

Deer, predators, and the emergence of Lyme disease

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Lyme disease is the most prevalent vector-borne disease in North America, and both the annual incidence and geographic range are increasing. The emergence of Lyme disease has been attributed to a century-long recovery of deer, an important reproductive host for adult ticks. However, a growing body of evidence suggests that Lyme disease risk may now be more dynamically linked to fluctuations in the abundance of small-mammal hosts that are thought to infect the majority of ticks. The continuing and rapid increase in Lyme disease over the past two decades, long after the recolonization of deer, suggests that other factors, including changes in the ecology of small-mammal hosts may be responsible for the continuing emergence of Lyme disease. We present a theoretical model that illustrates how reductions in small-mammal predators can sharply increase Lyme disease risk. We then show that increases in Lyme disease in the northeastern and midwestern United States over the past three decades are frequently uncorrelated with deer abundance and instead coincide with a range-wide decline of a key small-mammal predator, the red fox, likely due to expansion of coyote populations. Further, across four states we find poor spatial correlation between deer abundance and Lyme disease incidence, but coyote abundance and fox rarity effectively predict the spatial distribution of Lyme disease in New York. These results suggest that changes in predator communities may have cascading impacts that facilitate the emergence of zoonotic diseases, the vast majority of which rely on hosts that occupy low trophic levels.

coyote range expansion | *Ixodes* | mesopredator release | trophic cascade | zoonosis

There is growing recognition that changes in host community ecology and trophic interactions can contribute to the emergence of infectious diseases (1–3). In particular, the transmission of vector-borne zoonotic diseases to humans depends on multiple species interactions that influence host and vector abundance and infection prevalence. Most zoonotic pathogens are harbored by wildlife that occupy low trophic levels (1). The extirpation of top predators and the consequent restructuring of predator communities (4, 5) may thus increase the risk of zoonotic diseases if predation of reservoir hosts plays a key role in disease suppression. A paradigmatic case of disease emergence that is thought to be driven by changes in the host community is Lyme disease (Fig. 1).

Lyme disease is the most prevalent vector-borne disease in North America, and both the annual incidence and geographic range are still increasing (6). The disease is caused by the bacteria *Borrelia burgdorferi*, which is transmitted to humans in the eastern United States primarily by the nymphal stage of *Ixodes scapularis* ticks (7). The emergence of Lyme disease has been attributed to the century-long population recovery of deer, which are not competent hosts for transmitting *B. burgdorferi* to ticks but are nonetheless important reproductive hosts for adult ticks (7, 8). Support for this hypothesis comes partly from studies of experimental removal or exclusion of deer, which has often led to reduced tick densities (9). However, substantial research indicates that experimental or natural increases of deer density above a low threshold often have little effect on nymphal tick abundance (reviewed in ref. 10; see also refs. 11–13; Table S1). This research suggests that when deer are sufficiently abundant, other factors, such as hosts for immature ticks, may become limiting. Decades after the recolonization of deer, and despite

a shift in management objectives from increasing deer populations to stabilizing or reducing them (14), Lyme disease cases have increased enormously (380% increase in Minnesota, 280% in Wisconsin, and 1,300% in Virginia from 1997 to 2007; Fig. S1), which suggests that other previously unidentified ecological changes may now be facilitating the emergence of Lyme disease.

A growing body of evidence implicates small-mammal abundance as a key determinant of the density of infected nymphs, the primary measure of entomological risk for Lyme disease (12, 15, 16). Molecular evidence suggests that four species of small mammals (the white-footed mouse *Peromyscus leucopus*, Eastern chipmunk *Tamias striatus*, short-tailed shrew *Sorex brevicauda*, and masked shrew *Sorex cinereus*) are responsible for infecting 80–90% of ticks (17). Thus, it is possible that changes in the ecology of small mammals play a role in the continuing increase of Lyme disease. Small-mammal populations are influenced both by resource availability, which has been correlated with the subsequent density of infected nymphs (12, 15) and by predation (18). The latter finding has led to the suggestion that predation may play a key role in suppressing Lyme disease (1).

