Although recent work has demonstrated that a trade-off between the rate at which the virus can replicate and the rate of virion colonization of new cells can lead to a systemic infection (105), much remains to be learned about the conditions under which these rates are negatively correlated. We also would expect a much greater potential for coexistence via trade-offs between local replication and colonization of healthy cells for pathogen communities composed of both single-celled pathogens that depend on reproduction to disperse (bacteria, viruses, and fungi that rely on conidia to spread within hosts) and multicelled pathogens, like most fungi, that spread via hyphae.

Hosts as Patches

Pathogen movement within and among host individuals occurs at a spatial scale that has been frequently modeled using metapopulation and metacommunity approaches. This conception of pathogen dynamics considers hosts as discrete patches and models the presence or absence of an infectious agent within a single host and transmission among hosts to predict the epidemiological consequences for a host population (see sidebar, Modeling Pathogens: Compartmental, Metapopulation, and Metacommunity Models) (9, 11) (**Figure 1*c*,*d***). This framework provides a

MODELING PATHOGENS: COMPARTMENTAL, METAPOPULATION, AND METACOMMUNITY MODELS

Two conceptually and mathematically related theoretical lineages have been used extensively to describe disease dynamics: compartmental and metapopulation models. Compartmental [or SIR (susceptible, infected, recovered)] models are typically composed of differential equations representing host states with respect to the infection process [e.g., S, I, or R hosts] (9, 11, 70, 83). SIR models serve as a powerful tool for understanding and predicting host-pathogen dynamics. They have provided a common mathematical currency for predicting whether a disease will become epidemic, remain endemic, or go extinct.

The parallels between metapopulation and SIR models of pathogen-host interactions have been recognized for decades (84). In a step toward the metacommunity approach, SIR models have been used to demonstrate that coexistence of two pathogens (i.e., coinfection) (115, 136) depends strongly on pathogen interactions with host demography and immune responses.

Despite many parallels, a key difference between metapopulation and SIR is that metapopulation patches do not have dynamics coupled to their colonists, whereas SIR models have strong pathogen-host dynamic coupling (112). However, SIR host-pathogen coupling becomes mathematically intractable with increasing pathogen diversity (112). Recent work applying metacommunity theory to pathogens assumed static hosts (e.g., 112). We explore the implications of this difference in the section Patch Occupancy and Patch Persistence.

vantage point for examining the dynamic consequences of the biology, infection, and transmission among host individuals for a wide variety of host-pathogen systems. For example, the anther smut pathogen *Microbotryum violaceum* causes infected plants to produce flowers with anthers containing fungal spores that are transmitted to new hosts via pollinators, reducing population growth (13, 30). Empirical work with this pathogen has demonstrated that spatial aggregation of host individuals can reduce disease prevalence, whereas patchy, discontinuous host populations are less diseased (5, 31). Thus, the spatial organization and connectivity of host individuals (patches, in this conception) may alter the rate of infection spread and total prevalence across the metapopulation of hosts.

A metacommunity modeling framework is particularly well suited to questions focused on more diverse pathogen assemblages within hosts because a single host is often considered to be composed of a large number of open sites that can be infected, allowing for prediction of both within-host pathogen diversity and within-host relative abundance of individual pathogens (112). Empirical data support the utility of the metacommunity framework in this context. For example, coinfection of hosts by a suite of common foliar fungi alters disease severity in *Populus trichocarpa* by *Melampsora* rust disease and also may alter the probability of among-host pathogen transmission (29). Pathogen diversity (i.e., coinfection) within hosts also has been documented to increase with host size (86, 87, 124, 125), possibly because larger hosts tend to be longer lived, thus accumulating pathogens over a longer time period. The correlation between host size and diversity would be relatively straightforward to test within the metacommunity model framework by changing the number of infection sites that make up an individual host. Metacommunity models are also well suited to explore general relationships between local pathogen diversity within hosts (i.e., coinfection) and the diversity of pathogens in the larger landscape. This landscape level diversity can be an important driver of coinfection within individual hosts. For example, the diversity of barley and cereal yellow dwarf viruses within individual grass hosts can depend in part on the diversity of the viral community in the larger landscape (i.e., the diversity of the metacommunity) (115).

