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Submitted February 24, 2015; Accepted June 5, 2015; Electronically published September 18, 2015

Online enhancement: appendix. *Dryad data:* http://dx.doi.org/10.5061/dryad.972mv.

abstract: Many parasites circulate endemically within communities of multiple host species. To understand disease persistence within these communities, it is essential to know the contribution each host species makes to parasite transmission and maintenance. However, quantifying those contributions is challenging. We present a conceptual framework for classifying multihost sharing, based on key thresholds for parasite persistence. We then develop a generalized technique to quantify each species' contribution to parasite persistence, allowing natural systems to be located within the framework. We illustrate this approach using data on gastrointestinal parasites circulating within rodent communities and show that, although many parasites infect several host species, parasite persistence is often driven by just one host species. In some cases, however, parasites require multiple host species for maintenance. Our approach provides a quantitative method for differentiating these cases using minimal reliance on system-specific parameters, enabling informed decisions about parasite management within poorly understood multihost communities.

Keywords: control, reservoir hosts, spillover, emerging infectious diseases, zoonoses, basic reproduction number (R_0).

Introduction

Parasites typically infect multiple host species (Cleaveland et al. 2001; Woolhouse et al. 2001; Pedersen et al. 2005; Begon 2008; Rudge et al. 2013), with important consequences for their spread to and impact on alternative host species. Indeed, many of the most pressing concerns about emerging infectious disease in humans (e.g., pandemic influenza [Kuiken 2006], West Nile virus [Kilpatrick et al. 2006]) and wildlife (e.g., bovine tuberculosis in cattle and badgers [Krebs et al. 1998], squirrel pox in red squirrels [Tompkins et al. 2002]) arise through transmission from one host species to another. More broadly, parasites often circulate endemically within reservoir host communities comprising multiple host species (Haydon et al. 2002; Viana et al. 2014) that differ in their susceptibility, infectiousness, and behavior. Hence, host community composition and the network of transmission among species play vital roles in driving disease transmission and persistence at the community level (Haydon et al. 2002; LoGiudice et al. 2003; Fenton and Pedersen 2005; Keesing et al. 2006; Kilpatrick et al. 2006; Streicker et al. 2013).

To aid our understanding of multihost parasite systems, a range of general theory has been developed (Holt and Pickering 1985; Bowers and Begon 1991; Begon et al. 1992; Bowers and Turner 1997; Greenman and Hudson 1999, 2000; Haydon et al. 2002; Holt et al. 2003; Dobson 2004; Fenton and Pedersen 2005; Begon 2008). This body of theory shows that a parasite can persist only if its basic reproduction number across the whole community (denoted here as $R_{0,\text{tot}}$) exceeds 1 (Dobson 2004). Formally, R_0 (or $R_{0,\text{tot}}$) is a measure of the ability of a parasite to invade a completely naïve host population (or community), being able to do so if $R_0 > 1$. While it is true that stochastic forces may be important, particularly around this threshold value (i.e., parasites may fade out if R_0 is slightly greater than 1 or may persist considerably if R_0 is slightly less than 1; Fenton and Pedersen 2005; Lloyd-Smith et al. 2005, 2009), in the deterministic models described above, $R_0 > 1$ is a requirement for the parasite to be maintained endemically, thereby providing an intuitive criterion for parasite eradication (by driving $R_0 < 1$). We

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Am. Nat. 2015. Vol. 186, pp. 610–622.
DOI: 10.1086/683173

therefore use the criterion $R_{0,tot} > 1$ as our threshold for parasite persistence within a host community.

Importantly, the magnitude of $R_{0,tot}$ will depend on the competencies of the different host species in the community and the rates of between- and within-species transmission. These ideas are exemplified by the graphical framework developed by Holt et al. (2003), which elegantly illustrates how different combinations of host species' densities combine to determine whether the parasite persists. This framework provides a valuable conceptualization of the qualitative relationship between host abundance and parasite establishment or extinction. Such conceptual frameworks, however, do not in themselves provide a means to quantify the contributions of each host species to $R_{0,tot}$ for genuine host-parasite systems. Hence, they do not enable quantification of the importance of each host species for the endemic persistence of a parasite or provide quantitative predictions about the targeting of control measures toward each host species that would drive $R_{0,tot} < 1$.

Quantifying host species contributions to $R_{0,tot}$ and predicting their consequences for parasite maintenance and the impact of control are highly challenging. Determining the species origin of infections (who infects whom) in a multihost community using molecular tools has been possible in only a few host pathogen systems in which cross-species transmission is relatively rare (e.g., Streicker et al. 2010). Furthermore, experimental manipulations of host density or cross-species transmission, which could provide insight into host species contributions to parasite persistence, are rarely undertaken for logistical reasons (Donnelly et al. 2003; Bielby et al. 2014; Viana et al. 2015). As such, there is a need to develop analytical tools that can make inferences about host contributions to parasite transmission and persistence from observational data. Recently, methods have been developed that do this for certain multihost disease systems (Funk et al. 2013; Rudge et al. 2013). For example, Rudge et al. (2013) presented an analysis that quantified host species contributions to $R_{0,tot}$ of the human schistosome parasite *Schistosoma japonicum*. Using a system-specific transmission model parameterized from values in the literature and observed infection prevalences, Rudge et al. (2013) were able to partition contributions to $R_{0,tot}$ for a range of potential host species, allowing identification of those species that were most likely maintaining this parasite. Likewise, Funk et al. (2013) developed a similar approach for human African trypanosomiasis, showing that human infections were unlikely to be maintained without input from the animal reservoir. These studies required accurate estimates of various parameters for their system-specific models (e.g., mortality rates, recovery rates), which were facilitated by the detailed information available about those well-studied systems. However, such information is lacking for most parasites. For those species, it would be invaluable to be able to make quantified inferences about likely levels of host contributions to $R_{0,tot}$, based purely on easily obtainable, standard parasitological data. Here we generalize the approaches of Funk et al. (2013) and Rudge et al. (2013) to develop a flexible generic method for readily estimating host species contributions to $R_{0,tot}$ that can be applied across a range of multihost-parasite systems with minimal reliance on system-specific parameter estimates.

In what follows, we first modify the conceptual framework of multihost contributions to parasite persistence developed by Holt et al. (2003) to express their density-based axes in terms of host contributions to R_0 and formally categorize different types of multihost dynamics based on key thresholds in this multidimensional R_0 space. Second, we generalize the system-specific approaches of Funk et al. (2013) and Rudge et al. (2013) to allow host species contributions to $R_{0,tot}$ to be directly quantified. Third, we show how we can use the quantified contributions to $R_{0,tot}$ to assess the proximity of an empirical system to the different thresholds for parasite persistence and estimate likely responses to targeted control strategies. Finally, we illustrate this process using a data set of eight different parasite species circulating within communities of four potential host species. We emphasize that although variations on the two primary aspects of this work (a conceptual multihost framework and an analytical method of quantifying host contributions to $R_{0,tot}$) have previously been developed, they have remained largely independent of each other. We see great value in bringing these different approaches together. Specifically, their combination provides a powerful tool with which to (i) make quantified inferences about host contributions to a parasite's $R_{0,tot}$ using easily obtainable data, (ii) categorize the way parasites use the available host community by locating the empirical system directly within the conceptual framework, and (iii) use this information to make quantitative predictions about the effects of targeted control based on the proximity of the system to thresholds for disease eradication. This unified approach is crucial for wildlife systems where accurate data on infection parameters are difficult to obtain but understanding host contributions to parasite persistence is a vital conservation concern.

