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Using sensitivity analysis to identify factors promoting higher versus lower infection prevalence in multi-host communities

Michael H. Cortez *

Depart of Biological Science, Florida State University, Tallahassee, FL 32306, United States

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ABSTRACT

Relationships between host species richness and levels of disease in a focal host are likely to be context-dependent, depending on the characteristics of which particular host species are present in a community. I use a multi-host epidemiological model with environmental transmission to explore how the characteristics of the host species (e.g., competence and competitive ability), host density, and the pathogen transmission mechanism affect the proportion of infected individuals (i.e., infection prevalence) in a focal host. My sensitivity-based approach identifies the indirect pathways through which specific ecological and epidemiological processes affect focal host infection prevalence. This in turn yields predictions about the context-dependent rules governing whether increased host species richness increases (amplifies) or decreases (dilutes) infection prevalence in a focal host. For example, in many cases, amplification and dilution are predicted to occur when added host species are sources or sinks of infectious propagules, respectively. However, if the added host species have strong and asymmetric competitive effects on resident host species, then amplification and dilution are predicted to occur when the added host species have stronger competitive effects on resident host species that are sources or sinks of infectious propagules, respectively. My results also predict that greater dilution and less amplification is more likely to occur under frequency-dependent direct transmission than density-dependent direct transmission when (i) the added hosts have lower competence than resident host species and (ii) interspecific competition between the added host species and resident host species is lower; the opposite conditions promote greater amplification and less dilution under frequency-dependent direct transmission. This work helps identify and explain the mechanisms shaping the context-dependent relationships between host species richness and disease in multi-host communities.

1. Introduction

Most host-pathogen communities are made up of multiple host species that can be infected by the same pathogen (Cleaveland et al., 2001; Pedersen et al., 2005; Rigaud et al., 2010). Consequently, changes in host species biodiversity in a community can affect levels of disease in a focal host species. For example, greater host biodiversity can be correlated with higher (Levine et al., 2017; Hydeman et al., 2017) or lower (Telfer et al., 2005, 2009, 2017, 2018) levels of disease. In addition, some wildlife management strategies use the reduction or removal of alternative host species to control levels of disease in a focal host (Laurenson et al., 2004; Donnelly et al., 2006).

Relationships between host biodiversity and disease are often studied in terms of the relationships between host species richness (i.e., the number of host species in a community) and infection prevalence in a focal host (i.e., the proportion of infected individuals in a focal host population) (Keesing et al., 2006; Rohr et al., 2019). *Dilution* of disease occurs when there is reduced infection prevalence in the focal host with increasing host species richness; in this case, the presence of alternative host species decreases disease burden in the focal population. *Amplification* of disease occurs when there is greater infection prevalence in the focal host with increasing host species richness; in this case, the presence of alternative host species decreases disease burden in the focal host population.

Previous studies argue that host richness-prevalence relationships are likely to be context dependent and depend on the characteristics of each host species in the community (LoGiudice et al., 2008; Randolph and Dobson, 2012; Wood et al., 2016; Rohr et al., 2019). This is supported by reviews and meta-analyzes of empirical work showing that both dilution and amplification occur across empirical systems (Salkeld et al., 2013; Wood et al., 2014;

* Corresponding author.
E-mail address: mcortez@fsu.edu

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Venesky et al., 2014; Civitello et al., 2015). In addition, individual studies show that responses to changes in host species richness can depend on which particular species are added or present in a community. For example, the prevalence of the fungal pathogen *Metschnikowia bicuspidata* in the water flea *Daphnia dentifera* can increase (Searle et al., 2016) or decrease (Strauss et al., 2015) depending on which particular host species is added to the community. Similarly, the prevalence of trematodes (*Echinostoma* spp.) in the snail *Helisoma anceps* depends on the number and identity of other snail species in the community.

The context-dependence of host richness-prevalence relationships is also supported by epidemiological theory. Theoretical studies (Rudolf and Antonovics, 2005; Roberts and Heesterbeek, 2018; Cortez and Duffy, 2021) predict that context-dependent outcomes are driven by the interactions between the pathogen transmission mechanism and characteristics of the host species, including host competence (i.e., the ability of an infected individual to transmit the pathogen to susceptible individuals) and interspecific host interactions such as resource competition and between-species transmission. For example, amplification was observed in models of density-dependent direct transmission pathogens (transmission rates are proportional to the densities of susceptible and infected individuals) without interspecific competition between hosts (Begon et al., 1992; Rudolf and Antonovics, 2005; Faust et al., 2017), but dilution can occur when interspecific competition is sufficiently strong (Rudolf and Antonovics, 2005). In comparison, dilution is often the expected outcome for frequency-dependent direct transmission pathogens (transmission rates are proportional to the frequency of susceptible individuals) (Rudolf and Antonovics, 2005), but amplification can occur if added hosts have very high competence (Faust et al., 2017).

The above empirical and theoretical work points to a need for theory that provides the context-dependent rules shaping host richness-prevalence relationships and identifies which characteristics of host and pathogen species promote amplification versus dilution (Buhnerkempe et al., 2015; Halsey, 2019; Rohr et al., 2019). Current theory is limited in its ability to do this for two reasons. First, most of the analytical theory for predicting host richness-prevalence relationships is based on two-host models (Rudolf and Antonovics, 2005; O'Regan et al., 2015; Searle et al., 2016; Roberts and Heesterbeek, 2018). It is unclear if and how predictions from those models extend to communities with more host species. Second, other studies (Dobson, 2004; Roche et al., 2012; Joseph et al., 2013; Mihaljevic et al., 2014; Faust et al., 2017) have used numerical simulations to explore relationships between host species richness and prevalence in systems with more than two host species. However, the generality of those results is unclear because those studies make simplifying assumptions about species interactions that are known to strongly affect the dynamics in two-host models. For example, all of the above numerical studies assume interspecific host competition is absent, yet studies on two-host models show interspecific competition can alter how the addition a second host affects disease prevalence in a focal host (Cortez and Duffy, 2021; Rudolf and Antonovics, 2005).

Sensitivity analysis is one tool that may provide insight into mechanisms shaping host richness-prevalence relationships. Local sensitivity analysis and global sensitivity analysis, respectively, assess how small and large changes in model inputs (e.g., parameter values) affect variation in model outputs (e.g., values of specific variables); see Saltelli et al. (2004), Saltelli et al. (2008), and Marino et al. (2008) for reviews and details. Roberts and Heesterbeek (2018) and (Cortez and Duffy, 2021) recently used local sensitivity analysis to analyze factors affecting infection prevalence at endemic equilibria. The idea behind the approach is that the sensitivities identify host and pathogen characteristics that promote higher or lower prevalence in a focal host, which in turn yield insight into how host prevalence changes with the gain or loss of a host species. Importantly, Cortez and Duffy (2021) showed that when computed analytically, the sensitivities could be used to predict how specific ecological and epidemiological processes affect disease prevalence at equilibrium. This prior work suggests that sensitivity analysis could provide a way to identify the context-dependent rules governing amplification and dilution of disease. However, one limitation of the Roberts and Heesterbeek (2018) and Cortez and Duffy (2021) studies is that they primarily focused on two-host communities, which makes it unclear if and how the predictions from those studies extend to larger communities.

In this study, I apply the local sensitivity approach in Roberts and Heesterbeek (2018) and Cortez and Duffy (2021) to an n-host-one-pathogen model with environmental transmission (i.e., transmission via infectious propagules that are excreted by infected individuals). I show that the sensitivities of equilibrium densities to parameters can be interpreted in terms of a small number of indirect effects between host species, which helps identify mechanisms promoting higher versus lower disease prevalence in a focal host. While local sensitivity results only necessarily apply to small changes in parameters, my results still provide general insight into the mechanisms shaping host richness-disease relationships because the analytical formulas apply to all points in parameter space. In addition, while I focus on a model with environmental transmission, I show that the results also apply to pathogens with density-dependent or frequency-dependent direct transmission. Overall, my results provide insight about how host characteristics and the pathogen transmission mode jointly affect infection prevalence in a focal host, which in turn yields insight into the factors promoting amplification versus dilution of disease in multi-host communities.

2. Models

2.1. SIR-type environmental transmission model

I model a system where there are n host species and the pathogen is transmitted through an environmental pathway. Infection occurs when susceptible individuals encounter infectious propagules that were excreted by infected individuals into the environment. I assume all host species share the same environment and are equally exposed to the pool of pathogens. Empirical examples of such a system include the fungal pathogen *M. bicuspidata* of *Daphnia* species (Strauss et al., 2015; Searle et al., 2016), whirling disease in fish (Hedrick et al., 1998; Bartholomew, 2002), and the fungal pathogen *Batrachochytrium dendrobatidis* of frogs (Daszak et al., 2003; Skerratt et al., 2007).

In the SIR-version of the model, the variables are the densities of susceptible (S_i), infected (I_i), and recovered (R_i) individuals in each host population ($1 \leqslant i \leqslant n$) and the density of infectious propagules (P); this is the n-host version of the two-host model in Cortez and Duffy (2021). The SIR-version of the model is

$$\begin{aligned}
\frac{dS_i}{dt} &= \overbrace{F_i(\cdot)}^{\text{reproduction}} - \overbrace{m_i S_i}^{\text{mortality}} - \overbrace{\beta_i S_i P}^{\text{infection}} + \overbrace{\gamma_i R_i}^{\text{loss of immunity}} \\
\frac{dI_i}{dt} &= \overbrace{\beta_i S_i P}^{\text{infection}} - \overbrace{(\mu_i + m_i) I_i}^{\text{mortality}} - \overbrace{\nu_i I_i}^{\text{recovery}} \\
\frac{dR_i}{dt} &= \overbrace{\nu_i I_i}^{\text{recovery}} - \overbrace{(\xi_i + m_i) R_i}^{\text{mortality}} - \overbrace{\gamma_i R_i}^{\text{loss of immunity}} \\
\frac{dP}{dt} &= \overbrace{\sum_i \chi_i I_i}^{\text{excretion}} - \overbrace{\sum_i (u_{S_i} S_i + u_{I_i} I_i + u_{R_i} R_i) P}^{\text{uptake}} - \overbrace{\delta P}^{\text{degradation}}.
\end{aligned} \tag{1}$$

Table 1
Definitions of parameters and default values used in numerical simulations.

Parameter	Interpretation	Default value
r_i	maximum reproduction rate for susceptible individuals	1.1
b_i	reduction in reproduction rate for infected individuals	0.2
c_i	reduction in reproduction rate for recovered individuals	1
α_{ii}	per capita intraspecific competitive effect of host i	1
α_{ij}	per capita interspecific competitive effect of host j on host i	0
e_{ij}	relative strength of competitive effects of infected individuals	1
ϵ_{ij}	relative strength of competitive effects of recovered individuals	1
β_i	transmission coefficient	1
m_i	mortality rate due to non-disease effects	0.1
μ_i	disease-induced mortality rate for infected individuals	0.25
v_i	recovery rate	0.1
ξ_i	disease-related mortality rate for recovered individuals	0.1
γ_i	loss-of-immunity rate	1
χ_i	excretion rate of infectious propagules	20
u_{W_i}	infectious propagule uptake rate for class W ($W \in \{S,I,R\}$)	20
δ	infectious propagule degradation rate	10

Default values for all parameters are given in Table 1. For host species i, m_i is the mortality rate due to non-pathogen factors, β_i is the product of the per spore encounter rate and the probability of infection, μ_i is the pathogen-induced mortality rate, v_i is the recovery rate, $\xi_i + m_i$ is the total mortality rate of recovered individuals (which could be higher than the natural mortality rate if there are long-term consequences of infection), γ_i is the rate at which recovered individuals lose immunity, χ_i is the rate of excretion of infectious propagules, and u_{S_i}, u_{I_i}, and u_{R_i} are the rates at which susceptible, infected, and recovered individuals, respectively, take up infectious propagules. Encounters between hosts and infectious propagules are assumed to be proportional to their densities, which results in the uptake rate of infectious propagules by individuals in class W_i ($W \in \{S,I,R\}$) being modeled as $u_{W_i}W_iP$. The second sum in the infectious propagule equation is the total loss of infectious propagules due to uptake by all individuals in all host classes. The transmission coefficient (β_i) is the product of the uptake rate (u_{S_i}) and the per propagule probability of infection (p_i), yielding the constraint $\beta_i = p_i u_{S_i} < u_{S_i}$. In the following, β_i is varied independently of u_{S_i} by varying p_i and u_{S_i} is varied independently of β_i by compensating for changes in u_{S_i} with changes in p_i.