A metacommunity framework can also provide insights into trade-offs and coexistence of different pathogen species or genotypes. For example, coexistence of pathogens could be mediated by a trade-off between within-host competitive ability and other traits such as dispersal ability (79) and off-host survival (1, 120). Alternately, more virulent pathogens may have less potential for dispersal because of a shorter host life span but are better within-host competitors (10). Moreover, cheater genotypes may emerge that perform better in mixed infections than in single infections (16). Finally, genetic diversity of the pathogen population also may influence the frequency at which coinfections occur. López-Villavicencio et al. (82) observed that high genetic diversity within pathogen populations may result in reduced rates of coinfection, seemingly due to higher within-host competitive exclusion among unrelated strains. Thus, spatial structure and dispersal among hosts are critical for maintenance of pathogen diversity, and the intensity of competitive interactions within hosts alters how pathogens experience the spatial structure of their hosts.

To date, remarkably little is known about the role of the host in mediating its pathogen community or how resistance evolves under attack by multiple pathogen species. Wille et al. (138) demonstrated that the outcome of competition among pathogenic fungal endophyte genotypes can vary among host plant genotypes, thereby demonstrating a mechanism by which host plant genetic diversity may maintain fungal diversity. In a seminal study, Burdon (24) found significant within-population variation in resistance to two common foliar pathogens among individuals of the common legume host *Trifolium repens*, suggesting differing strength of selection imposed by these pathogens on their shared host. Jointly, these cases point to a key role of host genotypes and resistance traits in shaping within-host pathogen communities. Moreover, we can expect selection for resistance to be highly sensitive to the diversity of the within-host pathogen community. An exciting future avenue of research will be to investigate this further. Moreover, by mapping real data onto the different metacommunity paradigms, we can better understand the relative importance of pathogen diversity and infection prevalence of within-host resource competition among pathogens, among-host transmission, and variation among the internal environments (e.g., nutrients or pathogen resistance) of hosts. This understanding will inform our predictions for within-host pathogen diversity, long-distance transmission, and disease epidemiology at population and landscape scales.

Host Populations as Patches

Given that disease dynamics depend on transmission from one host individual to the next, it is not surprising to find that the spatial distribution of host individuals has major impacts on disease occurrence patterns. At the metapopulation level, the sizes of local host populations and their connectivity to other host populations have proven to be key parameters predicting landscape-scale disease occurrence patterns (12, 68, 89, 90, 117) (**Figure 1*e*,*f***). Spatial structure is also expected to impact the local diversity of infections for both within-pathogen genetic diversity and species-level diversity. In the metapopulation of powdery mildew *Podosphaera plantaginis* infecting a highly fragmented host population network in the Åland Islands, coinfection is higher in host populations with strong connection to other pathogen populations. Connectivity among pathogen populations likely increases host coinfection by increasing the probability of new strains immigrating into the local population, thereby increasing local genetic diversity (127). Spatial structure in pathogens also may reflect spatial environmental gradients that influence pathogen diversity. For example, environmental gradients underlie the spatial trends in pathogen diversity and the within-host diversity (coinfection) of barley and cereal yellow dwarf viruses in three host grass species across 26 natural grasslands spanning the Pacific coast of the United States (114). Within host populations, pathogen distribution and transmission are dependent on the density and spatial aggregation

of the hosts (25, 96). Previous studies have observed positive correlations between host density and infection prevalence for aerial and splash-dispersed aboveground fungal pathogens and some vector-transmitted viruses (22, 25, 90), with direct links between host density and the diversity of pathogen infections (3, 65, 72, 88).

Plant diversity within local populations may regulate the infection, transmission, and diversity of plant pathogens. The increased number of potential host species may support a diverse community of specialized pathogens (62) while also favoring the presence of generalists (46, 71). However, local plant community structure may decrease the density of susceptible hosts, particularly for specialized pathogens, with increased diversity having a negative effect on infection (5, 45, 145). Plant species diversity can affect host properties such as plant defense levels and nutritional status (34) as well as pathogen transmission mode (22, 90, 116). Moreover, the diversity, abundance, and behavior of pathogen vectors can be influenced by the diversity of the local plant community (25). Recent work on fungal pathogens suggests that reduced host diversity can reduce pathogen diversity within individuals (108).

Thus, when populations of hosts represent a patch within the metacommunity framework, among-patch movement occurs as transmission to a distant host population (**Figure 1*e*,*f***). The importance of the local host and nonhost community context at this spatial scale raises the question of whether locally co-occurring pathogens within host patches are more similar (77) or less similar (40) than a random draw from the global community. A metacommunity approach thus provides a framework for interpreting pathogen diversity and composition at the landscape scale.