The Multispecies Theoretical Framework

Our intention is to provide an intuitive, simple method of inferring host species contributions to parasite persistence using relatively easily obtained parasitological data. We therefore adopt a highly generic framework that is broadly applicable to both microparasites (e.g., viruses, bacteria) and macroparasites (e.g., parasitic helminths). Specifically, we model changes in the prevalence of infection in host species rather than, for example, modeling infection intensities, which are less easy to parameterize and can suffer

greatly from problems of sampling error (Barbour 1996; Rudge et al. 2013); we return to this point in the discussion. Here we first consider the case of homogenous transmission among host species; later we extend it to allow for heterogeneities in the rates of transmission within and among host species.

The Homogenous Transmission Framework

We consider a parasite species circulating within a community of n host species of abundance H_i ($i = 1, 2, \ldots, n$). For simplicity, we assume that these host species do not directly interact with each other (e.g., through competition), and so the presence or abundance of one species does not affect the presence or abundance of another species; such interactive scenarios have been considered in previous multihost-parasite models (Holt and Pickering 1985; Bowers and Turner 1997; Greenman and Hudson 2000). Here we assume that the parasite is transmitted via a single homogenous pool of infective stages (E) in the environment (e.g., spores, eggs, larvae, virions; fig. 1*A*), although a similar framework is easily developed for directly transmitted parasites (see appendix, available online). The dynamics of the system are given by

$$\frac{dP_i}{dt} = (1 - P_i)\beta_i E - b_i P_i, \tag{1a}$$

$$\frac{dE}{dt} = \sum_{i=1}^{n} \lambda_i P_i H_i - \gamma E, \tag{1b}$$

where P_i is the prevalence of infection in host species i, β_i is the transmission rate to host species i, b_i is the loss rate of infected individuals of host species i (incorporating recovery and natural and parasite-induced mortality), λ_i is the rate of infective stage production by infected individuals of host species i (here assumed to be independent of infection intensity; Rudge et al. 2013), and γ is the mortality rate of infective stages in the environment. For simplicity, we assume that the loss rate of infective stages from the environment through uptake by hosts is negligible; relaxation of this assumption would reduce the parasite's overall R_0 but would require explicit information about the rate of uptake in order to quantify, which may be very hard to obtain. Hence, we ignore this possibility in what follows. Following the next-generation method of Diekmann and Heesterbeek (2000), the parasite's overall basic reproduction number in the community of n host species is given by the dominant eigenvalue of the transmission matrix (Dobson 2004; see also Rudge et al. 2013):

$$R_{0,\text{tot}} = \sqrt{\sum_{i=1}^{n} R_{0,i}}, \tag{2}$$

where $R_{0,i} = \beta_i \lambda_i H_i / \gamma b_i$, corresponding to the parasite's R_0 value when host i is the only species in the community.

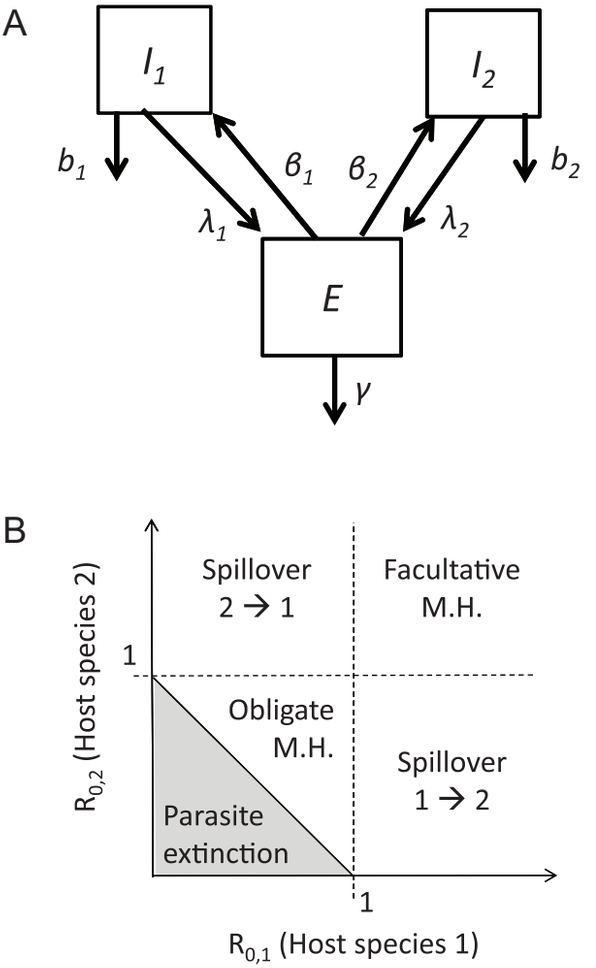

Figure 1: *A*, Schematic diagram of the homogenous transmission model, assuming a single pool of parasite infection stages in the environment. *B*, Graph of $R_{0,1}$–$R_{0,2}$ parameter space for the homogenous transmission model, showing the five regions of dynamic outcome: parasite exclusion, spillover ($H_1 \rightarrow H_2$), spillover ($H_2 \rightarrow H_1$), facultative multihost (M.H.), and obligate multihost.

Hence, when all hosts have equal access to a common pool of infective stages (fig. 1*A*), the parasite's overall basic reproduction number within the whole host community is simply proportional to (specifically, the square root of) the sum of the individual $R_{0,i}$ for each host species alone.

From this theoretical basis, we can modify the framework of Holt et al. (2003) to illustrate how the contributions of each host species combine to determine the parasite's overall $R_{0,\text{tot}}$; here we do that for two host species ($i = 1, 2$; fig. 1*B*), although the concepts apply to any number of host species. The different possible thresholds of disease persistence given by $R_{0,i} = 1$ and $R_{0,\text{tot}} = 1$ result in five regions of parameter space.

Region 1. The parasite cannot persist ($R_{0,\text{tot}} < 1$). The upper boundary of this region is given by the equation $R_{0,\text{tot}} = 1$, and due to the assumption of shared access to a common transmission pool (see below where this is relaxed), the two host species combine additively to determine the parasite's overall basic reproduction number (eq. [2]); this boundary is the straight diagonal from $R_{0,1} = 1$ to $R_{0,2} = 1$ (fig. 1*B*). This is equivalent to the substitutable hosts of Holt et al. (2003).

Region 2. The parasite is maintained solely by host species 1 (the reservoir or "maintenance" host in the terminology of Haydon et al. 2002; $R_{0,1} > 1$) but causes spillover infections in host species 2, which contributes little to parasite persistence and is unable to maintain the parasite on its own ($R_{0,2} < 1$).

Region 3. The reverse of region 2, with species 2 being the maintenance host and species 1 the spillover host ($R_{0,2} > 1$ and $R_{0,1} < 1$).