The reproduction rate for each host population is assumed to have the form

$$F_i(\cdot) = S_i f_{S_i}(\cdot) + I_i f_{I_i}(\cdot) + R_i f_{R_i}(\cdot) \tag{2}$$

where $(\cdot)$ is shorthand for $(S_1,\ldots,S_n,I_1,\ldots,I_n,R_1,\ldots,R_n)$ and f_{S_i}, f_{I_i}, and f_{R_i} are the per capita reproductive outputs of susceptible, infected, and recovered individuals, respectively. The functions f_{S_i}, f_{I_i}, and f_{R_i} are assumed to be non-increasing functions of their arguments due to intraspecific and interspecific host competition, i.e., $\frac{\partial F_{V_i}}{\partial W_j} \le 0$ for $V,W \in \{S,I,R\}$ and all i,j. For example, the numerical simulations use functions of Lotka-Volterra form,

$$F_i = r_i(S_i + b_i I_i + c_i R_i)\left(1 - \sum_j \alpha_{ij}\left[S_j + e_{ij}I_j + \epsilon_{ij}R_j\right]\right) \tag{3}$$

which allow for susceptible, infected, and recovered individuals to have different reproduction rates and intraspecific and interspecific competitive effects. Specifically, r_i, $b_i r_i$, and $c_i r_i$ are the maximum reproduction rates for susceptible, infected, and recovered individuals of host i, respectively. The terms $\alpha_{ij}\left[S_j + e_{ij}I_j + \epsilon_{ij}R_j\right]$ model how the reproduction rate of host i decreases linearly with increased density of host j due to competition. Each α_{ij} is the per capita competitive effect of susceptible individuals of host j on host i and each e_{ij} and ϵ_{ij} determines if infected and recovered individuals of host j, respectively, have weaker ($e_{ij} < 1, \epsilon_{ij} < 1$), equal ($e_{ij} = 1, \epsilon_{ij} = 1$), or stronger ($e_{ij} > 1, \epsilon_{ij} > 1$) per capita competitive effects than susceptible individuals of host j. In the special case where susceptible, infected, and recovered individuals have equal maximum reproduction rates and competitive effects, the functions simplify to the typical Lotka-Volterra form $F_i = r_i N_i\left(1 - \sum_j \alpha_{ij} N_j\right)$, where $N_i = S_i + I_i + R_i$ is the total population size of host i.

The basic reproductive number for the pathogen in the n-host community or a subcommunity can be derived using the next-generation matrix (Van den Driessche and Watmough, 2002; Diekmann et al., 2010); see Appendix S1.1 for details. The basic reproductive number for the pathogen in the n-host community is

$$\mathscr{R}_0 = \sum_i \frac{\beta_i \chi_i \bar{S}_i}{(\mu_i + m_i + v_i)\left(\delta + \sum_j u_{S_j}\bar{S}_j\right)} \tag{4}$$

where $\bar{S}_i$ is the density of host i at the disease-free equilibrium for the n-host community. Each term in the sum is similar in form to the basic reproductive number for the pathogen in a single-host community, $\mathscr{R}_{0,i} = \beta_i\chi_i\bar{S}_i / \left[(u_i + m_i + v_i)\left(\delta + u_{\bar{S}_i}\bar{S}_i\right)\right]$ where, with an abuse of notation, $\bar{S}_i$ is the density of host i at the disease-free equilibrium for the single-host community.

2.2. Relationship to direct transmission models

The environmental transmission (ET) model (1) reduces to a model with direct transmission when the excretion rates (χ_i) and some combination of the uptake (u_{V_i}) and degradation (δ) rates are sufficiently large such that there is a separation of time scales between the dynamics of the infectious propagules and the dynamics of the host classes. Cortez and Duffy (2021) showed this for the two-host version of model (1); the calculations for the n-host version are nearly identical. Briefly, when there is a separation of time scales, the infectious propagule density reaches a quasi-steady state equilibrium defined by $P = \sum_j \chi_j I_j / \left[\delta + \sum_j \left(u_{S_j}S_j + u_{I_j}I_j + u_{R_j}R_j\right)\right]$. Substitution into the host equations yields

$$\begin{aligned}
\frac{dS_i}{dt} &= \overbrace{F_i(\cdot)}^{\text{reproduction}} - \overbrace{m_i S_i}^{\text{natural mortality}} - \overbrace{\frac{\beta_i S_i \sum_j \chi_j I_j}{\delta + \sum_j \left(u_{S_j}S_j + u_{I_j}I_j + u_{R_j}R_j\right)}}^{\text{infection}} + \overbrace{\gamma_i R_i}^{\text{loss of immunity}} \\
\frac{dI_i}{dt} &= \overbrace{\frac{\beta_i S_i \sum_j \chi_j I_j}{\delta + \sum_j \left(u_{S_j}S_j + u_{I_j}I_j + u_{R_j}R_j\right)}}^{\text{infection}} - \overbrace{(\mu_i + m_i) I_i}^{\text{mortality}} + \overbrace{v_i I_i}^{\text{recovery}} \\
\frac{dR_i}{dt} &= \overbrace{v_i I_i}^{\text{recovery}} - \overbrace{(\xi_i + m_i) R_i}^{\text{mortality}} - \overbrace{\gamma_i R_i}^{\text{loss of immunity}} .
\end{aligned} \tag{5}$$

In model (5), there is direct transmission of the pathogen and the rate of transmission from host j to host i is $\beta_i S_i \chi_j I_j / \left[\delta + \sum_k \left(u_{S_k} S_k + u_{I_k} I_k + u_{R_k} R_k\right)\right]$.

When loss due to uptake is negligibly small compared to degradation ($\delta + \sum_k \left[u_{S_k} S_k + u_{I_k} I_k + u_{R_k} R_k\right] \approx \delta$), the transmission rates in model (5) reduce to the bi-linear form $\bar{\beta}_{ij} S_i I_j$ where $\bar{\beta}_{ij} = \beta_i \chi_j / \delta$. This is a density-dependent direct transmission (DDDT) form (Anderson and May, 1978; Anderson and May, 1979; May and Anderson, 1978; May and Anderson, 1979a) where host contact rates are proportional to host densities. In this case, transmission rates are governed by mass action and proportional to the densities of susceptible and infected individuals.

When there is no degradation of infectious propagules ($\delta = 0$), the transmission rates in model (5) reduce to the form $\bar{\beta}_{ij} S_i I_j / \sum_k \left(u_{S_k} S_k + u_{I_k} I_k + u_{R_k} R_k\right)$ where $\bar{\beta}_{ij} = \beta_i \chi_j$. This is a frequency-dependent direct transmission (FDDT) form (May and Anderson, 1979b; Begon et al., 1998; Begon et al., 1999) where host contact rates are independent of host density. In this case, the transmission rates are proportional to the weighted frequencies of susceptible individuals in the community, where the uptake rates $(u_{S_i}, u_{I_i}, u_{R_i})$ are the weights for the host classes.

While the above assumes a separation of time scales between the infectious propagule and host dynamics, the equilibria of the ET model (1) are identical to those of DDDT models when uptake is negligibly small compared to degradation and identical to those of FDDT models when there is no degradation of infectious propagules. Hence, all of the equilibrium-based results for the ET models apply to the DDDT and FDDT models.

2.3. NYZ environmental transmission model

To facilitate predictions about amplification and dilution, which are defined in terms of the proportion of infected individuals in a focal host, I transform model (1) into a form that follows the dynamics of the total density ($N_i = S_i + I_i + R_i$), proportion of infected individuals ($Y_i = I_i/N_i$), and proportion of recovered individuals ($Z_i = R_i/N_i$) of each host population. From these variables, the proportion of susceptible individuals is defined by $X_i = 1 - Y_i - Z_i$. The NYZ-version of the model is

$$\begin{aligned}
\frac{dN_i}{dt} &= \overbrace{F_i(\cdot)}^{\text{reproduction}} - \overbrace{m_i N_i}^{\text{natural mortality}} - \overbrace{\left(\mu_i Y_i N_i + \xi_i Z_i N_i\right)}^{\text{disease-related mortality}} \\
\frac{dY_i}{dt} &= \beta_i (1 - Y_i - Z_i) P - \left(\mu_i + m_i\right) Y_i - \nu_i Y_i - \frac{Y_i}{N_i}\frac{dN_i}{dt} \\
\frac{dZ_i}{dt} &= \nu_i Y_i - (\xi_i + m_i) Z_i - \gamma_i Z_i - \frac{Z_i}{N_i}\frac{dN_i}{dt} \\
\frac{dP}{dt} &= \overbrace{\sum_i \chi_i Y_i N_i}^{\text{excretion}} - \overbrace{\sum_i \left[u_{S_i}(1 - Y_i - Z_i) N_i + u_{I_i} Y_i N_i + u_{R_i} Z_i N_i\right] P}^{\text{uptake, UP}} - \overbrace{\delta P}^{\text{degradation}}.
\end{aligned} \tag{6}$$

The terms in the dY_i/dt equation describe how the proportion of infected individuals increases due to new infections and decreases due to mortality, recovery and production of new susceptible individuals. Similarly, the terms in the dZ_i/dt equation describe how the proportion of recovered individuals increases due to recovery of infected individuals and decreases due to mortality, loss of immunity, and the production of new susceptible individuals. To simplify notation, $U_i = u_{S_i}(1 - Y_i - Z_i) N_i + u_{I_i} Y_i N_i + u_{R_i} Z_i N_i$ denotes the per capita rate of loss of infectious propagules due to uptake by host i and $U = \sum_i U_i$ denotes the sum of those rates.

2.4. Jacobian of NYZ model (6)

This study focuses on analyzing endemic equilibria where all hosts coexist with the pathogen. I assume model (6) has an endemic equilibrium, p^* with equilibrium values N_i^*, Y_i^*, Z_i^*, and P^*. With an abuse of notation, the corresponding stable equilibrium of model (1) is denoted by p^*, where the equilibrium densities are S_i^*, I_i^*, R_i^*, and P^*. The equilibrium-based results are computed using the Jacobian, J. This section presents the Jacobian and interprets its entries; additional details are provided in Appendix S1.2. Assumptions about the signs of the entries and derived quantities are discussed in the next two subsections.

When evaluated at p^* the Jacobian of model (6) has the structure,

$$\mathbf{J}|_{p^*} = \begin{bmatrix} \mathbf{A} & \mathbf{B} & \mathbf{C} & \vec{0}_n \\ -\mathbf{D}_{Y/N}\mathbf{A} & -\mathbf{D}_{Y/N}\mathbf{B} - \mathbf{D}_\beta P^* - \mathbf{D}_\mu - \mathbf{D}_m - \mathbf{D}_\nu & -\mathbf{D}_{Y/N}\mathbf{C} - \mathbf{D}_\beta P^* & \overrightarrow{\beta X N} \\ -\mathbf{D}_{Z/N}\mathbf{A} & -\mathbf{D}_{Z/N}\mathbf{B} + \mathbf{D}_\nu & -\mathbf{D}_{Z/N}\mathbf{C} - \mathbf{D}_\xi - \mathbf{D}_m - \mathbf{D}_\gamma & \vec{0}_n \\ \vec{E}_N & \vec{E}_Y & \vec{E}_Z & -U^* - \delta \end{bmatrix}. \tag{7}$$

In the far right column, $\overrightarrow{\beta X N}$ is an $n \times 1$ vector with entries $\beta_1 X_1^* N_1^*, \ldots, \beta_n X_n^* N_n^*$, and $\vec{0}_n$ is an $n \times 1$ zero vector. These entries define how increased infectious propagule density causes an increase in infection prevalence and has no direct effect on the total density or proportion of recovered individuals in each host population. The bottom right entry $-U^* - \delta$ is the total per capita rate of loss of infectious propagules due to uptake by all hosts and degradation. In the bottom row, the $1 \times n$ vectors $\vec{E}_N$, $\vec{E}_Y$, and $\vec{E}_Z$ have entries $\frac{\partial}{\partial N_i}\frac{dP}{dt}$, $\frac{\partial}{\partial Y_i}\frac{dP}{dt}$, and $\frac{\partial}{\partial Z_i}\frac{dP}{dt}$, respectively; each entry defines how the net production rate of infectious propagules by host i changes with an increase in its total density, prevalence, or frequency of recovered individuals, respectively.

For entries in the middle rows, the matrix $\mathbf{D}_W$ denotes an $n \times n$ diagonal matrix whose diagonal entries are $W_1, \ldots, W_n$. For example, $\mathbf{D}_{Y/N}$ has diagonal entries $Y_1^*/N_1^*, \ldots, Y_n^*/N_n^*$ and $\mathbf{D}_\beta$ has diagonal entries $\beta_1, \ldots, \beta_n$. The entries in the middle rows define how a change in the total density or frequency of a host class of a host species affects the dynamics of a host class of the same or another host species.

The matrix $\mathbf{A}$ describes the effects of intraspecific competition on each host species (diagonal entries) and the direct effects of interspecific competition between host species (off-diagonal entries). The off-diagonal entries are zero when the species do not directly interspecifically compete and negative when there are direct competitive interactions. The matrices $\mathbf{B}$ and $\mathbf{C}$ describe how the competitive effects between species change if a small number of susceptible individuals are transferred to the infected or recovered class, respectively, while holding the total host densities constant. The diagonal entries of $\mathbf{B}$ and $\mathbf{C}$ are negative when susceptible individuals are much weaker intraspecific competitors than infected individuals or recovered individuals, respectively, and positive otherwise. The off-diagonal entries $\mathbf{B}_{ij}$ and $\mathbf{C}_{ij}$ $(i \neq j)$ are zero if host j does not directly compete with host i and otherwise negative, zero, and positive when susceptible individuals of host j are weaker, equal, and stronger interspecific competitors than infected or recovered individuals, respectively.