A major change in predator–prey interactions in North America over the last half-century has resulted from the range expansion and population growth of a new top predator—the coyote, *Canis latrans*, which has spread across the continent following the extirpation of gray wolves, *Canis lupus* (19). The expansion of coyotes likely suppressed the abundance of several small-mammal predators, with the reduction of foxes by interference competition with coyotes being the best documented (20–22). The replacement of foxes by coyotes would likely reduce predation rates on small-mammal prey (i.e., the reverse of mesopredator release) because red fox (*Vulpes vulpes*) densities are typically an order of magnitude higher than coyote densities (23–25), and small mammals make up a larger fraction of their diets, particularly in the eastern United States, where coyotes have hybridized with wolves (26) and rely far more on deer (27, 28). Further, red fox cache prey for later consumption and are thus capable of killing large quantities of prey when prey are abundant (e.g., after an acorn mast). The high abundance of foxes (29), their ability to kill large quantities of small mammals due to both dietary preference and prey-caching behavior, and their adaptability to human-dominated landscapes makes them potentially highly important to suppressing Lyme disease hosts in areas around human habitation. Thus, somewhat paradoxically, the expansion of coyotes likely decreased predation rates on small mammals by suppressing more-efficient predators (foxes).

Here we test the hypothesis that changes in predation have contributed to the continuing emergence of Lyme disease by analyzing disease models that explicitly incorporate predation intensity, and by examining spatial and temporal correlations at multiple scales between Lyme disease, coyote, fox, and deer abundance.

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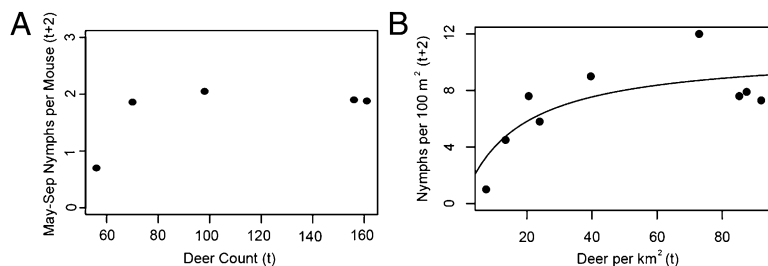


Fig. 2. Relationships between deer abundance and Lyme disease risk measured by the density of infected nymphs. (A) *I. scapularis* nymph abundance, measured as nymphs per mouse, in response to deer removal experiment in Deblinger et al. (30). (B) Nymph density (100 m^{-2}) as a function of deer density (per km^2) from Stafford et al. (31). When all data are included, there is a saturating relationship, and there is no significant relationship without the point with the lowest deer density despite nearly 10-fold variation in deer density.

is positively correlated with coyotes and negatively correlated with foxes (Fig. 4A and B), which suggests a more important role for variation in the abundance of predators than deer. Lyme disease is notably rare in western New York, where fox are abundant, despite having among the highest deer abundance in the state. It is worth noting that the nonlinear relationship between foxes and Lyme in Fig. 4B closely resembles model predictions (Fig. 1). Previously compiled data on catch-per-unit effort of red fox by trappers and buck harvest density match the spatial distribution of carnivores and deer derived from harvest-independent data (34).

Temporal Correlations at Smaller Spatial Scales. Harvest-independent data from multiple regions of Wisconsin also suggest that Lyme incidence is more tightly linked to changes in predator abundance (coyote increase and fox decrease leading to lower overall predation rates) than deer abundance. In Wisconsin, where Lyme disease incidence has increased greatly over the past decade, landowner wildlife surveys indicate that a fox decline and coyote increase occurred throughout the state (Fig. 5), which corroborates the statewide trends from hunter harvest data (Fig. 3). Deer observations have been stable or declining over this period (Fig. 5), although due to high deer abundance, these surveys may be a less-sensitive index for deer. However, on a fine spatial scale, deer density in management units with the highest Lyme incidence did not change over the last decade, whereas

Lyme disease cases increased 300% (Fig. S7). Deer densities increased at most sites from the early 1980s until the mid 1990s, which may have caused the initial emergence of Lyme disease in Wisconsin. However, in the past 15 y, deer abundance has slowed markedly, with one-fourth of units showing no increase and several others increasing only a small percentage (Fig. S7).

Discussion

The increase in deer during the early 20th century is thought to have allowed tick populations to grow and spread from small remnant populations, and this likely contributed significantly to the initial rise in Lyme disease cases (7). However, in recent decades, Lyme disease has continued to increase substantially in many places where deer populations have stabilized (Figs. 2 and 4). Further, we detected no relationship between the spatial distribution of Lyme disease and deer abundance in four states (Fig. 4). The weak correlations between changes in deer and Lyme disease incidence is consistent with a saturation in the probability that an adult tick finds a host (e.g., deer) with deer density (Fig. 2). Additionally, recent work from New York found no relationship between threefold variation in deer abundance and the density of infected nymphs over 13 y (12), and there was no response in nymph abundance to a recent deer culling program in New Jersey (13). Thus, though there is convincing evidence linking deer to high nymph densities from deer enclosure