Modes of Transmission

Dispersal of pathogen inoculum is central to the development of disease epidemics and, hence, pathogen community structure. Plant pathogens can be transmitted via a variety of biotic and abiotic pathways, including foraging animals, rain blowing or splashing, soil dispersal, and windblown transmission. Here, we focus on vector- and directly transmitted pathogens, as these represent transmission pathways that lead to substantial differences in a pathogen's perception of scale. Vectoring of pathogens among hosts via arthropods (e.g., aphids, leafhoppers, thrips, and mites) is the main transmission mode for many plant pathogens. Vector specificity varies widely, from opportunistic association of some bacteria and fungi with a wide variety of foraging insects to highly specific associations between a pathogen species and a single vector species (e.g., many viruses and some bacteria; 101). Although (or perhaps, because) the association with a vector species is a key step in the among-host transmission of many economically important pathogens, this represents an enormous literature and is beyond the scope of the current review. However, we point our readers to a variety of excellent reviews on this topic (e.g., 33, 47, 53, 92, 101, 137).

Vector behavior and competence can alter the composition and diversity of the pathogen community. For example, viruses that can be transmitted by the same vector species are more likely to coinfect individual hosts and to be spatially and temporally correlated, as has been shown for a suite of aphid-vectored phytoviruses (115). Vector foraging preferences can also alter disease risk among different hosts. For example, grass hosts that are preferred by foraging aphids tend to have a higher prevalence of multiple plant viruses (113). Most importantly, from the perspective of metacommunity theory, foraging vectors that actively seek out food plants that are also competent hosts for the pathogens they carry increase the likelihood that a pathogen will be transmitted to a new, competent host individual or population (134). Thus, the degree of vector specificity determines the probability of any individual pathogen's successful colonization of a new host patch.

In contrast to insect-vectored pathogens, the spores of many plant-pathogenic fungi, such as those causing rusts, mildews, and leaf spots, are released into the air and can be dispersed by air

breezes or strong winds over distances varying from a few centimeters up to several kilometers (15). Recent studies have shown high levels of coinfection within host individuals and in populations of wind-dispersed pathogens (98). Strong gusts of wind promote both spore release and travel; hence, transmission of aerially dispersed pathogens inhabiting the same sites may be spatially and temporally correlated. A spore-trapping experiment over short distances revealed cotransmission of two pathogen strains in the powdery mildew *P. plantaginis*, resulting in new coinfection (127). Moreover, some plant phenotypes and genotypes are also more likely to capture and allow establishment of arriving spores (132), thereby potentially promoting coinfection. Although most research has focused on disentangling the abiotic factors that generate variation in dispersal gradients of passively dispersed pathogens, genetic variation of both the host and the pathogen can affect disease spread at small spatial scales (128, 132), with expected impacts on disease communities.

NUTRIENT SUPPLY AND HETEROGENEITY AMONG PATCHES

Our treatment of the spatial scales of local competition and long-distance dispersal for pathogens, the key elements necessary for application of metacommunity theory, has, so far, ignored the differences among patches that can clearly alter pathogen colonization, persistence, and transmission. Here, we focus on how variation in nutrient supply and nutrient content may alter pathogen persistence, coinfection, and dispersal. Host mineral nutrition has a long history in the study of plant disease (e.g., 17), and the role of nutrients has received revived attention in studies of the ecology of infectious disease (e.g., 51, 66). Such variation is included in the species sorting paradigm (78) and maps effectively onto the well-described variation among host tissues, individuals, and populations that can clearly alter infection dynamics.

Nutrient Supply and Host Tissues as Patches

Tissues within an individual plant can vary strongly in the content and ratio of growth-limiting nutrients such as nitrogen and phosphorus (102, 144), and plants can reallocate nutrients among tissues in response to infection (e.g., 4, 80, 95). In light of this within-host nutrient heterogeneity and because different pathogens differ in their nutrient requirements (41), occupy different plant tissues, and can have different within-host growth strategies, a single host individual may provide a suitable habitat for a wide range of pathogens. Indeed, partitioning of the resource niche may promote coexistence of pathogenic and nonpathogenic microbial species sharing the same host (118, 119). For example, coexistence of the pathogenic bacterium *Pseudomonas syringae* with several other epiphytic bacteria in the phyllosphere of hosts depends on the degree of niche differentiation in carbon source (141). However, little work has been done to directly link the nutrient variation among host tissues with the cell-to-cell movement or long-distance transport of microbes through a host's vascular system. Examining the effectiveness of the metacommunity concept for studying host-pathogen interactions at multiple spatial scales highlights that the link between local tissue nutrient content and pathogen resource competition, population growth, and long-distance transport through a host is a promising future direction for research into the rate and mechanisms by which infections transition from localized to systemic (105).