2.5. Assumptions

In order to simplify the analysis and to restrict it to biologically likely scenarios, I assume the following: (i) recovered and susceptible individuals have identical competitive abilities, reproductive output, and uptake rates; (ii) infected individuals are stronger, equal, or moderately weaker (but not much weaker) competitors than susceptible individuals; (iii) the endemic equilibrium is stable; (iv) all host species experience negative density dependence at equilibrium; (v) the direct and total interspecific competitive effects between each pair of host species are zero or negative; (vi) intraspecific competition is greater than interspecific competi-

tion; (vii) the competitive effects between all host species and the competitive effects between all subcommunities of $n-1$ host species are consistent with stability; (viii) increased prevalence in a host species at equilibrium has a negative total effect on its growth rate, and (ix) increased prevalence in host j at equilibrium has a negative and positive total effect on the growth rate of host i when infected individuals of host i are stronger and weaker competitors, respectively, then susceptible individuals. Conditions (v) through (ix) are guaranteed to hold if interspecific competition is sufficiently weak relatively to intraspecific competition, but they may not hold if interspecific competition is sufficiently strong and asymmetric. Mathematical details are summarized below and in Table 2; additional details are given in Appendices S1.2 and S1.3.

Susceptible and recovered individuals are assumed to be identical except that recovered individuals are immune to infection and possibly experience increased mortality (ξ_i) due to past exposure to the pathogen. Specifically, susceptible and recovered individuals have equal reproductive outputs ($f_{S_i}=f_{R_i}$), equal competitive abilities ($\partial f_{W_i}/\partial S_i=\partial f_{W_i}/\partial R_i$ for $W\in\{S,I,R\}$), and equal uptake rates ($u_{S_i}=u_{R_i}$). The former two conditions imply $C_{ii}<0$ and $C_{ij}=0$ for $i\neq j$. Infected individuals are assumed to be stronger, equal or moderately weaker competitors than susceptible individuals. I do not consider cases where infected individuals are much weaker competitors than susceptible individuals, e.g., $e_{ij}\ll 1$ in Eq. (3), because this often results in the total host density of one species increasing above its carrying capacity (e.g., $N_i^*>1/\alpha_{ii}$ a Lotka-Volterra model). This seems unlikely to arise in natural systems.

The endemic equilibrium, p^*, is assumed to be stable because the sensitivity-based analysis is unlikely to be biologically informative otherwise. This implies $\text{sign}(|\mathbf{J}|)=(-1)^{3n+1}$. Stability does not occur in all regions of parameter space (e.g., regions where interspecific host competition is sufficiently strong), but it is satisfied in all of the numerical simulations.

The conditions for negative density dependence and the direct and total effects of intraspecific and interspecific competition at equilibrium are defined by the entries of the matrix $\mathbf{A}$. Negative density dependence means $\mathbf{A}_{ii}<0$ for all i. The direct interspecific competitive effect of host j on host i ($j\neq i$) is assumed to be negative or zero, which means $\mathbf{A}_{ij}<0$ and $\mathbf{A}_{ij}=0$, respectively. Both conditions are direct consequences of the assumptions about the host reproductive rates in Eq. (2); see Appendix S1.2 for details. The assumption that intraspecific competition is stronger than interspecific competition implies $\mathbf{A}_{ii}>\mathbf{A}_{ij}$ for $i\neq j$. For the Lotka-Volterra function (3), this corresponds to assuming $\alpha_{ii}>\alpha_{ij}$ for all i,j.

The total interspecific competitive effect of host j on host i is the sum of the direct and indirect competitive effects. Let $|\mathbf{A}^{[-i,-j]}|$ denote the i,j-minor of $\mathbf{A}$, i.e., the determinant of the submatrix of $\mathbf{A}$ where row i and column j have been removed. The assumption that the total effect is negative or zero means the sign of the minor $|\mathbf{A}^{[-i,-j]}|$ is $(-1)^{n+i+j}$ or 0, respectively; see Remark S1.1 in Appendix S1.3 for details.

The competitive effects between all host species are assumed to be consistent with stability. Mathematically, this means the sign of $|\mathbf{A}|$ is $(-1)^n$. I expect this assumption to be met in most systems for the following reason; see Remark S1.2 in Appendix S1.3 for mathematical details. The matrix $\mathbf{A}$ determines the stability of the $\{N_k\}_{k=1}^n$-subsystem, i.e., the subsystem where the total host densities (N_i) are dynamic and all other variables are held fixed at their equilibrium values. If the sign of $|\mathbf{A}|$ is inconsistent with stability, then the $\{N_i\}_{i=1}^n$-subsystem satisfies the subsystem instability condition (*sensu* Cortez and Abrams, 2016). This means that (i) the interspecific competitive interactions between the host species are sufficiently strong to have a destabilizing effect on the equilibrium; (ii) stable coexistence is only possible because the pathogen has a strong stabilizing effect on the system; and (iii) the infectious propagules exhibit a hydra effect at equilibrium (e.g., increased infectious propagule density with increased removal, $\partial P^*/\partial\delta>0$) (Abrams, 2009; Cortez and Abrams, 2016). These seem unlikely to be satisfied in most empirical systems.

The competitive effects between subsets of $n-1$ host species are assumed to be consistent with stability. Mathematically, this corresponds to assuming $\text{sign}\left(|\mathbf{A}^{[-i,-i]}|\right)=(-1)^{n-1}$ for all i. The submatrix $\mathbf{A}^{[-i,-i]}$ determines the stability of the $\{N_k\}_{k\neq i}^n$-subsystem, i.e., the subsystem where the total densities of hosts $k\neq i$ are dynamic and all other variables are held fixed at their equilibrium values. This assumption corresponds to no host exhibiting a hydra effect when the epidemiological dynamics of the system (dY_i/dt, dZ_i/dt, and dP/dt equations) are frozen.

Finally, at equilibrium, an increase in infection prevalence (Y_j^*) is always accompanied by an increase in the frequency of recovered individuals (Z_j^*) because $Z_j^*=Y_j^*\nu_j/\left(m_j+\xi_j+\gamma_j\right)$. The total effect of simultaneous changes in Y_j^* and Z_j^* on the growth rate of host i is determined by the determinant $|\mathbf{A}_{I_j\to N_i}|$, where the matrix $\mathbf{A}_{I_j\to N_i}$ is constructed by replacing column i of $\mathbf{A}$ with column j of the sum $\mathbf{B}+\mathbf{C}\mathbf{D}_{Z/Y}$; see Remark S1.3 in Appendix S1.3 for details. Increased prevalence in a host species is assumed to have a negative total effect on its growth rate at equilibrium. Mathematically, this means the sign of $|\mathbf{A}_{I_j\to N_j}|$ is $(-1)^n$. The opposite sign is possible when infected individuals are very weak intraspecific competitors or use very few resource. However, as noted above, this leads to the biologically unlikely scenario where the disease causes the species'

Table 2
Signs and interpretations of quantities arising in sensitivity calculations.

Quantity		Sign†	Biological interpretation
$\lvert\mathbf{J}\rvert$		$(-1)^{3n+1}$	Endemic n-host equilibrium is stable
$\mathbf{A}_{ii}$		-1	Each host species experiences negative density dependence at equilibrium
$\mathbf{A}_{ij}$	$i\neq j$	-1 or 0	Presence or absence of a direct interspecific competitive effect of host j on host i
$\lvert\mathbf{A}\rvert$		$(-1)^n$	Competitive effects between all host species are consistent with stability; infectious propagules do not exhibit a hydra effect
$\lvert\mathbf{A}^{[-i,-i]}\rvert$		$(-1)^{n-1}$	Competitive effects between all host species except species i are consistent with stability
$\lvert\mathbf{A}^{[-i,-j]}\rvert$	$i\neq j$	$(-1)^{n+i+j}$	Increased density of host j has a negative total effect on the growth rate of host i
$\lvert\mathbf{A}_{Y_j\to N_j}\rvert$		$(-1)^n$	Increased prevalence in host j (Y_j) has a negative total effect on its own growth rate
$\lvert\mathbf{A}_{Y_j\to N_i}\rvert$	$j\neq i$		Total effect of increased prevalence in host j (Y_j) on the growth rate of species i is
		$(-1)^{n-1}$	positive when infected individuals of host j are weaker competitors than susceptible individuals
		$(-1)^n$	negative when infected individuals of host j are stronger competitors than susceptible individuals
φ_i			Net production rate of infectious propagules per infectious individual by host i at equilibrium
		-1	Host i is a sink, i.e., a net remover of infectious propagules
		1	Host i is a source, i.e., a net producer of infectious propagules

See Section 2.5 and Appendices S1.2 and S1.3 for definitions of quantities and additional details about assumed signs.† The signs of all quantities are assumed, except the signs of the φ_i, which are determined by the model parameters and the infectious propagule density at equilibrium.

density to increases above its carrying capacity. Increased prevalence in host species j is assumed to have a negative or positive total effect on the growth rate of host species i ($i \neq j$) when infected individuals of host j are stronger or weaker competitors, respectively, than susceptible individuals; mathematically, this means $\text{sign}(|\mathbf{A}_{I_j \to N_i}|) = (-1)^n$ or $\text{sign}(|\mathbf{A}_{I_j \to N_i}|) = (-1)^{n-1}$, respectively.

2.6. Definitions of competence, sink and source

The net production rate of infectious propagules by host i at equilibrium is $\chi_i I_i^* - (u_{S_i} S_i^* + u_{I_i} I_i^* + u_{R_i} R_i^*) P^*$. Dividing by the density of infected individuals and simplifying (see Remark S1.5 in Appendix S1.3 for details) yields the net production rate per infected individual,

$$\varphi_i = \chi_i - \frac{(\mu_i + m_i + \nu_i) u_{S_i}}{\beta_i} - u_{I_i} P^* - \frac{\nu_i u_{R_i}}{\xi_i + m_i + \gamma_i} P^*. \tag{8}$$

The first term in the equation defines the per capita production rate of infectious propagules and the other terms define the loss rates due to uptake by all host classes. A host is a *sink* or *source* of infectious propagules if the net production rate per infected individual is negative ($\varphi_i < 0$) or positive ($\varphi_i > 0$), respectively. The quantity defining sink/source in this study (φ_i) is similar to, but not identical to, the quantity ($\chi_i - u_{I_i} P^*$) used in Cortez and Duffy (2021). The key difference is that φ_i accounts for uptake by all host classes whereas the quantity in Cortez and Duffy (2021) only accounts for uptake by infected individuals. I use φ_i because that quantity arises naturally in the sensitivity equations; the results are qualitatively similar if the quantity in Cortez and Duffy (2021) is used instead.

The *competence* of a host is the ability of an infected individual to transmit the pathogen to a susceptible individual. In this study, the competence of host i is defined by $\mathscr{R}_{0,i}(\infty) = \chi_i \beta_i / u_{S_i}(\mu_i + m_i + \nu_i)$, which is the pathogen's basic reproductive number for a single-host community ($\mathscr{R}_{0,i}$) in the limit where the density of host i is infinite. Because changes in the parameter values that make $\mathscr{R}_{0,i}(\infty)$ larger or smaller also make $\mathscr{R}_{0,i}$ larger or smaller, respectively, statements about higher or lower competence based on $\mathscr{R}_{0,i}(\infty)$ can be directly translated to $\mathscr{R}_{0,i}$.

I note three things about the definitions of competence and sink/source. First, the quantities defining competence and sink/source were chosen because (i) they arise naturally in the sensitivity calculations, (ii) they only depend on the epidemiological parameters of a single host species, and (iii) they do not depend on the densities or frequencies of the host classes. As a consequence, all host species can be ordered from highest to lowest competence and from largest source to largest sink based solely on the epidemiological parameters for each host and the density of infectious propagules. However, both definitions depend on the hosts' environment through the natural mortality rates (m_i), which means an ordering based on competence or sink/source may differ across environments. In addition, because the definitions of sink and source depend on infectious propagule density, a given host can be a sink in one community (e.g., where infectious propagule density is low) and a source in another community (e.g., where infectious propagule density is high). Overall this means that while the hosts can always be ordered in terms of competence and sink/source, context-dependence can be important for defining the orderings, whether a host has high versus low competence, and whether a host is a large or small sink or source.