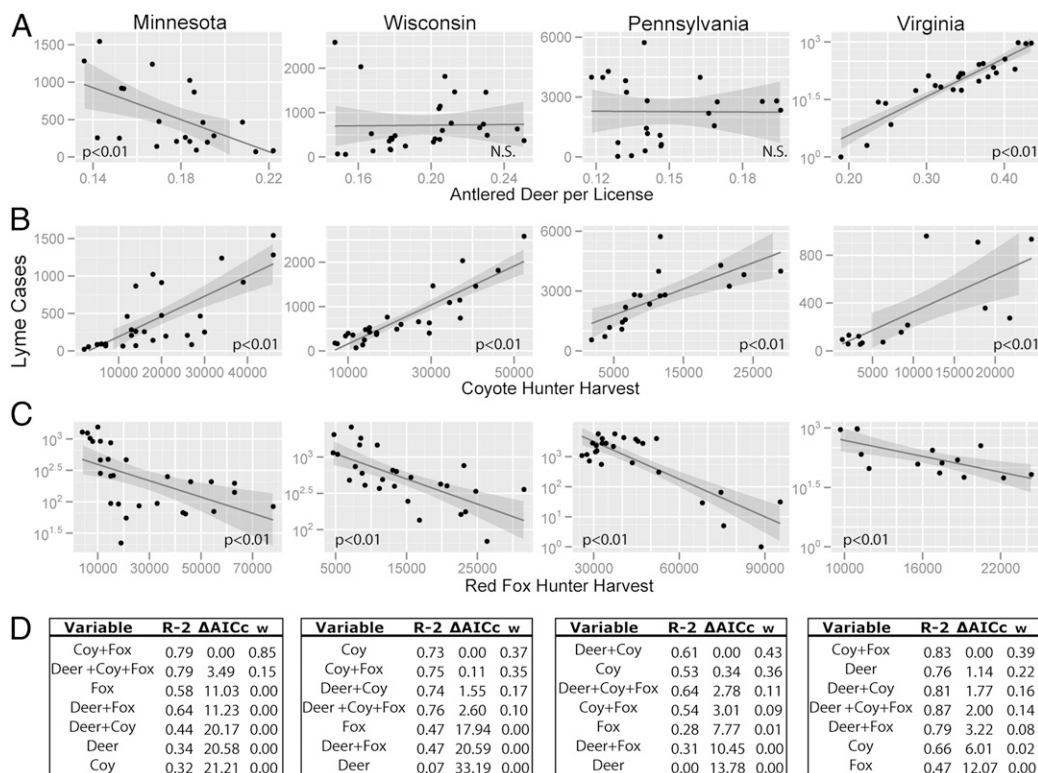


Fig. 3. Temporal trends between Lyme cases and (A) deer harvest per license, the hunter harvest of (B) coyotes, and (C) foxes are consistent with the predation hypothesis. As predicted by the model, the relationship between foxes and Lyme is nonlinear (Lyme cases are on a log scale). (D) Statistical models were compared with AICc. All models with greater than 1% model weight did not have temporally autocorrelated residuals ($P > 0.05$ Box-Pierce test). Model selection in Pennsylvania underestimates the importance of foxes because we use only data since 1990, the first year that coyote data were collected (fox-only model is best if coyotes are excluded and the full fox and deer time series are analyzed).

a combination of predator manipulation and severe reductions in deer densities necessary to reduce tick abundance.

More broadly, these results suggest a need to explore the role of predation in the community ecology of other emerging zoonotic diseases, which overwhelmingly rely on hosts that occupy low trophic levels (1). Due to the widespread eradication of large carnivores (4), top predators in many terrestrial ecosystems are now medium-sized carnivores such as coyotes (5). These medium-sized carnivores can indirectly increase the abundance and diversity of low trophic-level species, such as rodents and songbirds, by suppressing populations of smaller carnivores such as foxes (20). Strong interactions among predators (35) that lead to cascading effects on prey have been documented for over 60 systems worldwide (21). As top predators are extirpated in some parts of the world, and recolonize in others, it will be important to understand the consequences for community composition and for the abundance of low trophic-level species in particular. Such restructuring of predator communities may have unintended consequences for human disease.