Regions 4 and 5. Cases where infection is observed in both host species but through very different processes. In region 4 (which we term "facultative multihost parasitism"), either host species can maintain the parasite alone ($R_{0,i} > 1$ for $i = 1, 2$), whereas in region 5 (termed "obligate multihost parasitism"), the parasite needs both hosts in order to persist ($R_{0,i} < 1$ for $i = 1, 2$, but $R_{0,\text{tot}} > 1$).

Clearly, where a parasite lies within this framework will greatly alter the impact of control measures targeting either host species (Fenton and Pedersen 2005). As such, if the individual species' contributions to $R_{0,\text{tot}}$ (the $R_{0,i}$) can be empirically quantified, then it will be possible to determine which region a given host-parasite community resides in and make quantitative predictions regarding the control effort and targeting of particular host species required to shift the community below the threshold for disease persistence. Below, we describe an approach that can allow this. However, first we extend the framework to allow for more realistic transmission pathways among host species.

Improving the Framework: Allowing for Heterogeneous Sharing of Infective Stages

The homogenous transmission framework above assumes that all hosts are exposed to a single homogenous pool of parasite infective stages. In reality, however, this is unlikely to be the case. For environmentally transmitted parasites, for example, if different host species occupy relatively distinct spatial locations, infective stages released from one host will be more likely to be picked up by an individual of the same species than of the other species, giving rise to incomplete transmission overlap, or "assortative transmission." This will result in within-species transmission being greater than between-species transmission, thereby altering the overall R_0 and the relative contributions of the different species. Note that the methods we present can allow for disassortative transmission, where there is more between-species transmission than within-species transmission (see Holt et al. 2003 for a consideration of this case); however, we consider it less likely and so do not explicitly consider it here.

To model heterogeneous sharing of infective stages, we describe two distinct pools of infective stages in the environment, one (E_1) comprising infective stages released by host species 1 and the other (E_2) comprising those released by host species 2 (fig. 2*A*). Both species have access to either pool of infective stages, with infection occurring at rate β_{ij}, describing the rate at which host species i picks up infective stages released by host species j (in the case where $j = i$, this becomes β_{ii}, representing the rate of within-

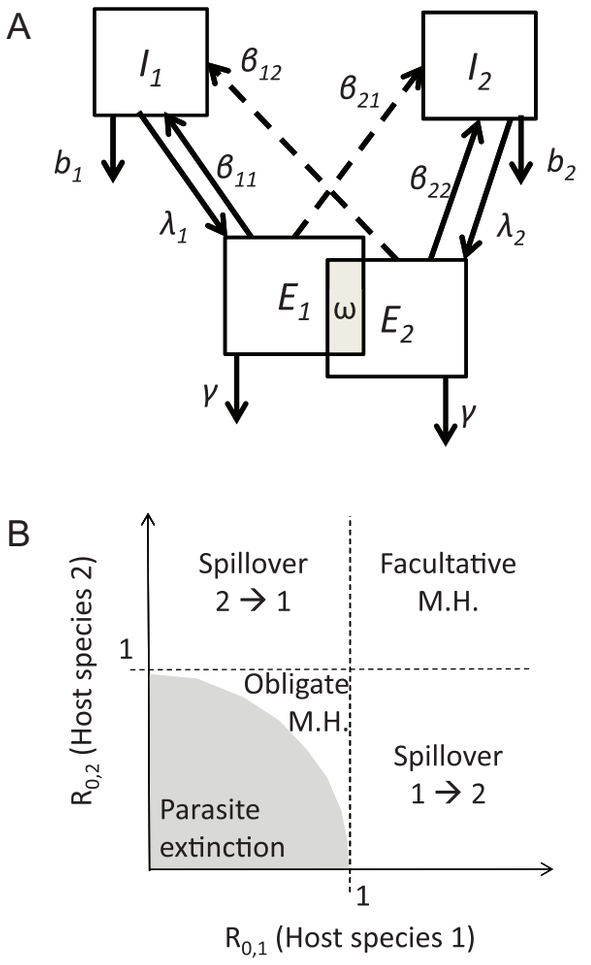

Figure 2: *A*, Schematic diagram of the heterogeneous transmission model, where ω represents the degree of transmission overlap. *B*, Graph of $R_{0,1}$–$R_{0,2}$ parameter space for the heterogeneous transmission model, showing the same five regions as in figure 1.

species transmission). The dynamics of the system are then given by

$$\frac{dP_i}{dt} = (1 - P_i)\beta_{ii}\left(\sum_{j=1}^{n} \omega_{ij}E_j\right) - b_iP_i, \tag{3a}$$

$$\frac{dE_i}{dt} = \lambda_iP_iH_i - \gamma E_i, \tag{3b}$$

where $\omega_{ij} = \beta_{ij}/\beta_{ii}$ is a measure of the degree of between-species transmission experienced by host species i relative to its rate of within-species transmission (see Rudge et al. 2013 for a description of a specific formulation for a parasite with an intermediate host stage). If $\omega_{ij} < 1$, then host species i is more likely to become infected by infective stages released from individuals of its own species than from those of the other species (between-species transmission is less than within-species transmission). However, if $\omega_{ij} = 1$, then the host is just as likely to encounter parasites released from either species (cross-species transmission equals within-species transmission), and we recover the homogenous model (eqq. [1], with $E = \sum_{i=1}^{n} E_i$). In what follows, we ignore the (perhaps rare) possibility that hosts are more likely to encounter infective stages released from a different host species than from its own ($\omega_{ij} > 1$). We also ignore the possibility of $\omega_{ij} < 0$ as a phenomenological representation of the dilution effect, where one species interferes with transmission to the other. A more accurate representation of this process would require explicit measurement of the rate of uptake of infectious stages from the environment, something that would be hard to quantify, so we do not consider it further here. Finally, note that the relative rates of cross-species transmission need not be symmetrical ($\omega_{ij} \neq \omega_{ji}$); for example, if the territory of species i is completely embedded within the territory of species j, then species i may be just as likely to encounter infective stages released from either host species ($\omega_{ij} \sim 1$), whereas species j may only rarely encounter infective stages from species i ($\omega_{ji} \ll 1$).

Incorporating assortative transmission alters how the host species combine to determine the parasite's overall R_0. Again, following the next-generation method of Diekmann and Heesterbeek (2000), the parasite's overall basic reproduction number within a community of two host species is now the following:

$$R_{0,\text{tot}} = \frac{1}{2}\left[R_{0,1} + R_{0,2} + \sqrt{(R_{0,1} + R_{0,2})^2 - 4R_{0,1}R_{0,2}(1 - \omega)}\right], \tag{4}$$

where $\omega = \omega_{12}\omega_{21}$. Deriving an analytical expression for $R_{0,\text{tot}}$ is more difficult (or even impossible) for more than two host species, but numerical solutions can readily be found (Dobson 2004). Now, unlike the previous case of homogenous mixing (eq. [2]), the contributions from each host species do not combine additively to determine $R_{0,\text{tot}}$. Furthermore, if $\omega < 1$, then the boundary separating the region where the parasite cannot persist and the region where it can only persist in the presence of the two host species bows outward (fig. 2*B*; see also Bowers and Turner 1997). Here the system becomes equivalent to the "weakly interacting hosts" scenario of Holt et al. (2003), showing that assortative transmission makes it less likely for a community of host species with $R_{0,i} < 1$ to maintain the parasite. In the limit when $\omega = 0$, the region of parasite extinction completely excludes the "obligate multihost" region, and it is no longer possible for two host species, each with $R_{0,i} < 1$, to combine to maintain the parasite, due to the lack of transmission between them (the "noninteractive hosts" scenario of Holt et al. 2003; see also Holt and Pickering 1985; Begon et al. 1992; Bowers and Turner 1997). The remaining regions in figure 2*B* are identical to those in the homogenous transmission framework (fig. 1*B*).