Nutrient Supply and Hosts as Patches

The nutrient content of individual hosts may be a function of the local environmental nutrient supply rate or host identity and can directly modify host susceptibility and within-host pathogen dynamics, or can act indirectly on epidemiology by altering host-vector interactions. Spatial variation

in environmental nutrient supply rates can directly alter a variety of vital rates that regulate host-pathogen interactions, including pathogen transmission and host resistance. For example, although many plant nutrients influence host susceptibility to foliar fungal pathogens, nitrogen supply frequently increases the incidence of powdery mildews and rusts (61). Hence, the global increase in nitrogen deposition is expected to have major influences on plant disease, as has been shown in fungal infection of the dwarf shrub *Vaccinium myrtillus* in northern Sweden (123). High potassium, manganese, and silicon content can enhance plant disease resistance to a wide range of pathogens and herbivorous insects in *Arabidopsis thaliana* (7), whereas phosphate may increase host susceptibility (64) to fungal pathogens. Plant nutrients can also have strong effects on prevalence and coinfection by plant viral pathogens. Host nutrient content can determine vector fecundity, competence, or preference, altering pathogen transmission (19, 113), and nitrogen, phosphorus, and micronutrients all have been shown to increase the prevalence of barley and cereal yellow dwarf viruses, a group of generalist, aphid-vectored pathogens of grass species (23, 74).

Host nutrient content may also determine the diversity of pathogens found within individual hosts. Although few experimental studies have tested this hypothesis, Lacroix et al. (74) found that an elevated supply of nitrogen and phosphorus caused a greater rate of coinfection by plant viruses than expected. Considering coinfection within a host from the vantage point of metacommunity theory suggests that this is an area ripe for exploration, as it predicts that spatial variability among patches, e.g., heterogeneity in nutrients among cells, tissues, or hosts, should typically increase the diversity of species within a single patch because of propagule subsidies from neighboring patches (i.e., mass effects) (78, 94, 112). These mass effects are analogous to (and may be a mechanism for) the spillover effects in which pathogen subsidies from reservoir hosts can increase pathogen prevalence in less competent hosts (71, 100).

Although host nutrient content may be altered by environmental nutrient supply, host nutrient content can also vary systematically among species along with a suite of correlated physiological traits, including growth rate and longevity, that act together to determine the potential of different host species to act as pathogen reservoirs and ultimately determine pathogen spread rates (38). Thus, many of the observed relationships between environmental nutrient supply and infection likely also exist across the species-level trait continuum of host nutrient content, suggesting that the species sorting and mass effects (i.e., pathogen spillover) paradigms of metacommunity theory may be particularly relevant for generating hypotheses about multihost pathogens.

Nutrient Supply and Host Populations as Patches

Soil nutrient availability plays a key role in determining the community structure and density of local plant host populations (36, 99), both of which are expected to impact the pathogen communities interacting with local plant individuals. Fertilization can increase the homogeneity of the abiotic environment, and for the species in natural plant communities that benefit from elevated nutrient supply, host populations can become more interconnected and less spatially structured (122). This change in spatial structuring of hosts in response to nutrient supply suggests a key role for metacommunity theory in generating testable hypotheses about the role of elevated nutrient supply in determining the dominant processes influencing infection.

Variation in environmental nutrient supply among host populations can also play a key role in determining nutrient availability to pathogens exploiting the host species and the host's ability to resist infection. Although there are limited data linking soil nutrient availability to local pathogen community composition, field level studies on the West Coast of the United States have shown that addition of nutrients differentially affects the prevalence of different species of the aphid-vectored barley and cereal yellow dwarf viruses, ultimately determining viral community composition (113).

