Parasite Transmission in Size-Structured Populations

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Abstract:

Host heterogeneity can impact parasite transmission, but determining underlying traits and incorporating them into transmission models remains challenging. Body size is easily measured and influences numerous ecological interactions, including transmission. In the snail-schistosome system, larger snails have a higher exposure to parasites but lower susceptibility to infection per parasite. We quantified the impact of size-based heterogeneity on population-level transmission by conducting transmission trials in differently size-structured snail populations and competing size-dependent transmission models. Populations with greater proportions of large snails had lower prevalence, and small snails were shielded from infection by co-occurring large conspecifics. Using the winning size-explicit model, we then estimated that schistosome transmission potential varies dramatically across time due to seasonal changes in snail population size structure. Thus, incorporating traits such as body size, which are impacted by and directly affect host ecology, into transmission models could yield insights for natural dynamics and disease mitigation in many systems.

I. Introduction:

Parasite transmission drives the ecological and evolutionary dynamics of host-parasite interactions. Therefore, demystifying the host and parasite factors that influence transmission is critical for characterizing disease dynamics and successfully managing any host-parasite system (Lloyd-Smith *et al.* 2009). In particular, transmission theory that ignores host variation and instead treats hosts as uniform individuals with identical infection risk matches data poorly and cannot address critical themes in disease ecology, such as superspreading and parasite aggregation (Lloyd-Smith *et al.* 2005). In order to more accurately predict disease dynamics in natural populations, it is important to consider the sources of host variation and their consequences for transmission because hosts can differ in many ways (Dwyer *et al.* 1997; Hall *et al.* 2007; Strauss *et al.* 2019).

Schistosomes are the causative agent of schistosomiasis, a Neglected Tropical Disease that is second only to malaria in its worldwide impact on human health and disproportionately affects individuals in poor, rural environments (Gryseels *et al.* 2006). Over 200 million people worldwide are currently infected, and schistosomiasis accounts for approximately 200,000 deaths per year (World Health Organization 2022). Schistosomes have a complex life cycle and obligately cycle between mammalian and snail hosts. One source of host heterogeneity that impacts schistosome transmission is snail body size: larger snails experience higher exposure rates but are less likely to become successfully infected on a per parasite basis (Niemann & Lewis 1990; Théron *et al.* 1998). The importance of body size in transmission to the snail host becomes even more apparent when considering the vast range in host snail body size. For example, a neonate *Biomphalaria glabrata*, an intermediate host species for *Schistosoma*

mansoni, is born at ~0.75 mm and can grow up to 40 mm under natural conditions over its lifetime (Jarne *et al.* 2011). This growth trajectory corresponds to a ~150,000-fold increase in biomass, akin to the difference between a mouse and an elephant (White 2010).

Despite the recognition that body size influences these mechanistic components of schistosome transmission decades ago in isolated, individual snails, the consequences of this relationship when scaled to size-structured populations have remained uninvestigated. Schistosome exposure in a host is irreversible, meaning a schistosome cannot leave a snail once it has entered, even if it fails to successfully infect the host. Therefore, snails that are invaded by parasites indirectly reduce the infection risk of others in the population (King *et al.* 2011). If size-dependent transmission effects scale up to the population level, then we predict that the presence of larger hosts will contribute to a within-species dilution effect by shielding their smaller conspecifics from parasite exposure while also being less likely to become infected themselves.

We investigated this hypothesis by conducting laboratory transmission trials of *Schistosoma mansoni* in *Biomphalaria glabrata* populations of varying size structures. We then used these data to compete candidate models of size-dependent transmission, and additionally used existing field data of *B. glabrata* population size structures to estimate how parasite success may change under natural conditions over time solely due to the dynamics of population size structure. In many host-parasite systems researchers are still in the nascent phase of breaking down the complex interaction of host traits that result in heterogeneous parasite transmission (Sweeny & Albery 2022). In the snail-schistosome system, body size is a measurable trait with the potential to influence parasite transmission via multiple mechanisms, but it remains relatively unexplored

how this individual-level trait scales up to influence transmission within and between populations. Incorporating this fundamental host trait into our understanding of schistosome transmission could yield important insights into transmission risk and disease control of this widespread and debilitating parasite, and this approach can be applied broadly to other disease systems and critical traits.