Second, in general a host can be any combination of high or low competence and a sink or source. This is because competence is a measure of transmission over the total period of infection whereas sink/source is a measure of instantaneous net production of infectious propagules. A high competence, source host can have large excretion (χ_i) and transmission (β_i) parameters and small uptake parameters ($u_{S_i}, u_{I_i}, u_{R_i}$). In contrast, a high competence, sink host can have a high per propagule probability of infection (p_i), large uptake parameters ($u_{S_i}, u_{I_i}, u_{R_i}$), and small excretion ($\chi_i$), mortality ($\mu_i + m_i$) and recovery ($\nu_i$) parameters. A low competence, sink can have small excretion (χ_i) and transmission (β_i) parameters and large uptake parameters ($u_{S_i}, u_{I_i}, u_{R_i}$). In contrast, a low competence, source host can have a low per propagule probability of infection (p_i), small uptake parameters ($u_{S_i}, u_{I_i}, u_{R_i}$), and large excretion ($\chi_i$), mortality ($\mu_i + m_i$) and recovery ($\nu_i$) parameters.

Third, the definitions of competence and sink/source extend to DDDT and FDDT pathogens. The definition of competence applies directly. For sink and source, all hosts are sources for DDDT pathogens because the uptake rates are negligibly small ($\varphi_i = \chi_i > 0$). Hosts of FDDT pathogens can be sources or sinks. Host j is a larger source (or smaller sink) for an FDDT pathogen when the inter-species transmission rate from host j to the focal host ($\bar{\beta}_{1j}$) is larger and the weights (u_{W_j} for $W \in \{S, I, R\}$) for host j are smaller; this corresponds to a larger excretion rate (χ_i) and smaller uptake rates (u_{W_j}) in the ET model. Host j is a larger sink or smaller source under the opposite conditions. For example, many studies (Rudolf and Antonovics, 2005; O'Regan et al., 2015; Faust et al., 2017; Roberts and Heesterbeek, 2018) use FDDT rates of the form $\bar{\beta}_{ij} S_i I_j / \sum_j N_j$ where all weights are equal to unity. In this case, host j is a source of the FDDT pathogen for host 1 when the inter-species transmission rate from host j to host 1 is larger than the intra-species transmission rate for host 1, i.e., $\bar{\beta}_{1j} > \bar{\beta}_{11}$.

3. Methods and results

In order to facilitate interpretation and without loss of generality, the following assumes host 1 is the focal host and computes the sensitivity of infection prevalence in the focal host (Y_1^*) to the characteristics and equilibrium density of host 2.

3.1. Responses in focal host infection prevalence to variation in competence or competitive ability of another host species

I first compute the sensitivities of focal host infection prevalence to parameters defining the competence and competitive ability of host 2 ($\partial Y_1^* / \partial \sigma$ where σ is a given model parameter). The sensitivities are analytically computed using the Jacobian-based method in Bender and Case (1984) and Yodzis (1988). In particular, consider the system of differential equations $dx_i/dt = g_i(x_1, \ldots, x_n)$ where σ is a parameter and $\mathbf{J}$ is the Jacobian evaluated at an equilibrium point $(x_1^*, \ldots, x_n^*)$. The (local) sensitivity $\partial x_i^* / \partial \sigma$ is

$$\frac{\partial x_i^*}{\partial \sigma} = \sum_j -\frac{\partial}{\partial \sigma}\left(\frac{dx_j}{dt}\right) \frac{(-1)^{i+j} |\mathbf{J}^{[-j,-i]}|}{|\mathbf{J}|} \tag{9}$$

where $\mathbf{J}^{[-j,-i]}$ is the submatrix of the Jacobian with row j and column i removed. For model (6), the sum has a small number of nonzero terms because only a few equations depend on any given parameter.

This analytical approach produces sensitivities in terms of the Jacobian entries. This has three advantages. First, it facilitates the biological interpretation of the sensitivities by identifying all of the indirect pathways through the community that influence the sign and magnitude of the response (summarized in Table 3). Second, it identifies the effects specific biological processes have on the signs of the sensitivities because each Jacobian entry corresponds to a specific set of biological processes. Thus, the approach identifies how specific characteristics of other species affect infec-

Table 3
Indirect pathways determining how the characteristics and density of host 2 affect focal host infection prevalence.

Sensitivity	Indirect Pathway		Sign of Indirect Effect†		
			Expected Sign	$\varphi_2 < 0$ & $u_{S_2} \ll u_{I_2}$	I_2 stronger competitors
$\frac{\partial Y_1^*}{\partial \chi_2}$	$\chi_2 \to P^* \to Y_1^*$		+		
$\frac{\partial Y_1^*}{\partial u_{W_2}}$	$u_{W_2} \to P^* \to Y_1^*$	$W \in \{S,I,R\}$	−		
$\frac{\partial Y_1^*}{\partial \beta_2}$	$\beta_2 \to Y_2^* \to P^* \to Y_1^*$		+	−	
	$\beta_2 \to Y_2^* \to N_2^* \to P^* \to Y_1^*$		$-\varphi_2$		
	$\beta_2 \to Y_2^* \to N_i^* \to P^* \to Y_1^*$	$i \neq 2$	φ_i		$-\varphi_2$
$\frac{\partial Y_1^*}{\partial \mu_2}$	$\mu_2 \to Y_2^* \to P^* \to Y_1^*$		−	+	
	$\mu_2 \to Y_2^* \to N_2^* \to P^* \to Y_1^*$		φ_2		
	$\mu_2 \to Y_2^* \to N_i^* \to P^* \to Y_1^*$	$i \neq 2$	$-\varphi_i$		φ_i
	$\mu_2 \to N_2^* \to P^* \to Y_1^*$		$-\varphi_2$		
	$\mu_2 \to N_2^* \to N_i^* \to P^* \to Y_1^*$	$i \neq 2$	φ_i		
$\frac{\partial Y_1^*}{\partial \alpha_{2k}}$	$\alpha_{2k} \to N_j^* \to P^* \to Y_1^*$		$-\varphi_j$		
	$\alpha_{2k} \to N_j^* \to N_i^* \to P^* \to Y_1^*$	$i \neq j$	φ_i		
$\frac{dY_1^*}{dN_2^*}$	$N_2^* \to P^* \to Y_1^*$		φ_2		
	$N_2^* \to N_i^* \to P^* \to Y_1^*$	$i \neq 2$	$-\varphi_i$		

† Column "Expected Sign" shows the expected signs of the indirect effects for most systems with the sign structure given in Table 1. Column "$\varphi_2 < 0$ & $u_{S_2} \ll u_{I_2}$" shows the different signs that can occur when host 2 is a sink and the uptake rates of infected individuals of host 2 are much larger than the uptake rate of susceptible individuals. Column "I_2 stronger competitors" shows the different signs that can occur when infected individuals of host 2 are stronger interspecific competitors than susceptible individuals. Host i is a sink and source if $\varphi_i < 0$ and $\varphi_i > 0$, respectively.

tion prevalence in the focal host and if and why those characteristics have context-dependent effects. Third, because the analytical formulas apply to all points in parameter space, they provide insight about what characteristics of other hosts promote higher or lower infectious prevalence in the focal host. However, because the approach is based on a local sensitivities, it may not accurately capture the effects of large changes in parameters.

3.1.1. Effects of varying excretion (χ_2) and uptake (u_{W_i}) rates

Increased excretion of infectious propagules by host 2 (larger χ_2) increases focal host infectious prevalence. Increased uptake of infectious propagules by host 2 (larger u_{W_i} for $W \in \{S,I,R\}$) decreases focal host infection prevalence. The intuition is that increases in excretion and uptake, respectively, cause an increase and decrease in infectious propagule density, which increases and decreases contacts between infectious propagules and susceptible individuals of the focal host.

The sensitivity of focal host infection prevalence to the excretion rate of host 2 is

$$\frac{\partial Y_1^*}{\partial \chi_2} = \frac{-|\mathbf{A}|}{|\mathbf{J}|} \overbrace{Y_2^* N_2^*}^{\chi_2 \to P^*} \overbrace{\beta_1 X_1^* N_1^*}^{P^* \to Y_1^*} Q_{\chi_2}. \tag{10}$$

where Q_{χ_2} is a positive quantity; see Appendix S2.1 for details. The sensitivities for the uptake rates of host 2, $\partial Y_1^*/\partial u_{W_2}$ for $W \in \{S,I,R\}$, are the same except that $Y_2^* N_2^*$ is replaced with $-W_2^* P^*$; see Appendix S2.1 for details.

Pieces of Eq. (10) can be interpreted in terms of indirect pathways. First, the product $Y_2^* N_2^* \beta_1 X_1^* N_1^*$ represents the indirect pathway $\chi_2 \to P^* \to Y_1^*$. In this pathway, increased excretion by host 2 increases the density of infectious propagules ($\chi_2 \to P^*$) and increased infectious propagule density increases contacts between infectious propagules and susceptible individuals of the focal host, which causes an increase in focal host infection prevalence ($P^* \to Y_1^*$). Similarly, in the sensitivity for the uptake rate of class W_2, the product $-W_2^* P^* \beta_1 X_1^* N_1^*$ represents the indirect pathway $u_{W_2} \to P^* \to Y_1^*$. In that pathway, increased uptake by host 2 decreases the density of infectious propagules ($u_{W_2} \to P^*$) which reduces contacts with susceptible individuals of the focal host and causes a decrease in focal host infection prevalence ($P^* \to Y_1^*$). Second, the determinant $|\mathbf{A}|$ represents the influence of all direct and indirect pathways that only involve intraspecific and interspecific competitive interactions between the host species. This set of pathways is denoted $\circlearrowleft\{N_i\}_{i=1}^n$. I expect the competitive interactions between all host species to be consistent with stability in most empirical systems; this means $\text{sign}(|\mathbf{A}|) = (-1)^n$.

When the competitive interactions between all host species are consistent with stability, Eq. (10) is positive and the corresponding equation for the uptake rates is negative. This means that increased excretion by host 2 increases focal host infection prevalence and increased uptake by any class in host 2 decreases focal host infection prevalence. The mechanism is simply that increased excretion and increased uptake indirectly affect focal host infection prevalence by increasing or decreasing, respectively, the density of infectious propagules.

In rare cases, the competitive interactions between host species may be inconsistent with stability, i.e., $\text{sign}(|\mathbf{A}|) = (-1)^{n-1}$. Under this condition, the infectious propagules exhibit a hydra effect, which means that any process that increases the growth rate of infectious propagules (e.g., χ_i) causes a decrease in its equilibrium density. Consequently, increased excretion by host 2 decreases focal host infection prevalence and increased uptake by any class in host 2 increases focal host infection prevalence. This shows that the general predictions about excretion and uptake in the previous paragraph can be reversed if the infectious propagules exhibit a hydra effect. However, in the following sections I do consider such systems because I expect them to be rare in nature.

3.1.2. Effects of varying the transmission coefficient (β_2)

In most cases, increasing the transmission coefficient of host 2 (β_2) increases infection prevalence in the focal host. The intuition is that increased transmission leads to increased prevalence in host 2, which leads to greater infectious propagule density and increased contact between infectious propagules and susceptible individuals of the focal host. This prediction can be reversed if (i) host 2 is a sink and infected individuals of host 2 have larger uptake rates than susceptible individuals, (ii) host 2 is a source and infected individuals of host 2 are stronger competitors than susceptible individuals, or (iii) host 2 has stronger interspecific competitive effects on sink hosts than source hosts.

The sensitivity of focal host infection prevalence to the transmission coefficient of host 2 is

$$\frac{\partial Y_1^*}{\partial \beta_2} = \overbrace{X_2^* N_2^* P^*}^{\beta_2 \to Y_2^*} \left[\overbrace{\frac{-|\mathbf{A}|}{|\mathbf{J}|} \frac{N_2^*}{Y_2^*} \left(\varphi_2 Y_2^* + u_{S_2} P^* \right)}^{Y_2^* \to P^*} + \overbrace{\sum_{i=1}^{n} \frac{|\mathbf{A}_{Y_2 \to N_i}|}{|\mathbf{J}|} \varphi_i Y_i^*}^{Y_2^* \to N_i^* \to P^*} \right] \overbrace{\beta_1 X_1^* N_1^* Q_{\beta_2}}^{P^* \to Y_1^*} \tag{11}$$

where Q_{β_2} is a positive quantity; see Appendix S2.2 for details. Eq. (10) shows that increasing the transmission coefficient of host 2 affects focal host infection prevalence through three kinds of indirect pathways: (1) $\beta_2 \to Y_2^* \to P^* \to Y_1^*$, (2) $\beta_2 \to Y_2^* \to N_2^* \to P^* \to Y_1^*$, and (3) $\beta_2 \to Y_2^* \to N_i^* \to P^* \to Y_1^*$ for $i \neq 2$.

The first pathway is defined by the first term in brackets. In that pathway, increased transmission increases infection prevalence in host 2 ($\beta_2 \to Y_2^*$), increased prevalence in host 2 affects the production rate of infectious propagules by host 2 ($Y_2^* \to P^*$), and changes in infectious propagule density affect focal host infection prevalence ($P^* \to Y_1^*$). Under the assumption $\text{sign}(|\mathbf{A}|) = (-1)^n$, the sign of the indirect effect for this pathway is $\varphi_2 Y_2^* + u_{S_2} P^*$. As shown in Remark S1.1 in Appendix S1.3, that quantity is positive unless host 2 is a sufficiently large sink (φ_2 negative and large in magnitude) and infected individuals have greater uptake rates than susceptible individuals ($u_{I_i} > u_{S_i}$). Consequently, this pathway has a positive indirect effect unless host 2 is a sufficiently large sink and infected individuals of host 2 have greater uptake rates than susceptible individuals.