Locating Host-Parasite Systems within the Multihost Framework

To quantify the contributions of each host species to overall R_0 of a given parasite and locate it within the above conceptual framework, we generalize the approaches of Funk et al. (2013) and Rudge et al. (2013) to describe a generic environmentally transmitted parasite. As in their approaches, we quantify the host species contributions using a prevalence-based framework such as the one presented in equations (3), assumed to be at steady state (although results appear robust to deviation from this assumption; see "Discussion" for details). However, instead of having to estimate each parameter in the model independently, we estimate the $R_{0,i}$ directly. Specifically, by assuming the system is at equilibrium, we set equations (3) equal to 0 and rearrange to give

$$R_{0,i} = \frac{1}{(1 - P_i^*)\sum_{j=1}^{n}(\delta_{ij}\varepsilon_{ij}\upsilon_{ij}\omega_{ij})}, \tag{5}$$

where, as before, $R_{0,i} = \beta_{ii}\lambda_iH_i/\gamma b_i$, and P_i^* is the prevalence of infection in host species i, $\delta_{ij} = \lambda_j/\lambda_i$, $\varepsilon_{ij} = H_j/H_i$, $\upsilon_{ij} = P_j^*/P_i^*$, and $\omega_{ij} = \beta_{ij}/\beta_{ii}$. The infection prevalence can typically be measured, or at least estimated, for most host-parasite systems, as can the relevant variables for the δ_{ij}, ε_{ij}, and υ_{ij} composite parameters (host abundance, H_i, and the release of parasite infective stages per infected host, λ_i). Furthermore, if there is complete overlap of transmission between the host species (cross-species transmission equals within-species transmission, $\omega_{ij} = 1$), the contribution of each host species to the parasite's overall R_0 can be fully quantified, allowing the system to be placed directly within the multihost framework (e.g., fig. 1*B*).

In the case of heterogeneous transmission, the quantification must account for $\omega_{ij} \neq 1$. In some cases, it might be possible to use natural history observations as a proxy for the degree of transmission overlap among host species—for example, the observed degrees of home-range overlap among the different species or the degree of spatial correlation among species (e.g., Funk et al. 2013). In the absence of such information, one can investigate how uncertainty in the value of ω_{ij} affects the estimated $R_{0,i}$ by sampling across a plausible range of values for each of the ω_{ij} (e.g., Rudge et al. 2013). This procedure then asks what level of $R_{0,i}$ is needed to generate the observed prevalence in that host species under different degrees of input (cross-species transmission) from the other host species. Clearly, if there is little input from the other host species ($\omega_{ij} \sim 0$), then $R_{0,i}$ must be relatively high in order to generate the observed prevalence in host species *i*. Conversely, if there is complete transmission overlap ($\omega_{ij} = 1$), then $R_{0,i}$ is likely to be low. In the next section, we illustrate this process using empirical data for eight parasite species within their host communities of up to four host species.

Empirical Illustration of the Framework

Description of Empirical System

We collected data on small mammal (*Rodentia*) community composition and gastrointestinal parasite occurrence across 19 grids in six sites in Virginia, Tennessee, New York, and Connecticut (see Streicker et al. 2013 for details). Animals were captured for two to three consecutive nights at each site, and fecal samples were collected from Sherman live traps to identify gastrointestinal parasites and quantify parasite egg/oocyst shedding rates. We present results for the eight most common parasite species or pseudospecies (two nematodes, three cestodes, and three coccidia species) for which we have the greatest confidence in identification. We acknowledge limitations in this data set that would have to be overcome in order to make predictions for disease systems of more practical concern (e.g., the need for accurate parasite identification, ideally using molecular techniques, and longer-term sampling to accurately quantify prevalence). We therefore emphasize that we use these data purely as a convenient means to illustrate the application of the approaches described here. The data are deposited in the Dryad Digital Repository: http://dx.doi.org/10.5061/dryad.972mv (Fenton et al. 2015).

Estimating Host Species' Contributions to R_0 *from Our Empirical Data*

For each parasite species, we used equation (5) to calculate the host species–specific contributions to the parasite's basic reproduction number ($R_{0,i}$) using empirical data on species-specific patterns of abundance, parasite shedding, and prevalence of infection. To assess uncertainty in the contribution of each host species under different cross-species transmission scenarios, we calculated $R_{0,i}$ using a series of values of ω_{ij} ranging from 0 (no between-species transmission) to 1 (equal between- and within-species transmission) in steps of 0.01 (fig. 3, colored circles; the mean values of those 100 calculations are denoted by crosses, with error bars showing 2.5%–97.5% quantiles). Note that this procedure assumes complete symmetry in overlap among all the hosts ($\omega_{ij} = \omega_{ji}$, $\forall_{i,j}$), so we repeated the process, drawing all ω_{ij} values at random from a uniform distribution between 0 and 1 (thereby allowing $\omega_{ij} \neq \omega_{ji}$; fig. A1, red circles; figs. A1–A5 available online). However, there was very little difference in the subsequent predicted values of $R_{0,i}$ (cf. fig. 3 with fig. A1), so we focus here on the results of the former procedure. In what follows, given the variation in predicted $R_{0,i}$ values (arising from the variation in ω_{ij} values), we classify contributions of each host species depending on whether the majority of $R_{0,i}$ values are greater or less than 1.

Across the eight parasite species, we found a range of host-sharing scenarios (fig. 3). Four parasite species (*Eimeria* A, *Eimeria* B, *Eimeria delicata*, and *Capillaria americana*) clearly had one dominant host species with individual $R_{0,i}$ values greater than 1 and substantially greater than that of the other host species in the community, almost regardless of the values of ω_{ij}; in these cases, the dominant host is an obvious maintenance host, even in the absence of any other host species. For two of those species (*Eimeria* A and *Eimeria* B), there was evidence that a second host species could also be making a significant contribution to overall parasite maintenance, depending on the values of the ω_{ij}. Indeed, under some values of transmission overlap (particularly when ω_{ij} was very small; fig. 3, red circles), the estimated $R_{0,i}$ values for these secondary hosts often exceeded 1, suggesting that they could be maintenance hosts in their own right. Finally, for *Hymenolepis* A, it appears unlikely that any of the host species alone would be able to maintain the parasite under most scenarios of transmission overlap ($R_{0,i} < 1$ for all host species); hence, under the assumptions of our model, and with the quality of data available to us, it seems that this parasite may require multiple host species to be maintained (i.e., it is an obligate multihost parasite).