II. Methods

Snail Maintenance. *B. glabrata* snails of the NMRI strain were maintained under favorable conditions. Snails were kept in HHCOMBO artificial lake water (Baer & Goulden 1998) at 26°C with a 12:12 light:dark cycle. Snails were fed a diet of fish flakes (Omega One) and chicken feed (Nutrena Meatbird Crumbles) suspended in 1% agar *ad libitum.*

Experimental Design. We conducted the experiment using a fully factorial design: five population size-structures, each with a total of 18 snails, were exposed to three densities of parasites in 24-hour transmission trials in 15-liter tanks, creating 15 total treatment combinations. *B. glabrata* were first assigned into three size classes by shell diameter: "small" (2-3 mm), "medium" (6-8 mm), and "large" (12-15 mm). Different size-structures were determined by the ratio of snails from each of the three size classes. The uniform size structure consisted of 18 snails from the same size class: "uniform small" (1:0:0), "uniform medium" (0:1:0), and "uniform large" (0:0:1). "Equal" size-structured mesocosms had 6 snails from each size class (1:1:1). "Small skewed" size structures contained 12 snails from the smallest size class and 3 snails from both the medium and large size classes (4:1:1). Parasite densities also varied between the tanks: 36 (2 miracidia/snail), 144 (8 miracidia/snail), and 256 parasites per tank (14 miracidia/snail). We obtained *S. mansoni* eggs from experimentally infected mice livers and

96 purified and hatched eggs to obtain miracidia (Dinguirard *et al.* 2018). We conducted four
97 randomized blocks of these trials in which each block contained one replicate of each treatment.
98 To control for potential batch effects on parasite infectivity across the temporal blocks, a control
99 group consisting of all medium snails individually placed in 24 well plates was simultaneously
100 exposed to each of the parasite densities.

101 To quantify size-based susceptibility we also conducted transmission experiments in which 120
102 snails ranging from 0.5mm to 15mm were individually placed in well plates with 5 mL COMBO.
103 These snails were exposed to either 2 or 6 miracidia over 24 hours. Due to the small volume of
104 water used in the individual well plate exposures, we assume that snails were exposed to all
105 parasites present in these trials, an assumption justified by prior experiments (Niemann & Lewis
106 1990).

107 **Infection Diagnosis.** 24 hours post-exposure, all snails were collected, sorted by size and
108 treatment group, and maintained for 5 weeks (longer than the minimal prepatent period for *S.*
109 *mansoni* in favorable conditions). Snails were diagnosed visually by parasite shedding in
110 individual well plates at 4- and 5-weeks post-exposure to obtain prevalence data (Asch 1972).
111 Snails were diagnosed as "infected" if we observed *S. mansoni* cercariae in their well plate, or
112 "uninfected" if no cercariae were detected. Snails infected at week 4 were sacrificed, while
113 uninfected snails were returned to their tanks to repeat this process at week 5. Snails that died
114 while prepatent or between weeks 4 and 5 of the shedding process were not included in our
115 results (6.25% of all snails).

116 **Model Creation and Maximum Likelihood Estimation of Parameters**. We then built
117 deterministic size-dependent transmission models for parameterization and competition using the
118 experimental data (Box 1). Each model separates the transmission process into two underlying

processes: exposure to parasites and susceptibility to infection given exposure. The models varied based on whether these processes were functions of snail body size (represented as the longest shell diameter, hereafter "length"). In the null model, all functions of length are constants, therefore no variation in prevalence by size-structure can be predicted. We also considered two models in which one parameter varied with body size: (1) the size-dependent exposure-only, in which only exposure is a function of host body size, and (2) the size-dependent susceptibility only, in which only susceptibility is a function of body size. Finally, we considered a fully size-dependent model, which varies both exposure (ε) and susceptibility (σ) with host body size. The three models that contain some element of size-dependence all predict that different size classes within a single size-structured population can experience different levels of infection prevalence and that populations of differing size-structures can vary in their overall population infection prevalence. For all models with a size-dependent component, we investigated two alternative parsimonious representations: linear and exponential functions of host length. For each model, we solved for the expected prevalence in each size class present analytically, given the size structure and parasite density of that treatment. We then used the bbmle package in R to conduct maximum likelihood estimation to estimate parameters for ε and σ for each model using the binomial error distribution with the probability of "success", i.e., infection, equal to the expected prevalence for that size class given the experimental conditions and parameter values (Strauss *et al.* 2019; Bolker & R Development Core Team 2021). Lastly, to control for potential differences in infectivity among parasites across the different temporal blocks, we incorporated a block effect for the baseline susceptibility parameter, σ_0. Using corrected Akaike's information criteria (AICc) in R (R Core Team 2021), we competed the fully

size-dependent model against the size-dependent exposure only, the size-dependent susceptibility only, and the size-independent null model.