The second pathway is defined by the $i = 2$ term in the sum in brackets. In that pathway, increased transmission increases infection prevalence in host 2 ($\beta_2 \to Y_2^*$); increased prevalence decreases the density of host 2 due to disease-induced mortality and intraspecific competition between infected and susceptible individuals ($Y_2^* \to N_2^*$); decreased density of host 2 affects infectious propagule density ($N_2^* \to P^*$), which depends on whether host 2 is a source ($\varphi_2 > 0$) or sink ($\varphi_2 < 0$); and changes in infectious propagule density affect focal host infection prevalence ($P^* \to Y_1^*$). Under the assumed signs in Table 2, the sign of the indirect effect for this pathway is $-\varphi_2$. Thus, this pathway has a positive indirect effect when host 2 is a sink and a negative indirect effect when host 2 is a source. In addition, because this indirect pathway involves intraspecific competition between susceptible and infected individuals, the magnitude of the indirect effect is larger when infected individuals of host 2 are stronger intraspecific competitors than susceptible individuals.

The third kind of pathway is defined by the $i \neq 2$ terms in the sum in brackets. These pathways are similar to the previous pathway, except that they account for how increased prevalence in host 2 alters the total interspecific competitive effect of host 2 on host i ($Y_2^* \to N_i^*$) and how changes in the density of host i affect infectious propagule density ($N_i^* \to P^*$), which depends on whether host i is a source ($\varphi_i > 0$) or sink ($\varphi_i < 0$). Under the assumed signs in Table 2, the sign of the indirect effect for these pathways are $-\varphi_i$ when infected individuals of host 2 are weaker competitors than susceptible individuals and φ_i when infected individuals of host 2 are stronger competitors than susceptible individuals. In addition, because these indirect pathways involve interspecific competition, the magnitude of each indirect effect is stronger when host 2 has stronger direct and indirect interspecific competitive effects on host i.

Responses in focal host infection prevalence to increases in the transmission coefficient of host 2 are determined by the three kinds of indirect pathways in the following way. Increases in β_2 often cause higher focal host infection prevalence (increasing curves in Fig. 1A-D) because the indirect effects of the first pathway and some of the other pathways are often positive. There are three cases under which the prediction can be reversed. First, if host 2 is a sink and infected individuals of host 2 have larger uptake rates than susceptible individuals, then increases in β_2 can cause lower focal host infection prevalence because the indirect effect of the first pathway is negative (decreasing blue exes in Fig. 1B). Second, if host 2 is a source and infected individuals are stronger competitors than susceptible individuals, then increases in β_2 can cause lower focal host infection prevalence because the indirect effect of the second pathway is negative and large in magnitude (decreasing parts of red plus signs and magenta open circles in Fig. 1C). Third, if host 2 has strong interspecific competitive effects on sink hosts, then increases in β_2 can cause lower focal host infection prevalence (decreasing parts of red plus signs and magenta open circles in Fig. 1D) because the indirect effects of the third kind of pathway are negative and large in magnitude. In principle, increases in β_2 can cause lower focal host infection prevalence if host 2 has strong interspecific competitive effects on source hosts and infected individuals of host 2 are stronger competitors than susceptible individuals. However, I was unable to find numerical examples of this, which suggests it may be unlikely to arise in nature.

3.1.3. Effects of varying disease-induced mortality (μ_2)

In most cases, increasing disease-induced mortality in host 2 (μ_2) decreases infection prevalence in the focal host. The intuition is that increased disease-induced mortality leads to decreased prevalence in host 2, which leads to lower infectious propagule density and decreased contact between infectious propagules and susceptible individuals of the focal host. This prediction can be reversed if (i) host 2 is a sufficiently large sink or (ii) if host 2 is a small sink and infected individuals of host 2 have sufficiently larger uptake rates than susceptible individuals.

The sensitivity of focal host infection prevalence to the disease-induced mortality rate of host 2 is

$$\frac{\partial Y_1^*}{\partial \mu_2} = \overbrace{Y_2^*}^{\mu_2 \to Y_2^*} \left[\overbrace{\frac{|\mathbf{A}|}{|\mathbf{J}|} \frac{N_2^*}{Y_2^*} \left(\varphi_2 Y_2^* + u_{S_2} P^* \right)}^{Y_2^* \to P^*} - \overbrace{\sum_i \frac{|\mathbf{A}_{Y_2 \to N_i}|}{|\mathbf{J}|} \varphi_i Y_i^*}^{Y_2^* \to N_i^* \to P^*} \right] \overbrace{\beta_1 X_1^* N_1^* Q_{\mu_2}}^{P^* \to Y_1^*}$$
$$+ \overbrace{Y_2^* N_2^*}^{\mu_2 \to N_2^*} \left(\overbrace{\sum_i \frac{(-1)^{i-1} |\mathbf{A}^{[-2,-i]}|}{|\mathbf{J}|} \varphi_i Y_i^*}^{N_2^* \to N_i^* \to P^*} \right) \overbrace{\beta_1 X_1^* N_1^* Q\prime_{\mu_2}}^{P^* \to Y_1^*} \tag{12}$$

where Q_{μ_2} and $Q\prime_{\mu_2}$ are positive quantities; see Appendix S2.3 for details. Eq. (12) shows that increasing the disease-induced mortality rate of host 2 affects focal host infection prevalence through five kinds of indirect pathways: (1) $\mu_2 \to Y_2^* \to P^* \to Y_1^*$, (2) $\mu_2 \to Y_2^* \to N_2^* \to P^* \to Y_1^*$, (3) $\mu_2 \to Y_2^* \to N_i^* \to P^* \to Y_1^*$ for $i \neq 2$, (4) $\mu_2 \to N_2^* \to P^* \to Y_1^*$, and (5) $\mu_2 \to N_2^* \to N_i^* \to P^* \to Y_1^*$. The first three kinds of pathways are the same as the pathways for $\partial Y_1^*/\partial \beta_2$, except that the signs of the indirect effects are reversed because increased disease-induced mortality has a negative direct effect on prevalence in host 2 ($\mu_2 \to Y_2^*$); see Table 3 for a summary of the signs of the indirect effects associated with each indirect pathway.

The fourth kind of pathway is defined by the $i = 2$ term in the second sum. In that pathway, increased mortality reduces the density of host 2 ($\beta_2 \to N_2^*$); reduced density of host 2 increases or decreases infectious propagule density ($N_2^* \to P^*$) depending on whether host 2 is a sink ($\varphi_2 > 0$) or source ($\varphi_2 < 0$), respectively; and changes in infectious propagule density affect focal host infection prevalence ($P^* \to Y_1^*$). Under the assumed signs in Table 2, the sign of the indirect effect for this pathway is $-\varphi_2$. Thus, this path-

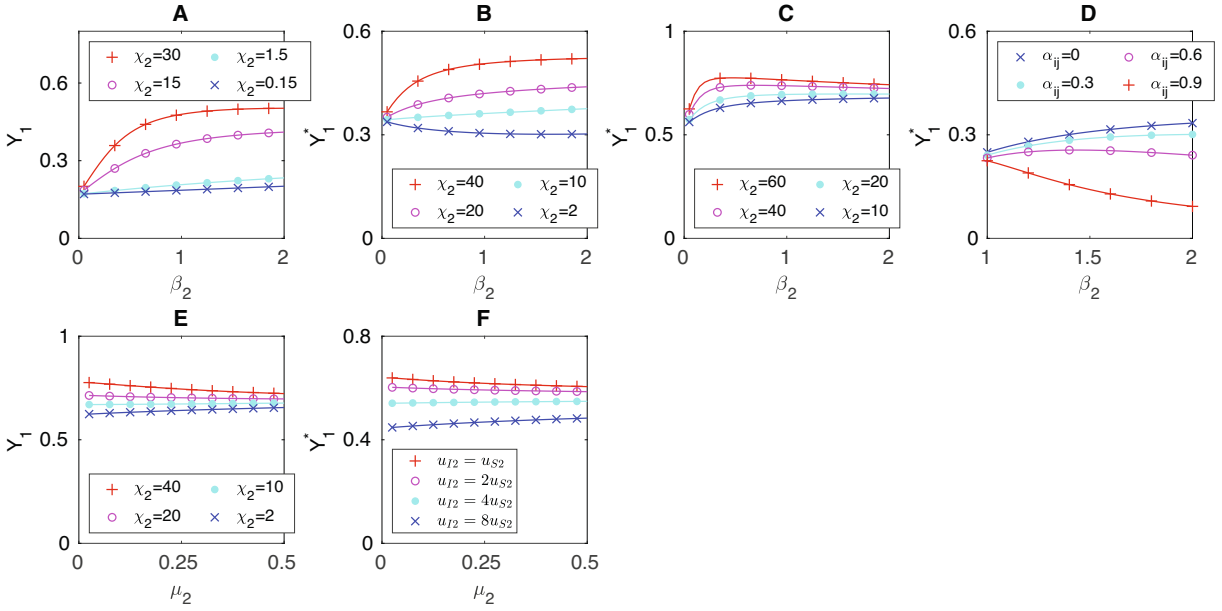

Fig. 1. Responses in focal host infection prevalence (Y_1^*) to increased competence of a non-focal host depend on the competence and competitive interactions of the non-focal host. (A) Increases in the transmission parameter of host 2 often cause increased focal host infection prevalence when host 2 is a sink (blue exes, cyan filled circles) or source (red plus signs, magenta open circles). (B) If infected individuals of host 2 have larger uptake rates then susceptible individuals, then increases in the transmission parameter of host 2 cause focal host infection prevalence to increase when host 2 is a source (red plus signs, magenta open circles) or small sink (cyan filled circles) and decrease when host 2 is a sufficiently large sink (blue exes). (C) If infected individuals of host 2 are stronger competitors than susceptible individuals, then increases in the transmission parameter of host 2 cause focal host infection prevalence to increase when host 2 is a sink (blue exes, cyan closed circles) and decrease when host 2 is a source (red plus signs, magenta open circles). (D) If host 2 has stronger interspecific competitive effects on sink hosts than source hosts, then increases in the transmission parameter of host 2 cause focal host infection prevalence to increase when interspecific competition is sufficiently weak (blue exes, cyan closed circles) and decrease when interspecific competition is strong (red plus signs, magenta open circles). (E) Increases in disease-induced mortality of host 2 cause focal host infection prevalence to decrease when host 2 is a source (red plus signs, magenta open circles) or small sink (cyan closed circles) and increase when host 2 is a sufficiently large sink (blue exes). (F) If host 2 is a source, then increases in disease-induced mortality of host 2 cause focal host infection prevalence to decrease unless infected individuals have sufficiently larger uptake rates than susceptible individuals (cyan filled circles, blue exes). Simulations are from a four-host models with parameter values defined as in Table 1 except those denoted in the legends and (A) $\delta = 0.1, \chi_1 = \chi_3 = \chi_4 = 15$, (B) $\delta = 0.1, u_{I_2} = 60$, (C) $\delta = 1, e_{ij} = 2, u_{S_i} = u_{I_i} = u_{R_i} = 10$ (D) $\delta = 0.9, \chi_2 = 20, \chi_1 = \chi_3 = \chi_4 = 10$, (E) $\delta = 1, u_{S_i} = u_{I_i} = u_{R_i} = 10$, (F) $u_{S_i} = u_{I_i} = u_{R_i} = 10$..

way has a positive indirect effect when host 2 is a sink (because there is a decrease in the density of sink hosts) and a negative indirect effect when host 2 is a source (because there is a decrease in the density of source hosts).

The fifth kind of pathway is defined by the $i \neq 2$ terms in the second sum. These pathways are similar to the previous pathway, except that they account for how decreased density of host 2 alters the total interspecific competitive effect of host 2 on host i ($N_2^* \to N_i^*$) and how changes in the density of host i affect infectious propagule density ($N_i^* \to P^*$), which depends on whether host i is a source ($\varphi_i > 0$) or sink ($\varphi_i < 0$). Under the assumed signs in Table 2, the sign of the indirect effect for this pathway is φ_i. Each pathway has a positive indirect effect when host i is a source, because there is an increase in density of source hosts; each pathway has a negative indirect effect when host i is a sink, because there is an increase in density of sink hosts. In addition, because these indirect pathways involve interspecific competition, the magnitude of each indirect effect is stronger when host 2 has stronger direct and indirect interspecific competitive effects on host i.