Figure 4 locates each of these parasites within the two-dimensional $R_{0,1}$–$R_{0,2}$ framework for the top two contributing host species for each parasite (the dominant host species is plotted on the *X*-axis in each case; note that we assume transmission heterogeneity is not constrained [$\omega_{ij} \neq \omega_{ji}$] for full characterization of uncertainty). Many parasite species (*Eimeria* B, *E. delicata*, *A. americana*, *C. americana*) appear to show spillover dynamics, occupying

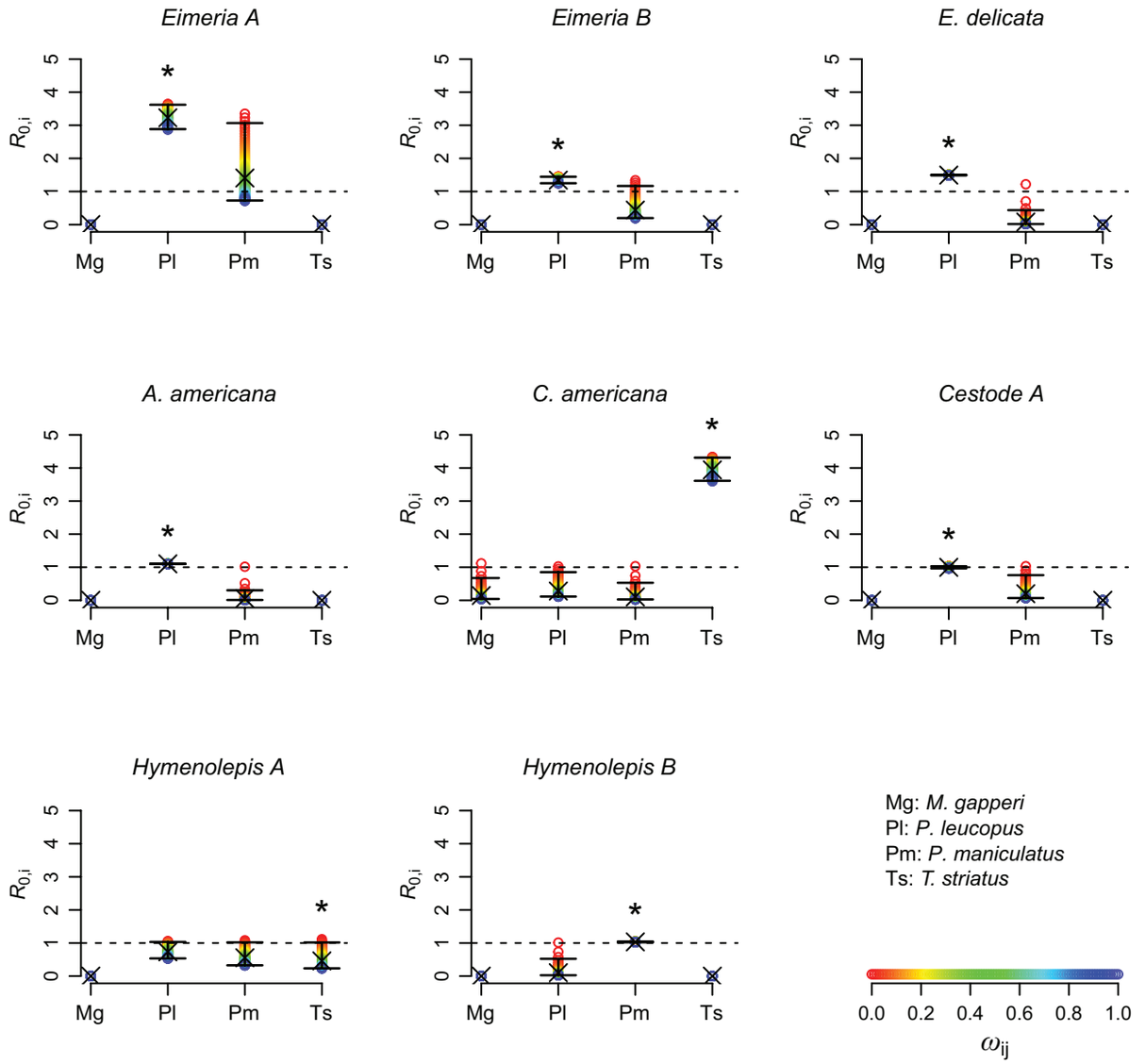

Figure 3: Estimated $R_{0,i}$ values for each of the four host species for the eight parasite species in the data set. Colored circles refer to the different values of ω_{ij} used for each calculation (color coded from red [$\omega_{ij} = 0$] to blue [$\omega_{ij} = 1$], assumed to be symmetrical for all host species in the community; $\omega_{ij} = \omega_{ji}$, $\forall_{i,j}$). Crosses denote the mean $R_{0,i}$ across the different ω_{ij} values, and error bars represent 2.5%–97.5% quantiles. Asterisks denote the dominant host species, based on the number of infected individuals.

the lower right-hand region of panels in figure 4, while two parasite species (Cestode A and *Hymenolepis* B) lie on the border with the region of obligate multihost parasite. In all these cases, there is a clear maintenance host species, with the other host(s) being unable to maintain transmission alone, suggesting that targeted removal of the maintenance host would eradicate the parasite from the community (assuming no compensatory growth by the remaining species in the community postremoval). For two species (*Eimeria* A and possibly *Eimeria* B), there is evidence that these species may be facultative multihost parasites (lying toward the top right-hand region of panels in fig. 4), depending on the precise network of transmission (i.e., the ω_{ij} values) among the host species. If so, this would suggest that these parasite species can be maintained by more than one host species alone. Finally, *Hymenolepis* A seems to sit firmly within the region of being an obligate multihost parasite, suggesting that it cannot be maintained by any single host species alone (assuming no compensatory growth in host abundance), but it requires transmission among multiple host