There are more studies on single-host, single-pathogen interactions, and these suggest that such links are also expected at the community level. In the interaction between *Hesperolinon californicum*, a plant in the flax family, and the pathogenic rust fungus *Melampsora lini*, plants growing in more stressful low-calcium soils experienced higher rates of rust infection, suggesting that soil calcium may modulate host susceptibility (121) at the population level. Soil calcium levels were also shown to mediate interactions between yellow star thistle, *Centaurea solstitialis*, its foliar pathogen, and three insect seed predators (130). Nutrient conditions were additionally shown to affect adaptation of host defense mechanisms in the interaction between the perennial grass *Holcus lanatus* and its rust pathogen, *Puccinia coronata*, in the 150-year-long Park Grass Experiment in the United Kingdom (63). Thus, nutrients can modify host defenses, nutrient supply to pathogens, and spatial structuring of hosts in the landscape, highlighting the links between variation in environmental nutrient supply and the local and long-distance transmission of pathogens. The multiple paradigms of metacommunity theory provide a promising approach for asking new questions about the role of nutrients in coinfection and the transition from endemic to epidemic infections at the landscape scale.

MISMATCHES BETWEEN THE METACOMMUNITY CONCEPT AND PATHOGEN-HOST INTERACTIONS

In spite of the effective description and new questions generated by examining pathogen-host interactions through a metacommunity lens, the existing metacommunity concept does not easily describe all aspects of pathogen-host interactions. Here, we explicitly examine biological attributes of host-pathogen interactions in which the existing metacommunity concept does not map directly onto this set of spatial interactions, namely that hosts have some fundamental differences from habitat patches in the landscape and, related, that occupancy of a host patch by one or more pathogens can feed back to affect host survival (i.e., patch persistence).

Hosts and the Metacommunity Patch Concept

The metapopulation and metacommunity theories generally assume a large number of static patches that are equidistant from one another or that patches are lost or become unoccupied at a constant rate (e.g., 54, 93, 133). In contrast, one of the most defining characteristics of host-pathogen systems is that host populations are dynamic in space and time. The dynamics of plant hosts may be largely independent of their microbial flora, arising as a result of infection-independent changes in host vital rates (37). For example, habitat loss can serve as a density-independent force removing host patches from the landscape (54, 93, 133), and metacommunity theory has demonstrated that patch removal through habitat loss or host vaccination can reduce infection prevalence in a host population while favoring species with higher dispersal or transmission rates (84). However, we are not aware of any metacommunity models that have examined the effect of temporally dynamic patches (i.e., patch births and deaths) or patches with a fixed life span. Thus, incorporation of patch dynamics into metacommunity models will enhance the relevance of metacommunity theory for generating predictions about most disease systems (85, 112).

Like individual hosts, many host populations are highly spatially structured because of the combined effects of spatial variability in the environment, dispersal limitation, and competition with neighboring individuals (18, 111). The spatial variability in host density is likely to alter the persistence or density of host populations, which will alter the infection risk of host individuals, especially for pathogens with strongly density-dependent transmission, such as wheat stripe rust (*Puccinia striiformis*), a wind-dispersed pathogen (91). Thus, incorporating variable distance among patches into metacommunity models will be an important step toward increasing the relevance of this framework, particularly for pathogens with density-dependent transmission.

Patch Occupancy and Patch Persistence

Pathogen infection often controls host dynamics, a linkage which can feed back to control the dynamics of the pathogen. Yet, in addition to assuming that patches are not dynamic in time or space, metacommunity theory generally includes no feedback between patch occupancy and patch persistence (78). Although this is a reasonable assumption for patches of habitat, feedbacks between the infection status of a plant host and its persistence are defining characteristics of disease models. Infection by one or more pathogens can feed back to alter host survival and fecundity (76, 131), determining the persistence and spatial structure of plant hosts and populations. Biological control of agricultural weeds using plant pathogens, for example, is the targeted use of pathogens to reduce host population size (107, 139) and is successful when, in metapopulation terms, patch occupancy (host infection) reduces the total number of patches (host population size). Similar effects of pathogens can occur in nursery and nonagricultural environments; for example, epidemics such as Dutch elm disease (69), chestnut blight (8), and Sudden Oak Death (104) are notorious for dramatically reducing their host populations.