Responses in focal host infection prevalence to increased disease-induced mortality in host 2 are determined by the five kinds of indirect pathways in the following way. Increases in μ_2 often cause lower focal host infection prevalence (decreasing red plus signs and magenta open circles in Fig. 1E,F) because the indirect effects of the first pathway and some of the other pathways are often negative. There are two cases under which the prediction can be reversed when host 2 is a sink. First, if host 2 is a sufficiently large sink, then increases in μ_2 can increase focal host infection prevalence because the indirect effect of the fourth pathway is positive (increasing cyan filled circles and blue exes in Fig. 1E). Second, if host 2 is small sink and infected individuals of host 2 have sufficiently larger uptake rates than susceptible individuals, then increases in μ_2 can increase focal host infection prevalence because the indirect effect of the first pathway is positive (increasing cyan filled circles and blue exes in Fig. 1F).

In principle, when host 2 is a source, increases in μ_2 can increase focal host infection prevalence if either (i) infected individuals of host 2 are weaker competitors than susceptible individuals and host 2 has strong competitive effects on sink hosts or (ii) infected individuals of host 2 are stronger competitors than susceptible individuals and host 2 has strong competitive effects on source hosts; these responses are driven by the indirect effects of the third and fifth pathways, respectively. I was unable to find numerical examples of this, which suggests these scenarios may be unlikely to arise in nature. In addition, condition (i) causes the terms with matching indices in the two sums in Eq. (12) to have opposite signs. The counteracting indirect effects from the different pathways make it less likely that the indirect effects from one of the pathways will be sufficiently strong to reverse the prediction. Overall, this suggests that focal host infection prevalence will decrease when a source host experiences increased mortality.

3.1.4. Effects of varying the level of competition experienced by a host

Increasing the competition experienced by host j often decreases focal host infection prevalence when host j is source and increases focal host infection prevalence when host j is sink. However, if interspecific competition is sufficiently strong and asymmetric, then increasing the competition experienced by host j can decrease or increase focal host infection prevalence when

host j has stronger competitive effects on source and sink hosts, respectively.

Let α_{jk} be a parameter that only has a negative effect on the reproduction rate of host j, i.e., $\partial F_j/\partial\alpha_{jk} < 0$ and $\partial F_i/\partial\alpha_{jk} = 0$ for $i \neq j$. Increases in α_{jk} are interpreted as an increase in the intraspecific or interspecific competition experienced by host j. For example, in a Lokta-Volterra competition model α_{jk} would be the competition coefficient describing the competitive effects of host k on host j. The sensitivity of focal host infection prevalence to competition coefficients affecting the focal host and competition coefficients affecting host 2, respectively, are

$$\frac{\partial Y_1^*}{\partial \alpha_{1k}} = \overbrace{-\frac{\partial F_1}{\partial \alpha_{1k}}}^{\alpha_{1k}\to N_1^*} \left(\overbrace{\sum_{i=1}^{n} \frac{(-1)^i \left|\mathbf{A}^{[\neg 1,\neg i]}\right|}{|\mathbf{J}|} \varphi_i Y_i^*}^{N_1^*\to P^* \;\&\; N_1^*\to N_i^*\to P^*} \right) \overbrace{\beta_1 X_1^* N_1^* Q_{\alpha_{1k}}}^{P^*\to Y_1^*} \tag{13}$$

$$\frac{\partial Y_1^*}{\partial \alpha_{2k}} = \overbrace{-\frac{\partial F_2}{\partial \alpha_{2k}}}^{\alpha_{2k}\to N_2^*} \left(\overbrace{\sum_{i=1}^{n} \frac{(-1)^{i-1} \left|\mathbf{A}^{[\neg 2,\neg i]}\right|}{|\mathbf{J}|} \varphi_i Y_i^*}^{N_2^*\to P^* \;\&\; N_2^*\to N_i^*\to P^*} \right) \overbrace{\beta_1 X_1^* N_1^* Q_{\alpha_{2k}}}^{P^*\to Y_1^*} \tag{14}$$

where $Q_{\alpha_{1k}}$ and $Q_{\alpha_{2k}}$ are positive quantities; see Appendices S2.5 and S2.6 for details. Eqs. (13) and (14) show that increased competition experienced by host j affects focal host disease prevalence through two kinds of pathways: (1) $\alpha_{jk} \to N_j^* \to P^* \to Y_1^*$ and (2) $\alpha_{jk} \to N_j^* \to N_i^* \to P^* \to Y_1^*$ for $i \neq j$.

In the first kind of pathway, increased competition reduces the density of host j ($\alpha_{jk} \to N_j^*$); reduced density of host j increases or decreases infectious propagule density ($N_j^* \to P^*$) depending on whether host j is a sink ($\phi_j < 0$) or source ($\phi_j > 0$), respectively; and changes in infectious propagule density affect focal host infection prevalence ($P^* \to Y_1^*$). Under the assumed signs in Table 2, the sign of the indirect effect for this pathway is $-\varphi_j$. This pathway has a positive indirect effect on focal host infection prevalence when host j is a sink, because increased competition decreases the density of the sink host, which causes an increase in infectious propagule density. The pathway has a negative indirect effect on focal host infection prevalence when host j is a source, because increased competition decreases the density of the source host, which causes a decrease in infectious propagule density.

The second kind of pathway is similar, except that decreased density of host j reduces the effects of competition on host i ($N_j^* \to N_i^*$), which causes its density to increase, and increased density of host i increases or decreases infectious propagule density ($N_i^* \to P^*$) depending on whether host i is a source ($\phi_i > 0$) or sink ($\phi_i < 0$), respectively. Under the assumed signs in Table 2, the signs of the indirect effects for these pathways are φ_i. Consequently, these pathways have positive and negative indirect effects on focal host infection prevalence when host i is a source and sink, respectively. Because these indirect pathways involve interspecific competition, the magnitude of each indirect effect is stronger when host j has stronger direct and indirect competitive effects on host i. In addition, if host j has asymmetrically strong competitive effects on other host species, then the pathways involving hosts experiencing stronger competition will be larger in magnitude.

Responses in focal host infection prevalence to host j experiencing increased competition are determined by the two kinds of pathways in the following way. If interspecific competition is sufficiently weak, then the indirect effects for the first kind of pathway will be larger in magnitude than the indirect effects for the second kind of pathway. Consequently, if interspecific competition is sufficiently weak, then the effect of the host j experiencing increased competition is an increase in focal host infection prevalence when host j is a sink (increasing blue exes and magenta open circles in Fig. 3A,C) and a decrease in focal host infection prevalence when host j is a source (decreasing blue exes and magenta open circles in Fig. 3B,D). If interspecific competition is sufficiently strong (but still weaker than intraspecific competition), then the indirect effects for the second kind of pathway will be large in magnitude. In this case, if host j has stronger competitive effects on sink hosts than source hosts, then focal host infection prevalence will decrease when host j experiences increased competition (decreasing red plus signs in Fig. 3A,C). Alternatively, if host j has stronger competitive effects on source hosts than sink hosts, then focal host infection prevalence will increase when host j experiences increased competition (increasing red plus signs in Fig. 3B, D).

3.2. Responses in focal host infection prevalence to variation in the density of other hosts

When host 2 is a weak interspecific competitor, responses in focal host infection prevalence to increased density of host 2 are driven by whether host 2 is a source or sink: focal host infection prevalence increases when host 2 is a source and decreases when host 2 is a sink. The intuition is that increased density of a source host results in increased infectious propagule density whereas increased density of a sink host results in decreased infectious propagule density. In contrast, when host 2 has asymmetric and strong interspecific competitive interactions on other host species, responses in focal host infection prevalence to increased density of host 2 can be driven by whether the other host species are sinks or sources: focal host infection prevalence can increase when host 2 has stronger competitive effects on sink hosts and decrease when host 2 has stronger competitive effects on source hosts. The intuition is that increased density of host 2 suppresses the densities of sink and source hosts (via interspecific competition), which causes infectious propagule density to increase and decrease, respectively.

The sensitivity of focal host infection prevalence to the equilibrium density of host 2 is computed using the ratio,

$$\frac{dY_1^*}{dN_2^*} = \frac{\partial Y_1^*}{\partial \alpha_{22}} \Big/ \frac{\partial N_2^*}{\partial \alpha_{22}}. \tag{15}$$

Throughout, I assume that increase in α_{22} cause a decrease in the equilibrium density of host 2, i.e., $\partial N_2^*/\partial\alpha_{22} < 0$. The opposite condition ($\partial N_2^*/\partial\alpha_{22} > 0$) is only satisfied when host 2 experiences a (generalized) hydra effect (Abrams, 2009), wherein reduced reproductive output of the host causes an increase in its density. Generalized hydra effects are possible in model (6) when interspecific host competition is sufficiently strong, however I expect most empirical systems will satisfy $\partial N_2^*/\partial\alpha_{22} < 0$ because hydra effects at stable equilibria are less likely in parameter space than not.

The analysis of Eq. (15) is similar to the analysis of Eq. (14). Specifically, the effect of increased density of host j on focal host infection prevalence is determined by two kinds of pathways: (1) $N_j^* \to P^* \to Y_1^*$ and (2) $N_j^* \to N_i^* \to P^* \to Y_1^*$ for $i \neq j$. In the first pathway, increased density of host 2 directly increases or decreases infectious propagule density ($N_j^* \to P^*$) depending on whether host 2 is a source ($\varphi_2 > 0$) or sink ($\varphi_2 < 0$), respectively. The indirect effect of that pathway on focal host infection prevalence is positive when host 2 is a source and negative when host 2 is a sink. In the second kind of pathway, increased density of host 2 suppresses the density of host i ($N_j^* \to N_i^*$) and decreased density in host i causes a decrease or increase in infectious propagule density ($N_i^* \to P^*$) depending on whether host i is a source ($\varphi_2 > 0$) or sink

($\varphi_2 < 0$), respectively. For each pathway of the second kind, the indirect effect on focal host infection prevalence is negative when host i is a source and negative when host i is a sink.

Responses in focal host infection prevalence to increased density of 2 are determined by the two kinds of pathways in the following way. When interspecific competition is weak, the indirect effect of the first kind of pathway is larger in magnitude than the indirect effects of the second kind of pathway. In this case, the responses to increased density of host 2 only depend on the characteristics of host 2. Specifically, increased density of host 2 increases focal host infection prevalence when host 2 is a source (increasing red plus signs and magenta open circles in Fig. 3A; increasing blue exes and magenta open circles in Fig. 3B) and decreases focal host infection prevalence when host 2 is a sink (decreasing cyan filled circles and blue exes in Fig. 3A; decreasing blue exes and magenta open circles in Fig. 3C). As interspecific competition becomes stronger, the indirect effects of the second kind of pathway become larger in magnitude. If host 2 has strong and asymmetric competitive effects on other host species, then the responses to increased density of host 2 may be driven by the characteristics of the host species experiencing the stronger competitive effects. Specifically, if host 2 has stronger competitive effects on source hosts than sink hosts, then increased density of host 2 can cause focal host prevalence to decrease (decreasing red plus signs in Fig. 3B). If host 2 has stronger competitive effects on sink hosts than source hosts, then increased density of host 2 can cause focal host prevalence to increase (increasing red plus signs in Fig. 2C).

The above yields the following predictions about how the addition or removal of host 2 affects focal host infection prevalence. In many cases, the addition of host 2 will increase or decrease focal host infection prevalence when host 2 is a source or sink, respectively. However, if host 2 has strong and asymmetric competitive effects on other host species, then the addition of host 2 can increase or decrease focal host infection prevalence when host 2 has stronger competitive effects on sink and source hosts, respectively. These predictions are guaranteed to be accurate if the sign of Eq. (15) is constant for all values of α_{22} and the removal of host 2 does not cause any other host species to go extinct (true for Fig. 3). However, if the sign of Eq. (15) is not constant or removal of host 2 causes the extinction of other host species, then the prediction may be inaccurate.

3.3. Responses in focal host infection prevalence to pathogen transmission mechanism

I now explore how the pathogen transmission mode influences changes in focal host infection prevalence in response to the addition of one or more hosts to the community. After a host is added to a community, focal host infection prevalence is lower under frequency-dependent direct transmission (FDDT) than density-dependent direct transmission when (i) the introduced hosts have lower competence compared to resident hosts and (ii) introduced hosts and resident hosts have weak interspecific competitive effects. Under the opposite conditions, the addition of a host to a community leads to higher focal host infection prevalence under FDDT than DDDT.

The approach in this section involves three steps. First, I assume there is a subcommunity where a subset of the host species stably coexist with the pathogen and the other host species are initially absent. To simplify the presentation, I focus on the case where host 2 is initially absent and the other $n-1$ host species stably coexist; cases where two or more host species are absent have similar results and are addressed in Appendix S2.7. Let $\hat{p}$ denote the stable endemic equilibrium of the subcommunity where host 2 is absent (hereafter, the 'subcommunity equilibrium') and let $\widehat{U}$ denote the total per infectious propagule uptake rate evaluated at the subcommunity equilibrium.