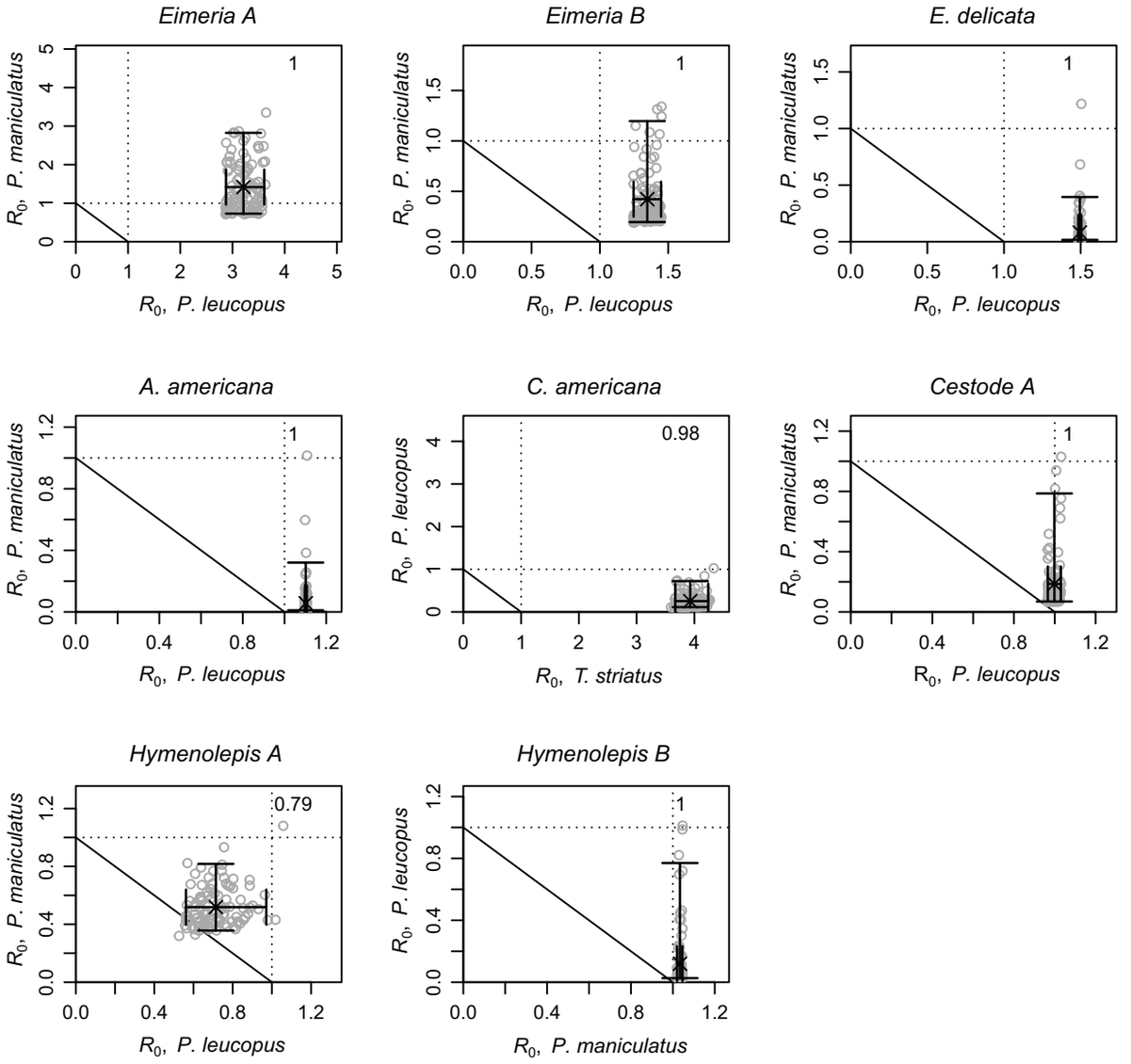

Figure 4: Graph of $R_{0,1}$–$R_{0,2}$ parameter space for the two dominant host species for each of the eight parasite species in the data set. Circles refer to the different values of ω_{ij} used for each calculation (assumed to vary between all host species pairs in the community; $\omega_{ij} \neq \omega_{ji}$). Crosses denote the mean $R_{0,i}$ across the different ω_{ij} values, and error bars represent 2.5%–97.5% quantiles. The number in the upper-right corner of each plot denotes the proportion of $R_{0,\text{tot}}$ explained by $R_{0,1}$ and $R_{0,2}$.

species in order to be maintained. Note that, for this species, the top two hosts only contribute ~80% of $R_{0,\text{tot}}$, highlighting that there is a third host species making a not insignificant contribution to transmission (fig. 3).

Predicted Impact of Targeted Control

The above section illustrates how placing host species contributions to $R_{0,\text{tot}}$ within the framework provides an intuitive appreciation of how host community configuration affects parasite persistence. Here we extend those insights to make specific predictions about the likely consequences of control for parasite persistence and prevalence. We use equation (5), parameterized with the estimated values of $R_{0,i}$ for each parasite species, to calculate the resulting equilibrium prevalence (P_i^*) for the remaining host species in the community following targeted control (e.g., treatment or culling) of the host species with the highest initial number of infected individuals. Control is assumed to be 100% effective, such that contribution to parasite transmission

from the targeted host species is completely blocked. Note that we assume that the imposed control does not alter the abundances of the remaining host species in the community (the H_i are unchanged from precontrol levels). Clearly, the effect of targeted control would be altered if remaining host species increased following control. For example, as shown by Bowers and Turner (1997), competition between hosts could suppress combined densities sufficiently to keep $R_{0,\text{tot}} < 1$, such that the system sits in the "parasite extinction region" (fig. 2*B*); in this scenario, removal of one of the host species may then allow the remaining species to increase sufficiently to drive $R_{0,\text{tot}} > 1$, allowing the parasite to persist (see also Begon 2008). This interplay between competition and community $R_{0,\text{tot}}$ could be incorporated within the framework by allowing the remaining species to increase in abundance following removal of the target host species, based on estimated or hypothesized competition coefficients among species (Holt and Pickering 1985; Bowers and Turner 1997; Greenman and Hudson 2000; Begon 2008). However, for simplicity, we ignore this possibility here.

Overall, the previous intuitive predictions about the consequences of targeted control were upheld by this quantitative analysis; removal of the dominant host species (fig. 5, asterisks) was nearly always predicted to bring about elimination of the parasite in the remaining host community (fig. 5). In most cases, infection persisted only when transmission overlap was negligible ($\omega_{ij} \sim 0$, such that each host species maintains infection in virtual isolation from other hosts). However, there was strong evidence to suggest that *Eimeria* A infection could be maintained by *Peromyscus maniculatus*, even in the complete absence of the dominant host *Peromyscus leucopus*. Hence, this parasite species appears to be something of a "facultative multihost parasite," able to infect and be maintained on more than one host species. Furthermore, there was some evidence that *Eimeria* B, as well as *Hymenolepis* A, was able to persist in the absence of the dominant host species but only if transmission overlap was low ($\omega_{ij} \to 0$), such that those secondary host species were able to maintain infection in relative isolation.

Discussion

Understanding the spread of parasites and pathogens through multihost communities and quantifying the contributions each host species makes to the transmission, persistence, and abundance of parasites within those communities remain major challenges in the management of infectious diseases. To address these challenges, we first modified an existing conceptual framework (Holt et al. 2003) to provide an intuitive method for classifying different kinds of parasite-host sharing within empirical multihost communities, based on host contributions to the parasite's overall basic reproductive number across the host community ($R_{0,\text{tot}}$). This framework clearly delineates parasites that show spillover dynamics (maintained by one key host) from those that either require multiple host species in order to persist or can persist on any of several host species. Importantly, we show how we can use this not just as a conceptual framework but as a practical tool in evaluating host species contributions to parasite persistence. Specifically, we combined this framework with a generalized analytical approach (modified from the system-specific approaches presented by Funk et al. 2013; Rudge et al. 2013) and showed how to quantify host-species contributions to a parasite's community-level R_0, infer proximity of the system to important thresholds of parasite persistence/eradication, and predict the community-wide outcomes of targeted control, all using readily collected parasitological data. Together, this combination of approaches provides a powerful method of identifying optimal management approaches for circulating diseases within natural ecological communities, where detailed understanding of system dynamics is rarely available.