Although plant pathologists have historically focused on infection and control of single pathogens (76), there is growing evidence of widespread coinfection of most hosts by more than one pathogen (43, 76). Coinfection of a wide variety of hosts, including vegetables, grains, and fruits, by pathogen complexes of bacteria, fungi, or viruses have been documented to induce greater mortality in their hosts than single infections (reviewed in 76), suggesting that synergistic interactions among pathogens within hosts may be both widespread and important for determining the population dynamics of their hosts (76, 115, 131, 136). Thus, patch occupancy, patch persistence, and the composition of the within-patch community are important considerations for modeling the dynamics of plant disease as a metacommunity.

A theory formulated explicitly to examine the effect of patch loss on metacommunity dynamics suggests that feedbacks between patch occupancy and patch persistence may lead to substantial changes in the dynamics of a metacommunity. For example, random loss of habitat patches or hosts from a metacommunity can cause continued declines in species persistence long after patches are lost, owing to low colonization rates (133), or may lead to a decline in the total pathogen diversity of the remaining hosts (131). However, linking patch loss to patch occupancy or within-patch species composition could fundamentally alter these predictions. In addition, although a transmission-virulence trade-off is often assumed in epidemiological and evolutionary models of disease, the empirical evidence for the ubiquity of this relationship for plant pathogens is inconclusive (44). Explicitly including virulence as a function of infection and coinfection further alters the predictions for metacommunity dynamics, suggesting that the total number of pathogens will be largely unaffected in the long run, whereas the average pathogen virulence (host death rate) will be reduced (84). However, in this metacommunity formulation, multiple pathogens persist only at the host population level, because only a single pathogen can infect a host at any point in time (84).

Thus, given the reduction in host population size induced by many plant pathogens and the growing number of examples of plant pathogens for which coinfection synergistically increases the titer (or pathogen load), transmission efficiency, and virulence (e.g., 2, 76, 131, 142), a metacommunity theory of disease that explicitly feeds back from individual and multiple pathogen infections to host population dynamics will fill a gap for predicting the role of pathogen diversity in host population dynamics (112).

CONCLUSIONS AND FUTURE DIRECTIONS

Only rarely in plant pathology or the ecology of infectious disease are the dynamics of multi-pathogen assemblages conceived of as the interplay between local- and regional-scale processes,

leading to predictable patterns of coinfection within hosts or among host populations. Yet, mapping empirical evidence onto the metacommunity framework demonstrates that stochastic mechanisms and environmental tolerance can shape diversity at many spatial scales (78), generating predictable patterns of host species and multiple pathogen species within hosts, within host populations, and across landscapes. Examining the spatial distribution and co-occurrence of microbial species using the metacommunity framework to generate hypotheses will inform our understanding of the local and long-distance forces shaping disease dynamics in plant communities. In addition, this framework also promises new insights into the ways in which anthropogenic changes to host and vector composition and diversity, ecosystem eutrophication, and pathogen interactions within hosts and vectors will alter the spatial dynamics of pathogen competition and movement within and among hosts. The metacommunity conception of plant-pathogen dynamics will likely clarify emergent regional-scale patterns that may help identify risks of known pathogens and predict risks of those yet to be discovered.

Thus, the metacommunity theoretical framework, which has been important for identifying new questions, framing testable hypotheses, and deepening the understanding of spatial determinants of communities of free-living organisms (58, 78), also holds promise for a deeper understanding of plant-pathogen dynamics. A review of a cross section of the empirical evidence for multiple scales of spatial movement of fungal, viral, and bacterial pathogens suggests that the metacommunity framework can provide a useful lens for the study of movement scales of plant pathogens and their hosts. In particular, each of the metacommunity paradigms (78) suggests a variety of hypotheses about the dominant forces determining infection and coinfection of plant hosts. Testing these hypotheses with existing and new empirical data will elucidate the role of interactions among pathogen species within hosts (i.e., coinfection) as well as ways that host and pathogen community context may modify pathogen movement and accumulation among tissues, among hosts, and across landscapes. In addition to those raised in each section, we provide examples of predictions ripe for examination, in the form of hypothesis-based questions in the Future Issues section.

Ecological theory in its many forms serves as an important tool for the prediction of infection progression and pathogen epidemics. Theoretical models provide a powerful tool for assessing the efficacy of control strategies for devastating pathogens and the potential of pathogens to serve as biocontrol agents as well as for predicting the likelihood of epidemics (70). However, examining the multiple scales of pathogen infection and transmission in a diversity of different host-pathogen systems also highlights areas ripe for further theory development, such as explicit examination of the implications for pathogen dynamics in response to population dynamics of their host patches, variable distances among patches, and feedbacks between patch occupancy and patch persistence. These modifications of existing theory and development of new theory will likely generate novel dynamic predictions that are highly relevant for understanding infection, coinfection, and pathogen transmission at the scales of cells, hosts, and host populations.