Second, the infectious propagule equation is rewritten as

$$\frac{dP}{dt} = \sum_i \chi_i Y_i N_i - f(q)UP - q\delta P \tag{16}$$

where the change of parameters function, $f(q)$, transforms the environmental transmission (ET) model from a form that behaves like a frequency-dependent direct transmission (FDDT) model ($q = 0$) to a form that behaves like a density-dependent direct transmission (DDDT) model ($f(q) = 0$). Here, $f(q)$ is a decreasing linear function

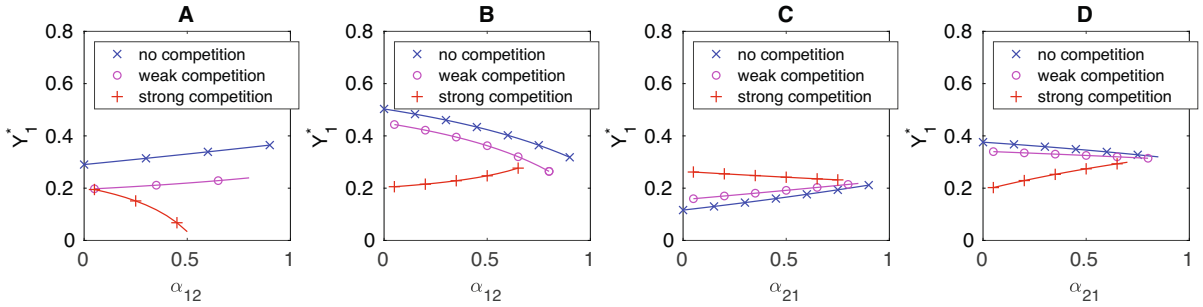

Fig. 2. Responses in focal host infection prevalence (Y_1^*) to increased competition experienced by the focal host (α_{12}) or a non-focal host (α_{21}). (A,B) If interspecific competition is sufficiently weak (blue exes, magenta open circles), then responses in focal host infection prevalence are driven by whether the host experiencing increased competition is a sink or source: focal host infection prevalence (A,C) increases when the host experiencing increased competition is a sink and (B,D) decreases when the host experiencing increased competition is a source. If interspecific competition is sufficiently strong (red plus signs), then responses in focal host infection prevalence are driven by whether the host experiencing increased competition has stronger interspecific competitive effects on sink or source hosts: focal host infection prevalence (A,B) decreases when the host experiencing increased competition has stronger competitive effects on source hosts and (B,D) increases when the host experiencing increased competition has stronger competitive effects on sink hosts. Simulations are from a four-host models with parameter values defined as in Table 1 except (A) $\delta = 30$, $(\beta_1, \beta_2, \beta_3, \beta_4) = (2, 1, 3, 2)$, $(\chi_1, \chi_2, \chi_3, \chi_4) = (1, 20, 20, 1)$, (B) $\delta = 30$, $(\beta_1, \beta_2, \beta_3, \beta_4) = (3, 2, 4, 3)$, $(\chi_1, \chi_2, \chi_3, \chi_4) = (20, 1, 1, 20)$, (C) $(\beta_1, \beta_2, \beta_3, \beta_4) = (1, 2, 3, 2)$, $(\chi_1, \chi_2, \chi_3, \chi_4) = (20, 1, 1, 1)$, (D) $\delta = 20$, $(\beta_1, \beta_2, \beta_3, \beta_4) = (1, 2, 3, 2)$, $(\chi_1, \chi_2, \chi_3, \chi_4) = (1, 20, 20, 20)$. The competition coefficients α_{ij} are given by the entries of the matrices (A,B) $\begin{bmatrix} 1 & \alpha_{12} & 0.9a & 0.5a \\ 0.8a & 1 & 0.7a & 0.1a \\ 0.1a & 0.9a & 1 & 0.9a \\ 0.9a & 0.5a & 0.6a & 1 \end{bmatrix}$ and (C,D) $\begin{bmatrix} 1 & 0.1a & 0 & 0 \\ \alpha_{21} & 1 & 0.1a & 0.1a \\ 0 & 0.9a & 1 & 0.1a \\ 0 & 0.9a & 0.1a & 1 \end{bmatrix}$ where a is 1 (red plus signs), 0.3 (magenta open circles), or 0 (blue exes)..

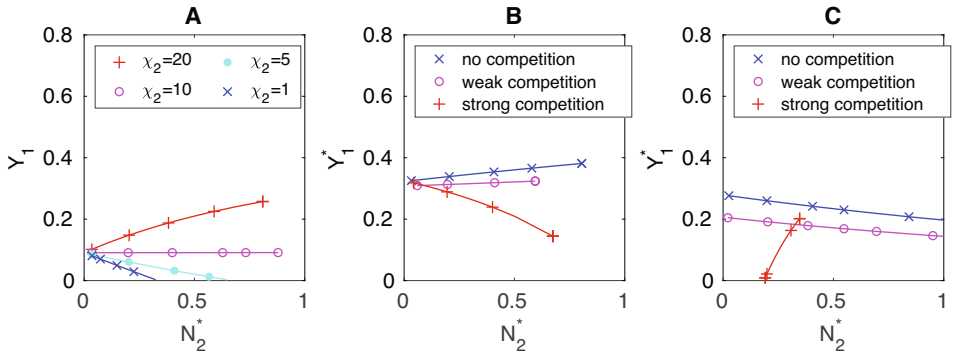

Fig. 3. Responses in focal host infection prevalence (Y_1^*) to increased density of a non-focal host (N_2^*). (A) In the absence of interspecific competition, increased density of a non-focal host causes focal host infection prevalence to increase when the non-focal host is a source (red plus signs, magenta open circles) and decrease when the non-focal host is a sink (blue exes, cyan closed circles). (B,C) If interspecific competition is sufficiently weak (blue exes, magenta open circles), then responses in focal host infection prevalence are driven by whether the non-focal host is a sink or source: focal host infection prevalence (B) increases when the non-focal host is a source and (C) decreases when the non-focal host is a sink. If interspecific competition is sufficiently strong (red plus signs), then responses in focal host infection prevalence are driven by whether the non-focal host has stronger interspecific competitive effects on sink or source hosts: focal host infection prevalence (B) decreases when the non-focal host has stronger competitive effects on source hosts and (C) increases when the non-focal host has stronger competitive effects on sink hosts. Simulations are from a four-host model with parameter values defined as in Table 1 except those denoted in the legends and (A) $\delta = 0.1, \chi_1 = \chi_3 = \chi_4 = 10$, (B) $\delta = 30$, $(\beta_1, \beta_2, \beta_3, \beta_4) = (2, 1, 3, 2)$, $(\chi_1, \chi_2, \chi_3, \chi_4) = (5, 20, 20, 5)$, (C) $\delta = 20$, $(\beta_1, \beta_2, \beta_3, \beta_4) = (1, 2, 3, 2)$, $(\chi_1, \chi_2, \chi_3, \chi_4) = (20, 1, 20, 1)$. In (B,C) the competition coefficients α_{ij} are given by the entries of $\begin{bmatrix} 1 & 0.9a & 0.8a & 0.1a \\ 0.4a & \alpha_{22} & 0.7a & 0.7a \\ 0.1a & 0.9a & 1 & 0.5a \\ 0.9a & 0.9a & 0.6a & 1 \end{bmatrix}$ where α_{22} varies from 1 to 25 and a is 1 (red plus signs), 0.3 (magenta open circles), and 0 (blue exes)..

that holds constant the total per capita loss rate of infectious propagules at the subcommunity equilibrium ($\widehat{U} + \delta$). The coefficients of $f(q) = aq + b$ are found by solving the equation $f(q)UP + q\delta P = \widehat{U}P + \delta P$, which yields $f(q) = 1 + \delta(1-q)/\widehat{U}$ for $0 \leqslant q \leqslant 1 + \widehat{U}/\delta$. The advantage of using this particular change of parameters function is that the subcommunity equilibrium ($\hat{p}$) is independent of the value of q. This simplifies the analysis because transforming the model from a FDDT-form ($q = 0$) to a DDDT-form ($q = 1 + \widehat{U}/\delta$) only affects the host densities and prevalences at the endemic equilibrium with all n species (p^*). The biological interpretation of this constraint is that focal host infection prevalence in the subcommunity is known, the pathogen transmission mechanism is unknown, and focal host infection prevalence in the full community is unknown. Small changes in q define how focal host infection prevalence (after the addition of host 2) depends on the relative contributions of degradation and uptake to the loss of infectious propagules. Varying q between 0 and $1 + \widehat{U}/\delta$ shows how focal host infection prevalence depends on whether environmental transmission behaves more like FDDT or DDDT, respectively. In particular, an increase or decrease in focal host infection prevalence between $q = 0$ and $q = 1 + \widehat{U}/\delta$ means that FDDT promotes lower or higher focal host infection prevalence, respectively, when host 2 is added to the community. The disadvantage of using this specific change of parameters function is that the competencies of the host species ($\chi_i\beta_i/u_{S_i}[\mu_i + m_i + v_i]$) are not held constant as the model is transformed between forms.

The third step is to compute the sensitivity,

$$\frac{\partial Y_1^*}{\partial q} = \frac{-|\mathbf{A}|}{|\mathbf{J}|} \overbrace{\frac{P^*\delta\widehat{U}}{f(q)}\left[\frac{\beta_2\chi_2}{\mu_2+m_2+v_2}X_2^*N_2^* + \sum_{i\neq 2}\frac{\beta_i\chi_i}{\mu_i+m_i+v_i}\left(X_i^*N_i^* - \widehat{X}_i\widehat{N}_i\right)\right]}^{q\to P^*} \overbrace{\beta_1 X_1^* N_1^*}^{P^*\to Y_1^*} Q_q \tag{17}$$

where Q_q is a positive quantity; see Appendix S2.7 for details. Eq. (17) shows that varying the relative magnitudes of degradation and uptake affects focal host infection prevalence through the indirect pathway $q \to P^* \to Y_1^*$. Specifically, varying the magnitudes of degradation and uptake alters infectious propagule density ($q \to P^*$), which in turn affects contacts between infectious propagules and susceptible individuals of the focal host and focal host infection prevalence ($P^* \to Y_1^*$).

The sign of Eq. (17) depends on the competences of all hosts and the competitive effects of host 2 on the other host species. As proven in Appendix S2.7, Eq. (17) is positive in the absence of interspecific competition, unless host 2 has sufficiently high competence (specifically, χ_2 is sufficiently large). This means that if there is no interspecific competition, then focal host infection prevalence is higher under DDDT than FDDT (three increasing curves in Fig. 4A), unless host 2 has very high competence relative to the other host species (decreasing red plus signs in Fig. 4A). More generally, Eq. (17) is positive, unless $\beta_i\chi_i\left(S_i^* - \widehat{S}_i\right)/(\mu_i + m_i + v_i)$ is negative and sufficiently large in magnitude for some $i \neq 2$. Each term $\beta_i\chi_i\left(S_i^* - \widehat{S}_i\right)/(\mu_i + m_i + v_i)$ is negative when S_i^* is small, which is more likely when host 2 has higher competence than host i and host 2 has strong total competitive effects on host i. For example, if the competence of host 2 is sufficiently greater than the competences of all other host species, then focal host infection prevalence is higher under FDDT than DDDT regardless of whether host 2 is a weak or strong interspecific competitor (decreasing curves in Fig. 4B). In contrast, if the competence of host 2 is similar to or lower than the competences of the other host species, then focal host infection prevalence is higher under FDDT than DDDT only when host 2 has sufficiently strong interspecific competitive effects on the other host species (decreasing red plus signs in Fig. 4C,D).

The above results and those in Appendix S2.7 predict the following about how the pathogen transmission mode influences changes in focal host infection prevalence in response to the addition of one or more host species to a community. The introduction of additional host species causes lower focal host infection prevalence under FDDT than DDDT when (i) resident hosts have higher competence and the introduced hosts have lower competence, (ii) resident hosts have weak interspecific competitive effects on the introduced hosts, and (iii) the introduced hosts are weak interspecific and intraspecific competitors. Under the opposite condition, the introduction of additional host species to the subcommunity causes higher focal host infection prevalence under FDDT than DDDT.