Methods

Host-Vector Disease Model. We use a vector-borne, susceptible-infected (36) modeling framework that describes the dynamics of ticks and small-mammal hosts, and includes parameters to account for the density of alternate hosts and deer. We group multiple species into a functional group of small-mammal hosts with density, N_m . The small-mammal host population growth rate, $G(N_m)$, is logistic with maximum intrinsic growth rate, r , and carrying capacity, K . The mortality rate, $M(N_m)$, follows a Holling type III functional response, which is characteristic of prey-switching generalist predation, with maximum predation rate, a , half-saturation parameter, c , and predator density, P (37–39). This functional response can exhibit alternative stable states in a small region of parameter space, but we stress that our results depend only on an S-shaped functional response, which is characteristic of switching or aggregating behavior in response to more-abundant prey (Fig. S3). An S-shaped functional response is also obtained with a type II functional response when predators respond numerically to increasing prey density (i.e., a combined numerical and functional response; *SI Text, Parameters and Derivations*).

The differential equation for the total host population is

$$\begin{aligned} \frac{dN_m}{dt} &= G(N_m) - M(N_m) \\ &= rN_m \left(1 - \frac{N_m}{K}\right) - \frac{aPN_m^2}{c^2 + N_m^2} \end{aligned} \quad [1]$$

The small-mammal host population consists of susceptible, S_m , and infected, I_m , classes. Susceptible hosts become infected with probability T_{mt} when bitten by an infected nymph, I_t . A fraction of tick bites occur on incompetent “dilution” hosts, F , so that these hosts divert blood meals away from small mammals but also increase total host abundance. The tick bite rate, $\beta(N_m + F)$, follows a type II functional response. Because each tick life stage requires a single blood meal, the functional response saturates at 1 as the abundance of hosts increases (i.e., all ticks can feed if there are infinite hosts). The half-saturation parameter, b_0 , represents the density of small mammals where half of ticks would be expected to feed. Thus, the tick bite rate can be interpreted as the fraction of ticks that successfully feed given the total population of hosts, $N_m + F$.

The differential equations for susceptible and infected small-mammal hosts are

$$\begin{aligned} \frac{dS_m}{dt} &= G(N_m) - T_{mt}I_t \frac{S_m}{N_m + F} \beta(N_m + F) - \frac{S_m}{N_m} M(N_m) \\ &= rN_m \left(1 - \frac{N_m}{K}\right) - \frac{T_{mt}I_t S_m}{b_0 + N_m + F} - \frac{S_m aPN_m}{c^2 + N_m^2} \end{aligned} \quad [2]$$

and

$$\begin{aligned} \frac{dI_m}{dt} &= T_{mt}I_t \frac{S_m}{N_m + F} \beta(N_m + F) - \frac{I_m}{N_m} M(N_m) \\ &= \frac{T_{mt}I_t S_m}{b_0 + N_m + F} - \frac{I_m aPN_m}{c^2 + N_m^2}, \end{aligned} \quad [3]$$

where susceptible hosts are created by birth and lost by infection or predation, and infected hosts are created by infection and lost by predation.

We assume no increase in predation risk associated with being infected. Therefore, the relative abundance of the susceptible and infected classes determines the relative predation rate of each class.

Larval ticks, S_t , which are all susceptible, have birth rate ν and per-capita death rate μ_t . We use a constant birth rate that can be varied independently, because it is unknown how vertebrate biomass and community composition influence the tick birth rate. Any larval tick that successfully feeds on either a small-mammal host or dilution host leaves this class so that the differential equation for larva is

$$\begin{aligned} \frac{dS_t}{dt} &= \nu - \beta(N_m + F)S_t - \mu_t S_t \\ &= \nu - \frac{N_m + F}{b_0 + N_m + F} S_t - \mu_t S_t \end{aligned} \quad [4]$$

Nymphs die at rate, μ_n , and also leave their class by successfully feeding. Nymphs become infected when larva successfully contract *Borrelia* from an infected host (i.e., this depends on the frequency of infected hosts) with probability T_{tm} . Thus, the differential equation for infected nymphs, I_t , is

$$\begin{aligned} \frac{dI_t}{dt} &= \frac{I_m}{N_m + F} \beta(N_m + F) T_{tm} S_t - \beta(N_m + F) I_t - \mu_n I_t \\ &= \frac{T_{tm} I_m S_t}{b_0 + N_m + F} - \frac{N_m + F}{b_0 + N_m + F} I_t - \mu_n I_t \end{aligned} \quad [5]$$