One of the biggest challenges with understanding the movement of parasites through multihost communities is estimating the rates of between-species transmission relative to within-species transmission. We characterized these relative rates in terms of the degree of "transmission overlap" between the host species, described by the ω_{ij} terms. However, estimating this overlap for natural communities is not straightforward. Assuming such heterogeneous transmission arises primarily from spatial segregation of host species, it may be possible to infer likely degrees of transmission overlap from measures of home-range overlap or habitat usage between species (Carslake et al. 2006; Funk et al. 2013). Alternatively, analysis of parasite sequence data from across the host community could reveal likely rates of cross-species transmission (Streicker et al. 2010; Biek et al. 2012). If these approaches are not possible, it would be necessary to sample values of ω_{ij} across the feasible range, as we have done here, to assess uncertainty in parameter estimates (e.g., Rudge et al. 2013). Regardless of how it is done, estimating this transmission overlap can be important, as it affects both the boundary for parasite persistence (fig. 2; see also Holt et al. 2003) and the estimated values of species-specific contributions to $R_{0,\text{tot}}$ (estimated $R_{0,i}$ values increase as ω_{ij} decreases; fig. 3). Notably, however, for many of the communities analyzed here, uncertainty in the degree of transmission overlap did not greatly alter either the location of the system within the multihost framework (fig. 4) or the predicted consequences of targeted control (fig. 5). Indeed, although the circulation of parasites within these ecological communities appears highly complex, the dynamics of transmission in most cases appeared to be driven by just

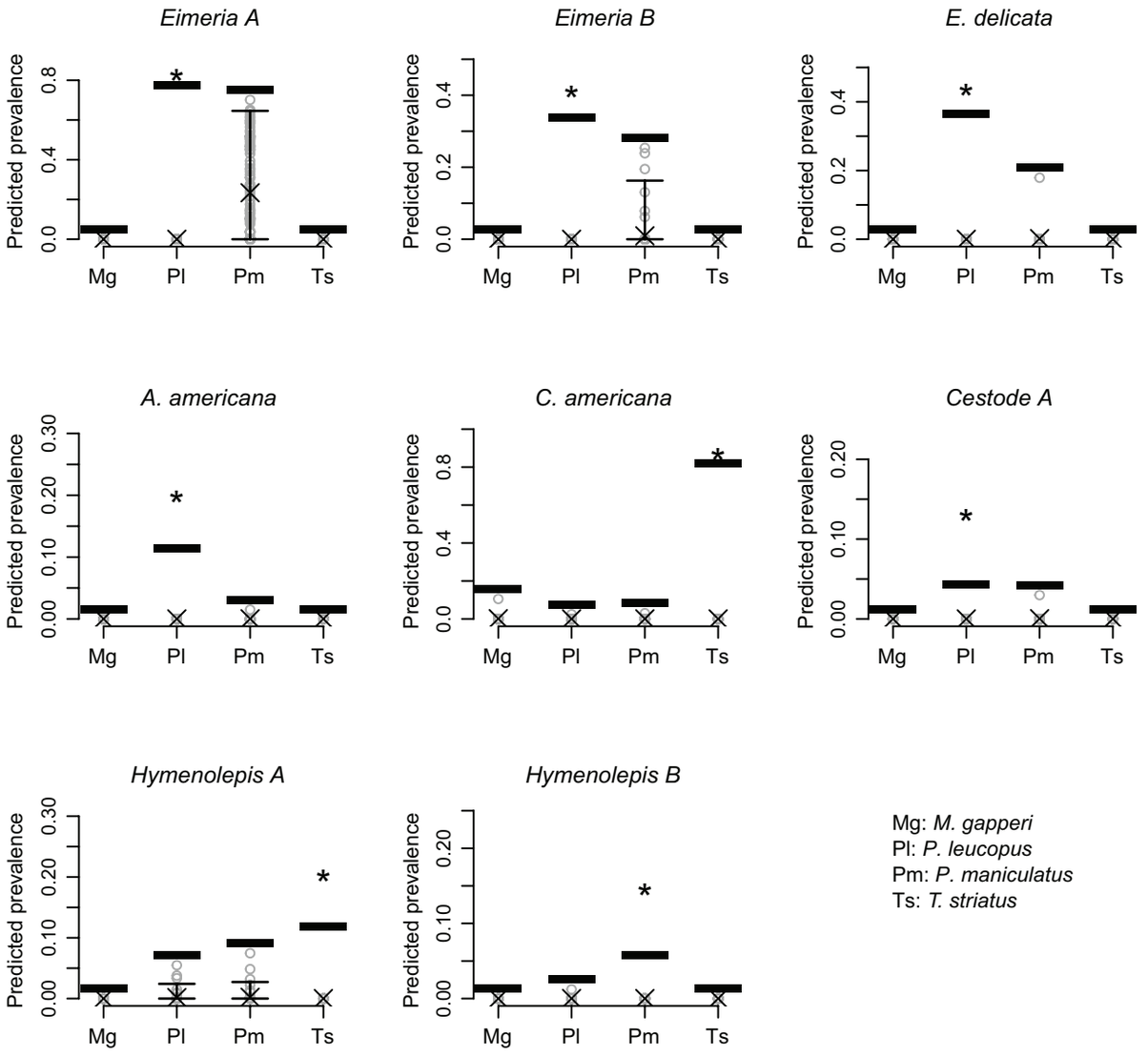

Figure 5: Predicted prevalence of infection in the remaining host species in the community following 100% efficacy control of the dominant host species (denoted by asterisks). Circles refer to the different values of ω_{ij} used for each calculation (assumed to vary between all host species pairs in the community; $\omega_{ij} \neq \omega_{ji}$). Crosses denote the mean predicted prevalence across the different ω_{ij} values, and error bars represent 2.5%–97.5% quantiles. Black bars show observed infection prevalence in the absence of control.

one host species. Studies of other multihost communities similarly suggest that there is often a dominant, key host responsible for the majority of transmission of the focal parasite or pathogen (e.g., LoGiudice et al. 2003; Kilpatrick et al. 2006; Lembo et al. 2007; Roeder et al. 2013). Hence, it may be that much of the apparent complexity of many multihost systems could reasonably be simplified to focus on one or two key components of the community. Clearly, there will be exceptions to this (e.g., *Eimeria* A and *Eimeria* B in our study), where it appears the parasite could be maintained by secondary species in the absence of the dominant species. Importantly, the approaches described here provide a clear, quantitative method for differentiating these cases.