Box 1. Model construction.

We constructed deterministic transmission models that tracked changes in the densities of susceptible hosts, S_i and infected hosts, I_i, in an arbitrary number of host size classes, *i*, as well as free-living parasites, P, with differential equations:

$$\frac{dS_i}{dt} = -\beta_i * S_i * P \qquad \text{Eq. 1}$$

$$\frac{dI_i}{dt} = \beta_i * S_i * P \qquad \text{Eq. 2}$$

$$\frac{dP}{dt} = -\sum_{i=1}^{n}(\varepsilon_i * (S_i + I_i)) * P \qquad \text{Eq. 3}$$

We parameterized these models based on a short-term infection experiment, therefore we ignored processes that occur at longer time scales such as birth and deaths of hosts and parasites (Civitello & Rohr 2014). For each model we broke down the transmission rate (β_i) into two main components, exposure (ε_i) and susceptibility (σ_i), that we allowed to vary with size (L_i). Prevalence can be directly calculated within each size class (i), based on the initial density of susceptible individuals in each size class, $S(0)_i$, :

Model	Transmission rate (β)	Prevalence Equation
Size-independent (Null)	$\varepsilon_0 * \sigma_0$	$1 - e^{\left(-\sigma_0\left(\frac{\varepsilon_0}{\sum \varepsilon_0 S(0)_i}\right)P_0\left(1-e^{\left(-t\left(\sum \varepsilon_0 S(0)_i\right)\right)}\right)\right)}$
Size-dependent exposure	$(\varepsilon_0 * e^{(\varepsilon_{sz} * L)}) * \sigma_0$	$1 - e^{\left(-\sigma_0\left(\frac{\varepsilon_i}{\sum \varepsilon_i S(0)_i}\right)P_0\left(1-e^{\left(-t\left(\sum \varepsilon_i S(0)_i\right)\right)}\right)\right)}$
Size-dependent susceptibility	$\varepsilon_0 * (\sigma_0 * e^{(\sigma_{sz} * L)})$	$1 - e^{\left(-\sigma_i\left(\frac{\varepsilon_0}{\sum \varepsilon_0 S(0)_i}\right)P_0\left(1-e^{\left(-t\left(\sum \varepsilon_0 S(0)_i\right)\right)}\right)\right)}$
Fully size-dependent	$(\varepsilon_0 * e^{(\varepsilon_{sz} * L)}) * (\sigma_0 * e^{(\sigma_{sz} * L)})$	$1 - e^{\left(-\sigma_i\left(\frac{\varepsilon_i}{\sum \varepsilon_i S(0)_i}\right)P_0\left(1-e^{\left(-t\left(\sum \varepsilon_i S(0)_i\right)\right)}\right)\right)}$

Application to field data

We then estimated the influence of population size structure on schistosome transmission for a snail population in an endemic setting experiencing natural variation in size structure throughout the year. We used WebPlotDigitizer (Rohatgi 2020) to gather snail size data over time from a

168 population of *Biomphalaria tenagophilia* in del Plata Basin, Argentina from 2000-2001 (Rumi *et*
169 *al.* 2009). Then, using these size structures, we used the fully size-dependent transmission model
170 to estimate the probability of successful infection by a schistosome given that schistosome makes
171 irreversible contact with a snail in the population for each time point. Specifically, for each size
172 class (1 mm increment), we estimated the probability that the miracidium would contact and
173 subsequently infect a snail in that size class based on the relative abundance of snails in that size
174 class and the size-dependent exposure and susceptibility traits of all snails in the population at
175 that time. We then summed infection probabilities across all snail size classes for each time point
176 to get an overall probability of infection (Eq. 4):

177 $$P(Infection|Snail\ contact) = \sum_{i=1}^{n} 1 - e^{-\sigma_0 * \left(\frac{\varepsilon_0}{\varepsilon_0 * S_i}\right) * P_0 * (1 - e^{-t(\varepsilon_0 * S_i)})} \quad \text{(Eq. 4)}$$

178 We estimated 95% confidence intervals for this quantity by drawing estimated transmission
179 parameters from the joint 95% confidence interval set inferred from the experimental results
180 (Bolker 2008). We contrasted these estimates to the 95% confidence interval for infection
181 success given exposure for the size-independent (null) model, which makes a constant prediction
182 of parasite success, independent of size structure.