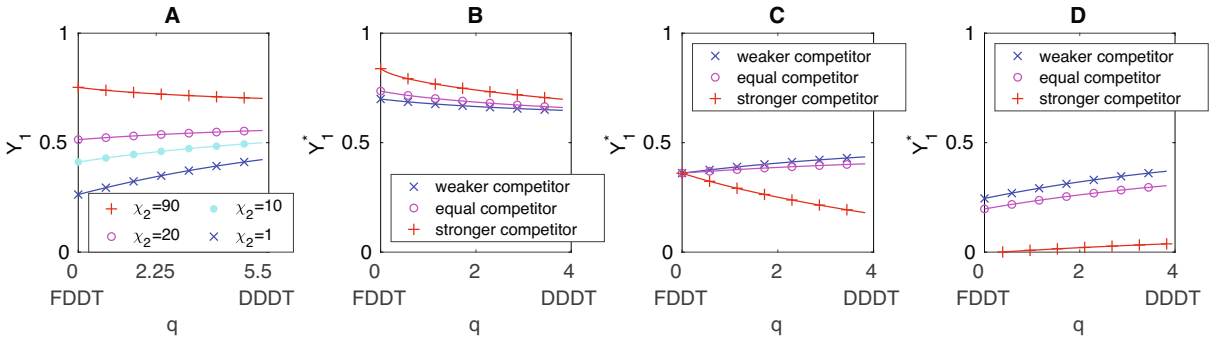

Fig. 4. Responses in focal host infection prevalence (Y_1^*) to changes in the pathogen transmission mode. The environmental transmission model transitions from a frequency-dependent direct transmission (FDDT) form to a density-dependent direct transmission (DDDT) form as q is varied from 0 to its maximum value; see text for details about the change of parameters. (A) When interspecific competition is low, focal host infection prevalence is higher under DDDT than FDDT (magenta open circles, cyan closed circles, blue exes), unless host 2 has much higher competence than the other hosts (red plus signs). (B-D) Increased interspecific competitive ability of the second host decreases the slope of the relationship when the second host has (B) higher competence, (C) equal competence, and (D) lower competence compared to other hosts. Simulations are from a four-host model where the pathogen dynamics are defined by Eq. (16) with (A) $\widehat{U} = 44.59$, (B) $\widehat{U} = 29.11$, (C) $\widehat{U} = 29.11$, and (D) $\widehat{U} = 29.11$. The other parameter values are defined as in Table 1 except those denoted in the legends, $\beta_i = 2, \chi_1 = \chi_3 = \chi_4 = 10$ and (B) $\chi_2 = 90, \alpha_{ij} = 0.3$ except the values of α_{i2} ($1 \leqslant i \leqslant 4$) are 0.9 (red plus signs), 0.3 (magenta open circles), and 0 (blue exes), (C) $\chi_2 = 10, \alpha_{ij} = 0.3$ except the values of α_{i2} ($1 \leqslant i \leqslant 4$) are 0.9 (red plus signs), 0.3 (magenta open circles), and 0 (blue exes), (D) $\chi_2 = 1$, and $\alpha_{ij} = 0.3$ except the values of α_{i2} ($1 \leqslant i \leqslant 4$) are 0.7 (red plus signs), 0.3 (magenta open circles), and 0 (blue exes)..

Translating these predictions to predictions about amplification and dilution of disease yields the following. Introduced hosts are more likely to amplify disease less and dilute disease more under FDDT than DDDT when (i) the introduced hosts have lower competence compared to resident hosts and (ii) interspecific competitive interactions between resident and introduced hosts are weak. In comparison, introduced hosts are more likely to amplify disease less and dilute disease more under DDDT when (i) the introduced hosts have higher competence compared to resident hosts and (ii) interspecific competitive interactions between resident and introduced hosts are strong.

4. Discussion

Host biodiversity-disease relationships are likely to be context-dependent (LoGiudice et al., 2008; Randolph and Dobson, 2012; Wood et al., 2016; Rohr et al., 2019), motivating calls for theory that identifies the specific characteristics of host and pathogen species that promote amplification or dilution of disease in natural communities (Buhnerkempe et al., 2015; Halsey, 2019; Rohr et al., 2019). Building on prior work (Roberts and Heesterbeek, 2018; Cortez and Duffy, 2021), I used local sensitivity analysis to explore the context-dependent ways host competence, host competition, host density, and the pathogen transmission mechanism influence infection prevalence in a focal host. My predictions about how host characteristics influence infection prevalence in a focal host are the following. Increased competence of a non-focal host increases infection prevalence in a focal host (Fig. 1A,E) unless (i) the non-focal host is a sufficiently large sink (Fig. 1D,E,F), (ii) the non-focal host is a source and infected individuals of the non-focal host are stronger competitors than susceptible individuals (Fig. 1B), or (iii) the non-focal host has stronger interspecific competitive effects on sink hosts than source hosts (Fig. 1C). In many cases, increased competition experienced by a non-focal host increases or decreases, respectively, focal host infection prevalence when the non-focal host is sink or source (blue exes and magenta open circles in Fig. 2). However, if a non-focal host has strong and asymmetric competitive effects on other hosts, then increased competition experienced by a non-focal host increases or decreases focal host infection prevalence when the non-focal host has stronger competitive effects on source and sink hosts, respectively (red plus signs in Fig. 2). These results provide support (albeit indirect) to prior claims that species characteristics are likely to have context-dependent effects on host biodiversity-disease relationships.

More direct support for context-dependent host biodiversity-disease relationships is provided by the results about how host density and the pathogen transmission mechanism affect infection prevalence. The interpretation of those results in terms of factors promoting amplification or dilution of disease are the following. First, in many cases, a non-focal host amplifies or dilutes disease in the focal host when the non-focal host is a source or sink, respectively (Fig. 3A). However, if the non-focal host has strong and asymmetric competitive effects on other host species, then the non-focal host amplifies or dilutes disease when the non-focal host has stronger competitive effects on sink and source hosts, respectively (Fig. 3B,C). Second, when a non-focal host is added to a community of resident host species, frequency-dependent direct transmission (FDDT) promotes greater dilution and less amplification than density dependent direct transmission (DDDT) when (i) the non-focal host has lower competence than the resident host species and (ii) interspecific competition between the non-focal host and the resident host species is lower. The opposite conditions promote less dilution and greater amplification under FDDT than DDDT (Fig. 4). Overall, these context-dependent predictions show that a given host or pathogen characteristic does not promote amplification or dilution in all settings, but instead its effects depend on feedbacks between epidemiological and ecological processes.

While the responses in n-host communities are more complex, the predictions in this study for n-host communities generally agree with the predictions for two-host communities (Cortez and Duffy, 2021). The one exception is how focal host infection prevalence responds to increased density or the addition of a sink host. Specifically, increased density of a sink host in a community with three or more host species can increase focal host infection prevalence if the sink host has strong interspecific competitive effects on other sink hosts in the community (Fig. 3C). In contrast, increased density of a sink host in a two-host community always decreases focal host infection prevalence. This is because if the second host is a sink, then the focal host must necessarily be a source, which results in the two indirect pathways defining $\partial Y_1^*/\partial N_2^*$ having negative indirect effects. Altogether, this means increased density of a sink host has a context independent effect in two-host communities, but a context dependent effect in communities with three or more host species. This highlights a limitation of extrapolating

empirical and theoretical results from two-host communities to larger communities.

The results of this study also highlight an important caveat of using short-term exposure experiments to predict patterns of amplification and dilution. Many empirical studies have used short-term exposure experiments to identify if the presence of other host species decreases, increases, or does not change infection prevalence in a focal host (Evans and Entwistle, 1987; Johnson et al., 2008; Searle et al., 2011; Orlofske et al., 2012; Becker et al., 2014; Venesky et al., 2014; Hopkins et al., 2020). In those studies, lower and higher focal host infection prevalence is interpreted to mean the non-focal hosts dilute and amplify disease, respectively. In some cases the results from these short-term experiments will accurately predict how infection prevalence in a focal host depends on the presence/absence of a non-focal host. For example, in a study on *Batrachochytrium dendrobatidis* (Bd) infections in frogs, infection prevalence in the community was positively correlated with the presence of species from the genus *Bufo* density and negatively correlated with the presence of species from the genus *Gastrophryne*. This matched results from short-term experiments where a third species (*Hyla cinerea*) was exposed to zoospores in the presence and absence of *Bufo terrestris* and *Gastrophryne carolinensis* (Venesky et al., 2014). However, the results in this study show that short-term experiments may not accurately predict long-term responses in focal host infection prevalence because the short-term experiments do not account for feedbacks involving excretion of infectious propagules (which influences whether a host is a sink or source) and competitive effects between species (which affects host species densities). For example, a sink host can amplify disease in a focal host if the sink host has strong interspecific competitive effects on other sink hosts in the community (Fig. 3C). This could affect the efficacy of population management strategies that control disease levels in a focal host through the reduction or removal of alternative host species (Laurenson et al., 2004; Donnelly et al., 2006).

While the sensitivity-based approach used in this study helps uncover context-dependent rules governing amplification and dilution of disease, it is important acknowledge two limitations of the approach. First, the results of this study only necessarily apply to small changes in parameter values or species' densities, which means they may not accurately predict responses to large changes in parameter values (e.g., converting the model from a FDDT to DDDT form) or large changes in a species' density (e.g., the addition or removal of a species). Nonetheless, because the analytical formulas for each sensitivity apply everywhere in parameter space, they can help explain patterns of amplification or dilution. In particular, the predictions are guaranteed to be accurate if a sensitivity has a constant sign. For example, Faust et al. (2017) found that focal host infection prevalence always increased with the addition of each non-focal host for DDDT pathogens (Fig. 1 right column and Fig. 2A in that study). The DDDT model assumed no interspecific competition, which means all hosts are sources ($\varphi_i > 0$ for all i) and Eq. (15) is positive for all host densities in any community. Thus, the observed increase of focal host infection prevalence under DDDT in Faust et al. (2017) was caused by the assumption that interspecific competition was absent. The current study also predicts that sufficiently strong interspecific competition can result in dilution under density-dependent direct transmission.

The second limitation is that these results cannot fully explain all patterns observed in multi-host DDDT, FDDT, and ET models. The reason is that models (1) and (6) assume all host species have completely overlapping habitats. This causes the DDDT-form and FDDT-form of the ET model to have within-host and between-host transmission coefficients ($\bar{\beta}_{ii}$ and $\bar{\beta}_{ii}$) that are not independent. Said another way, there is no onto mapping of parameterizations of the ET model (1) to parameterizations of an FDDT or DDDT model. To illustrate the consequences of this, Faust et al. (2017) found that focal host infection prevalence decreased with the addition of each non-focal host for FDDT pathogens (Fig. 1 middle column and Fig. 2c in that study), unless late arriving non-focal hosts had very high competence (Fig. 2b of that study). The FDDT model in Faust et al. (2017) assumed no interspecific competition and transmission rates of the form $\bar{\beta}_{ij}S_iI_j/(\sum_{k=1}^{n}N_k)$, where the interspecific transmission coefficients were defined by $\bar{\beta}_{ij} = \phi\sqrt{\bar{\beta}_{ii}\bar{\beta}_{jj}}$ for $0 < \phi < 1$. When translated to the ET model, these conditions correspond to all hosts having equal uptake rates ($u_{W_i} = 1$ for $i \leqslant n$ and $W \in \{S, I, R\}$) and the excretion rate of the focal host being greater than that of a non-focal host ($\chi_1 > \chi_i$ for $i \geqslant 2$), unless the added non-focal host has sufficiently higher competence than the focal host (β_{jj} sufficiently larger than β_{11}). This study predicts that focal host infection prevalence will decrease (increase) when an added non-focal host has lower (higher) competence than the focal host because the non-focal host is a sink (source). This prediction holds when the non-focal host is added to the community with just the focal host (yielding a two-host community). However, the predictions do not always hold when the non-focal host is added to a community with more than one host species (yielding a community with three or more host species) because a non-focal host can be a source for the focal host but a sink for a different non-focal host.

Despite the limitations of the current study, the sensitivity-based approach used in this study could be useful for advancing our understanding of biodiversity-disease relationships in two ways. First, a sensitivity-based approach could help explain when and why predictions for different metrics agree or disagree. Previous studies have shown that predictions based on infection prevalence, the density of infected individuals, and the pathogen basic reproductive number ($\mathscr{R}_0$) do not always agree (Roche et al., 2012; Wood et al., 2014; Wood et al., 2016; Roberts and Heesterbeek, 2018; Cortez and Duffy, 2021). These metrics provide different, but related, information about epidemics: the density and proportion of infected individuals measure disease burden in a population, with the latter being scaled relative to the total population size, and $\mathscr{R}_0$ is a measure of a community's risk of a outbreak. Applying the sensitivity-based approach could identify when and why the metrics agree or disagree. This in turn would yield understanding about when and why host biodiversity has similar versus different effects on different aspects of disease dynamics.

Second, the approach could help understand how diversity at other trophic levels affects disease. Predators of host species and species that consume infectious propagules can alter levels of disease (Thieltges et al., 2008; Borer et al., 2009; Cáceres et al., 2009; Orrock and Allan, 2011; Orlofske et al., 2012; Rohr et al., 2015). Chesson and Kuang (2008) showed that Lokta-Voterra multi-predator-multi-prey models can be reduced to models with a single trophic level, where the intraspecific and interspecific competition coefficients of the prey account for the competitive interactions between prey and the indirect interactions mediated by the predator species. Combining the approaches in Chesson and Kuang (2008) and this study could help identify how feedbacks involving competitive and predatory interactions between species shape disease dynamics and contribute to the context-dependent shapes of host biodiversity-disease relationships. Overall, the sensitivity-based approach used in this study could help identify the general rules governing how the characteristics of host and non-host species shape biodiversity-disease relationships in natural communities.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at https://doi.org/10.1016/j.jtbi.2021.110766.

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