Uninfected nymphs, J_t , can be uninfected because a larval tick fed on a susceptible or dilution host or because a larval tick fed on an infected host but did not contract *Borrelia*. The equation for uninfected nymphs thus has an additional term to account for the probability that feeding on an infected host did not cause infection, but can be simplified to

$$\begin{aligned} \frac{dJ_t}{dt} &= \frac{S_m + F}{N_m + F} \beta(N_m + F) S_t + (1 - T_{tm}) \frac{I_m}{N_m + F} \beta(N_m + F) S_t - \beta(N_m + F) J_t - \mu_n J_t \\ &= \frac{S_m + F + I_m(1 - T_{tm})}{b_0 + N_m + F} S_t - \frac{N_m + F}{b_0 + N_m + F} J_t - \mu_n J_t \end{aligned} \quad [6]$$

We solved for the steady states as a function of the steady-state small-mammal density $\bar{N}_m$. The closed-form solutions, which are presented in *SI Text, Steady-State Solutions*, explicitly demonstrate the strength of the known multiple drivers of Lyme disease.

Data Analysis. Spatial Analysis. New York enlists bow hunters to survey wildlife from tree stands. We averaged the observation rates of each species from 2005 to 2007 in each management unit to compare with Lyme disease incidence from 2006 to 2008. Lyme disease incidence is recorded at a county scale, so we allocated incidence to management units as a weighted average based on the relative area of each county in each wildlife management unit groupings.

In Virginia we used buck harvest per square mile reported in the Virginia deer management plan (14) as a proxy for deer density. Both the harvest data and Lyme disease data are on the county spatial scale. Wisconsin and Pennsylvania produce deer density estimates using the sex-age-kill model (40), which estimates density in management units using data on harvest, age, and sex structure, and fawn-to-doe ratios. Lyme disease incidence is recorded at a county scale. In Pennsylvania, wildlife management units are larger than counties, so we allocated Lyme incidence to management units as above. In Wisconsin, wildlife management units are smaller than counties, so we allocated deer density to counties based on the relative area of each wildlife management unit in each county. For Wisconsin, we additionally analyze changes in deer densities since 1981 in 25 randomly chosen management units intersecting counties with the highest incidence (Fig. S7).

Time-Series Methods. We use harvest-based proxies for white-tailed deer, coyote, and red fox abundance. To compare the populations of coyotes and foxes with annual Lyme disease cases, we use hunter harvest as a proxy for abundance. Any longitudinal changes in hunting effort are unlikely to be biased in favor of one of these species over another, suggesting that a decline in fox harvests and an increase in coyote harvests represent real population changes. Data on trapper harvest is more widely available but is not reliable because it is influenced by exogenous factors such as pelt prices and changes in trapping regulations designed to prevent incidental catch of high-value or endangered species. Many states, including the four we consider, have liberal

coyote- and fox-hunting regulations, including very long or continuous seasons and no bag limits. We therefore conduct our analysis on the subset of large states from which we could obtain hunter harvest time-series data: Wisconsin, Minnesota, Pennsylvania, and Virginia (New York does not collect hunter harvest data); the exception is Pennsylvania, for which we have only total harvest (hunter + trapper) data, which are not as reliable an index for foxes but are likely representative of the population expansion of coyotes as they colonized the state.

As a proxy for deer abundance, we use antlered deer harvest, which is routinely used by wildlife management agencies to monitor trends in deer abundance. Antlered deer harvest is a robust estimate of the statewide deer population due to the large number of hunters that sample the deer population with success rates dependent on the abundance of deer. We scale antlered deer harvest by hunting license sales to capture changes in hunter participation (Fig. S8). Analysis of the hunter functional response from 10 datasets supports a type I functional response (41), which suggests that hunter success rates are expected to increase linearly, rather than simply monotonically, with deer density. Additionally, hunter success rates (Fig. S8; <25% in MN, PA, and WI, and <40% in VA) suggest increases in deer abundance would be represented by increased harvests, because hunters are not saturated with deer. Longitudinal hunter harvest data has been shown to correlate well with trends in deer density and has been used in the

literature not only for crude population trends but also for more sophisticated time-series analysis (42–45).

Combining the available wildlife harvest time series, we evaluate the relative support of the predation and deer hypotheses. We additionally analyze antlered deer harvest data not corrected for license sales (Table S3) and harvests of deer, coyotes, and foxes all scaled by hunting license sales (Table S4) to ensure that our results are statistically robust to changes in hunter participation. We use deer (big game) license sales throughout because small-game hunters focus on a variety of species, and individuals may only report that they are coyote or fox hunters if they opportunistically kill one of these species incidental to other activities (46). The strength of each candidate model was evaluated using corrected Akaike Information Criterion (33, 47).

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