183 **<u>III. Results</u>**

184 **Experimental Transmission Experiments**

185 Population prevalence for snails varied by size structure and parasite density (Fig. 1). The
186 uniform small size structure had the greatest prevalence at each parasite density (36 parasites:
187 0.37 ± 0.026 [mean ± SE]; 144 parasites: 0.69 ± 0.078; 256 parasites: 0.83 ± 0.034). The uniform
188 large size structure had the smallest prevalence of the tanks at the lowest and highest parasite
189 densities (36 parasites: 0.13 ± 0.011; 256 parasites: 0.32 ± 0.13).

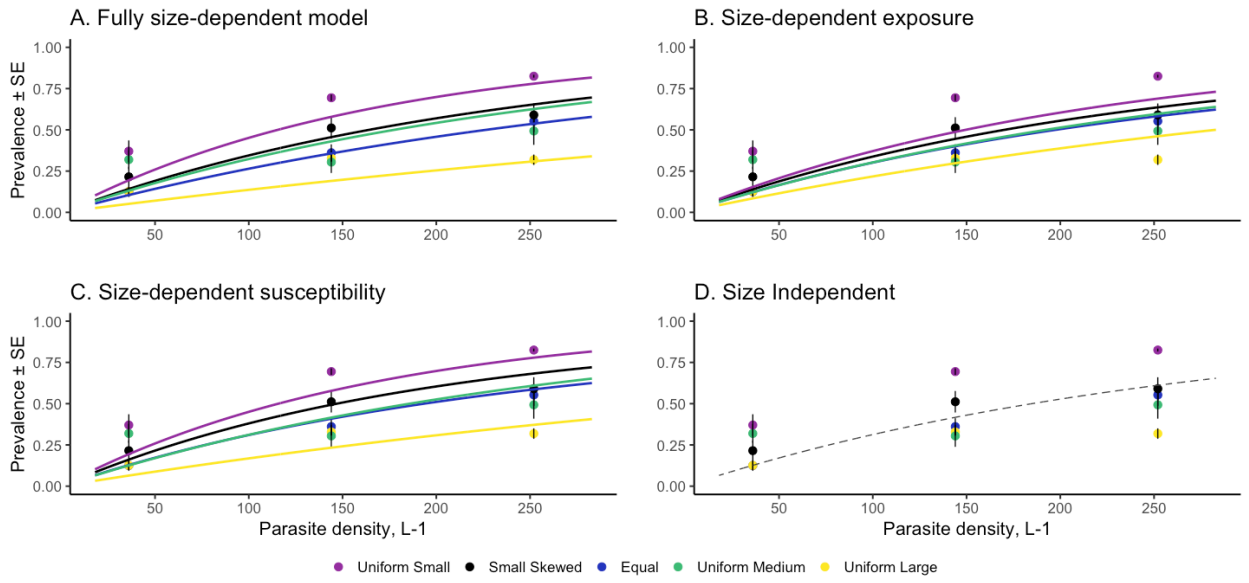

Figure 1. Schistosome prevalence in snail populations with differing size structures. Points represent mean ± SE prevalence in each population structure and lines represent best model fits. Each panel depicts one of the candidate transmission models; experimental data is identical between panels. A fully size-dependent transmission model (**A**) in which exposure and susceptibility vary with body size outperformed all other candidate models. Allowing only exposure to vary with body size (**B**) tended to underestimate prevalence in populations with a greater proportion of small individuals, while a model in which only susceptibility varies with body size (**C**) performed better than exposure-dependence, it did especially poorly at predicting prevalence of uniformly large populations. A null model with no size-dependence (**D**) is unable to make different predictions in differently size-structured populations, and thus has a very poor fit to the observed data.

Within size classes, the average prevalence for small snails varied by population size structure and parasite density (Fig 2). Small snails in the uniform small size structure had the highest prevalence across parasite densities (Fig 2.A, while medium and large snails did not show large differences between size structures (Fig 2.B,C).