The multiscale mechanisms addressed by metacommunity theory are often overlooked in plant pathology, disease ecology, and epidemiology; however, by exploring empirical evidence through a metacommunity lens, it is clear that the importance of spatial structure for determining infection dynamics has many parallels at scales spanning cells within a host to populations of hosts in a landscape. Using metacommunity theory as a conceptual framework allows us to identify plausible mechanisms shaping patterns of infection at each of these spatial scales. The empirical evidence reviewed here suggests that environmental changes leading to altered local movement, colonization, extinction, or long-distance transmission of pathogens serve to filter the composition of pathogen species, determining patterns of coinfection and feeding back to alter processes at larger and smaller spatial scales. Inquiry informed by metacommunity theory will allow us to ask and answer parallel questions about the role of local environments and competition compared

with regional transport spanning cell to landscape scales, potentially leading to an understanding of the scale-independent general characteristics of pathogen dynamics as well as species- and trait-dependent contingencies. Thus, this review suggests that explicitly using metacommunity theory to pose testable hypotheses about diverse microbial assemblages within hosts and host populations could be instrumental in further informing predictions about host infection risk and pathogen coinfection within a host. Our ability to predict and manage the dynamics of plant pathogens stands to benefit substantially from further development and empirical testing of the multiscale hierarchical metacommunity theory of pathogens.

SUMMARY POINTS

1. Plant populations and individual plants, tissues, or cells may be appropriately considered a patch within the metacommunity framework, whereas transport and infection distant from the population, in a different plant or in cells or tissues far from the point of pathogen entry, represent among-patch movement.
2. A review of empirical evidence at multiple spatial scales suggests that explicit testing and further development of the metacommunity framework will be a useful avenue for generating new hypotheses about plant-pathogen communities and their hosts.
3. Environmental nutrient supply can modify host allocation to defense, pathogen access to host nutrients, and the composition and spatial structuring of hosts, highlighting the links between environmental nutrients and the local composition and long-distance transmission of pathogen species.
4. Cells, hosts, and host populations have dynamics that may be simultaneously independent of and dependent on infection; thus, further development of metacommunity theory to include these dynamics and feedbacks will improve the predictive ability of these models for host-pathogen interactions and increase our understanding of the mechanisms generating correlations (positive and negative) among pathogen species at multiple scales.

FUTURE ISSUES

1. The patch dynamic paradigm of metacommunities raises a variety of testable hypotheses about pathogen co-occurrence. For example, are patterns of pathogen species presence and co-occurrence nonrandom among host tissues, hosts, or host populations? Do a host's constitutive or induced defenses shape its pathogen community? Do different host genotypes select for different pathogen communities? Does the order of infection alter host suitability for other pathogens?
2. The patch dynamic paradigm also predicts that coinfection will result from trade-offs. For example, are pathogen within-patch competition and among-patch dispersal negatively correlated, where patches are cells, tissues, hosts, or host populations?
3. The species sorting paradigm suggests that the abiotic environment may mediate pathogen infection and coinfection rates. For example, to what extent does host nutrient content alter selection at the host or host patch scale? Is there evidence for negative correlations among pathogen genotypes or species under different resource environments?

4. The species sorting paradigm also suggests that the pathogens' fitness will vary among patches at a variety of scales. For example, are locally co-occurring pathogens (within host cells, individual hosts, or host patches) more similar (77) or less similar (40) than a random draw from the global community?
5. The mass effects and neutrality paradigms suggest a key role of pathogen transmission in maintaining diversity. For example, is there density-dependent dispersal of pathogens (vector transmitted versus directly transmitted)?
6. The mass effects and neutrality paradigms also raise the possibility that a trade-off between pathogen evolution and transmission may determine pathogen diversity. For example, is the rate of plant-pathogen evolution faster than the rate of dispersal?
7. The mass effects and neutrality paradigms also suggest that there is a limit to the total infection load of a host (i.e., zero-sum game), thus raising questions such as whether an increase in one pathogen within a host necessarily leads to declines in other pathogens.

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