The accuracy of the quantitative predictions will obviously depend greatly on the quality of the data available. Of crucial importance is to ensure accurate identification of parasite species across the different host species, ideally using molecular techniques, to distinguish true multihost parasites from multiple apparently similar host-specific species (Streicker et al. 2010). Furthermore, it is essential that sampling errors and biases are minimized or at least quantified. For example, accurately quantifying infection status can

depend greatly on the sensitivity and the specificity of the diagnostic method used; hence, Rudge et al. (2013) used a Bayesian framework to quantify "true" prevalence, given uncertainties in the diagnostic tests. Such problems are magnified when attempting to quantify infection burdens (e.g., for parasitic helminths), making parameterization of intensity-based models highly problematic and tending to result in underestimation of R_0 (Barbour 1996). We therefore used a prevalence-based framework that, though ignoring heterogeneity in infection burdens, provides a more robust framework for quantifying transmission and is often used to aid parameterization of helminth models from field data (Hairston 1965; Williams et al. 2002; Ishikawa et al. 2006; Gray et al. 2008; Montresor et al. 2013; Rudge et al. 2013). Explicitly incorporating infection intensities is not possible within the current framework, and so the consequences of relaxing this assumption are unclear. However, this issue could be explored using either a classic host-macroparasite framework, where the degree of parasite aggregation is imposed on the system (Anderson and May 1978), or an individual-based framework, where it emerges dynamically (e.g., Fenton et al. 2010). Finally, it is important to consider sampling biases, particularly in the estimation of host abundances, where different host species may have different probabilities of being sampled (e.g., trap success varies between species) or infection status may influence capture success (e.g., whether infected animals are more/less likely to be caught than uninfected animals). Similar to the adjustment described in Streicker et al. (2013), if estimates of per capita trap probability for each species are available, they could be used to correct the observed host abundances in equation (5) (contained within the ε_{ij} terms). If such estimates are not available, then uncertainty arising from possible differential capture success could be incorporated by repeatedly sampling from a plausible distribution (Streicker et al. 2013).

Related to the above considerations, one key assumption we make is that the system is at equilibrium. Although it is unlikely that many natural systems are truly at equilibrium, they may not be far from it, and results may be relatively insensitive to deviations from this assumption. To assess the extent to which our estimated $R_{0,i}$ values are affected by this assumption, we ran a series of simulations of a hypothetical two-host community (see app. for details) in which we allowed the abundance of each host species to fluctuate around a mean value, either stochastically (fig. A2) or regularly (to mimic seasonal or periodic cycles in abundance), with the host species cycling either out of phase (figs. A3, A4) or in phase (fig. A5) with each other. Overall, the estimated $R_{0,\text{tot}}$ values and the estimated ratio of the $R_{0,i}$ values did not differ greatly from the true values in the models, even for large-amplitude fluctuations in host abundance (figs. A2, A3) and even if there were asymmetries in the extent of transmission overlap between the species (fig. A4). Only when host species underwent large-amplitude fluctuations completely in phase with each other did the estimated values begin to differ significantly from the true values (fig. A5). Clearly, this sensitivity analysis is not exhaustive, and there may be conditions under which the estimated values depart significantly from the true values. However, we suggest that our approach is relatively robust to the assumption of being at steady state. Crucially, however, this depends greatly on the accuracy of estimates of host abundance, a vital input parameter for the calculation (eq. [5]). For this reason, we would suggest that snapshot estimates of abundance are unlikely to be sufficient, so long-term data on host abundances should be used where possible. In systems where the equilibrium assumption might lead to significant errors in estimation, values of $R_{0,i}$ could be estimated by applying contemporary model-fitting techniques to long-term time series data on host abundances and infection prevalences (e.g., Ionides et al. 2006; Shrestha et al. 2013).

There is currently great appreciation of the community context of disease. Many parasites and pathogens of human health, economic, or conservation importance circulate within multihost reservoir communities. Without an understanding of how parasites flow within and between host species in these communities, it is impossible to anticipate disease emergence from them or assess how shifts in those communities (e.g., arising from host species losses or gains associated with land-use change, climate change, or human management) will affect disease risk and occurrence within them. The approaches we have described provide an intuitive and accessible means to quantify the contributions that individual host species make to parasite transmission and persistence, thereby providing a quantitative basis from which to make informed decisions about the management of multihost parasites.

Acknowledgments

A.F., A.B.P., and O.L.P. are supported by grants from the Natural Environment Research Council (NE/I024038/1 and NE/I026367/1), and A.B.P. is funded by an Advanced Fellowship as part of a Wellcome Trust Strategic Grant for the Centre for Immunity Infection and Evolution (grant 095831). D.G.S. was supported by National Science Foundation (NSF) grant DEB-1020966 and a Sir Henry Dale Fellowship jointly funded by the Wellcome Trust and the Royal Society (grant 102507/Z/13/Z). A.B.P. was supported by an NSF Dissertation Improvement Grant, Sigma Xi grants-in-aid, and a grant from the American Society of Mammalogists to fund the data collection. We thank the Mountain Lake Biological Station and the Cary Institute of Ecosystem Studies for use of their facilities and all the field assistants and landowners for their help with the data collection.

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Associate Editor: Pej Rohani
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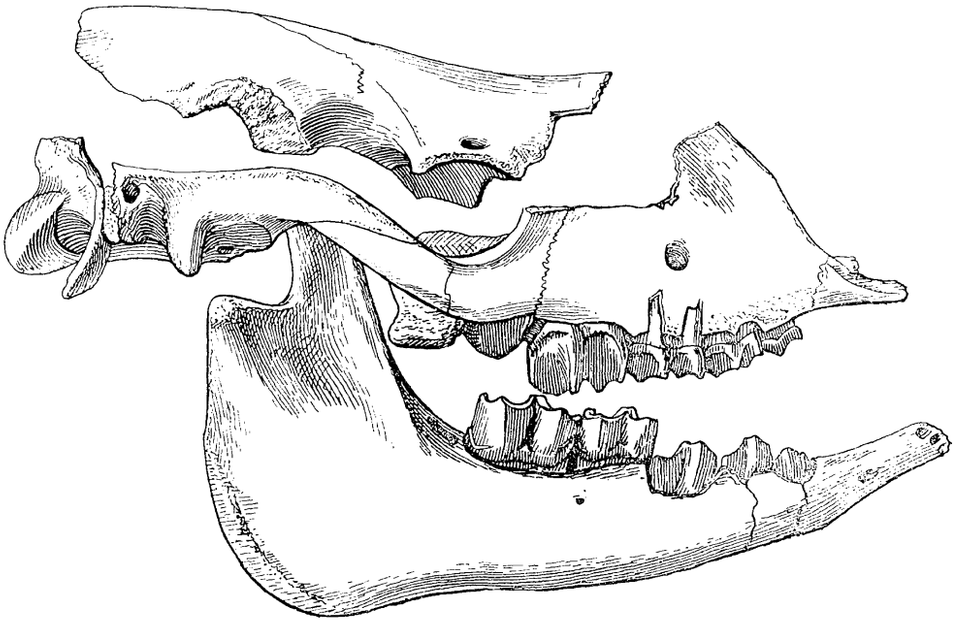

"The skeletal structure of Moropus is a unique combination of characters. The phalanges are highly modified, terminating in cleft ungues which were, no doubt, covered by heavy claws; otherwise the skeleton is distinctively of an ungulate type, most closely resembling the Perissodactyla.… Some species are as large as an African rhinoceros, or even larger." From "Preliminary Notes on Some American Chalicotheres" by O. A. Peterson (*The American Naturalist*, 1907, 41:733–752).