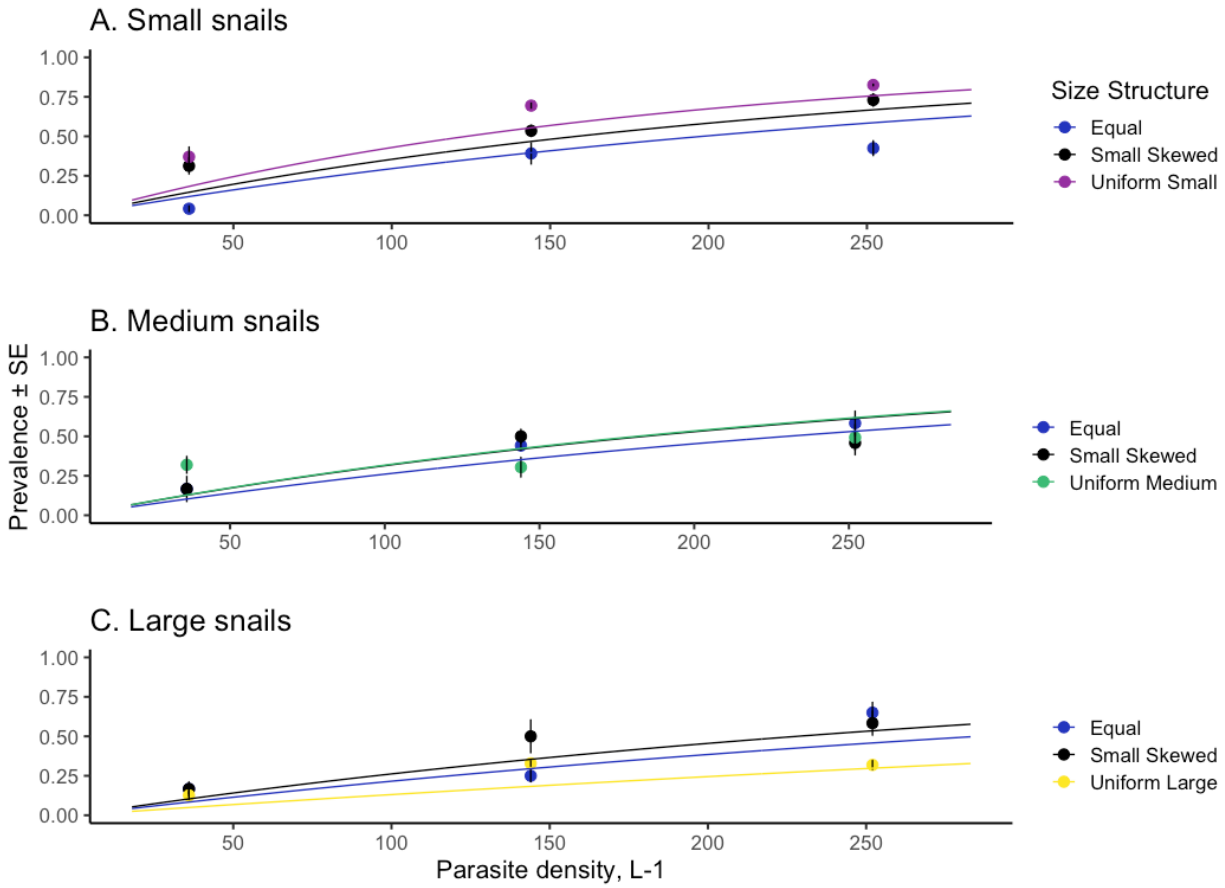

Figure 2. Schistosome prevalence within size classes in snail populations with differing size structures. Points represent average prevalence in each population structure, n=4 replicates per treatment; lines represent fits from the winning candidate model with full size dependence. A) Small snails B) Medium snails C) Large snails.

Transmission model competition

The size-independent null model performed poorly (Table 1). It either over or underestimated transmission depending on the population size-structure (Fig 1D). Exposure-only size dependence and susceptibility-only size dependence performed better (Table 1), but still tended to underestimate schistosome prevalence especially at lower parasite densities (Fig 1B, 1C). A fully size-dependent model performed far better than other candidate models (Table 1). An exponential relationship between body size and exposure and susceptibility outperformed a linear relationship

(Table S1, Fig S1), therefore we focus in the main text on comparing size-based models with exponential function(s) to the null model.

Table 1. Parameter estimates and model selection statistics

Model	Maximum Likelihood Parameter Estimates				AIC	ΔAIC	Akaike weight
	ε_0	ε_L	σ_0	σ_L			
Fully size-dependent	0.64	--	0.151	--	995.1	0	>.999
Size-dependent susceptibility	1.04	-0.085	0.162	--	1029.8	34.7	<0.001
Size-dependent exposure	0.669	--	0.305	-0.105	1083.6	88.5	<0.001
Size-independent (null)	0.25	0.184	0.609	-0.214	1116.8	121.6	<0.001

Maximum likelihood estimates for size-dependent exposure and susceptibility from the fully size-dependent model allow for predictions of exposure(ε), susceptibility(σ), and transmission ($\beta = \varepsilon \times \sigma$) based on body size (Fig 3). Experimental data on size-based susceptibility correspond well to these predictions (Fig 3B) and the transmission parameter is more strongly influenced by susceptibility, resulting in a prediction of overall lower transmission with increasing body size (Fig 3C).

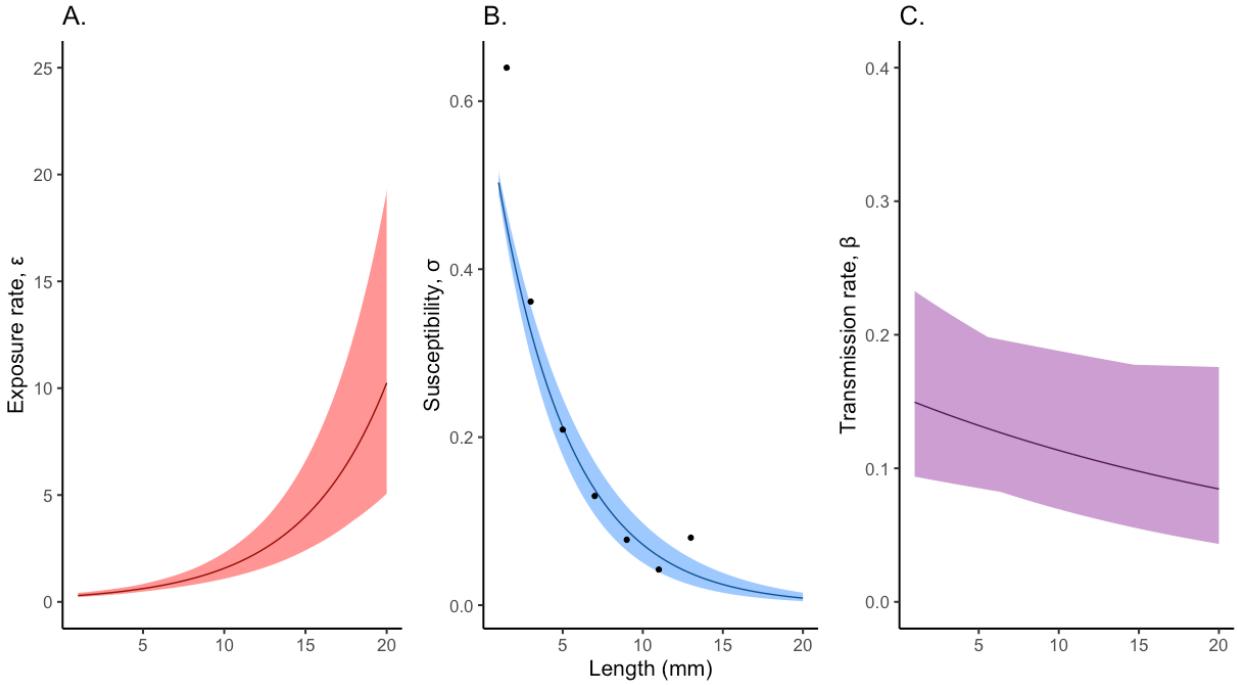

Figure 3. Estimates for exposure, ε(L), (A), susceptibility,σ(L), (B), and overall transmission rate, β(L) = ε(L)*σ(L) (C) as functions of snail length. Lines represent the maximum likelihood of estimated parameters across body size of snails. Shading represents the minimum and maximum from the 95% confidence interval of parameters estimated. Points in (B) are from experimentally observed schistosome susceptibility across snail sizes from individual exposures, while the other two parameters are inferred from the full dataset.

Implications for *S. mansoni* dynamics

The size structure of a natural *Biomphalaria* population varied substantially during the year (Fig 4A). Using these size structure data, we estimated that the probability of establishing a successful infection for a single schistosome miracidium encountering a snail in this population would also vary over the course of the year due to the influence of snail body size on transmission. When small snails are overrepresented in the population, e.g. day 150, the predicted success of a schistosome is much higher than when the population is skewed towards larger individuals, e.g. day 208 (Fig 4B). Importantly, the null and size-dependent models yielded similar estimates in

only 3 of 14 months. Overall, the size-dependent model predicted lower parasite success than the null model, suggesting that ignoring size structure could lead to overestimation of transmission potential.

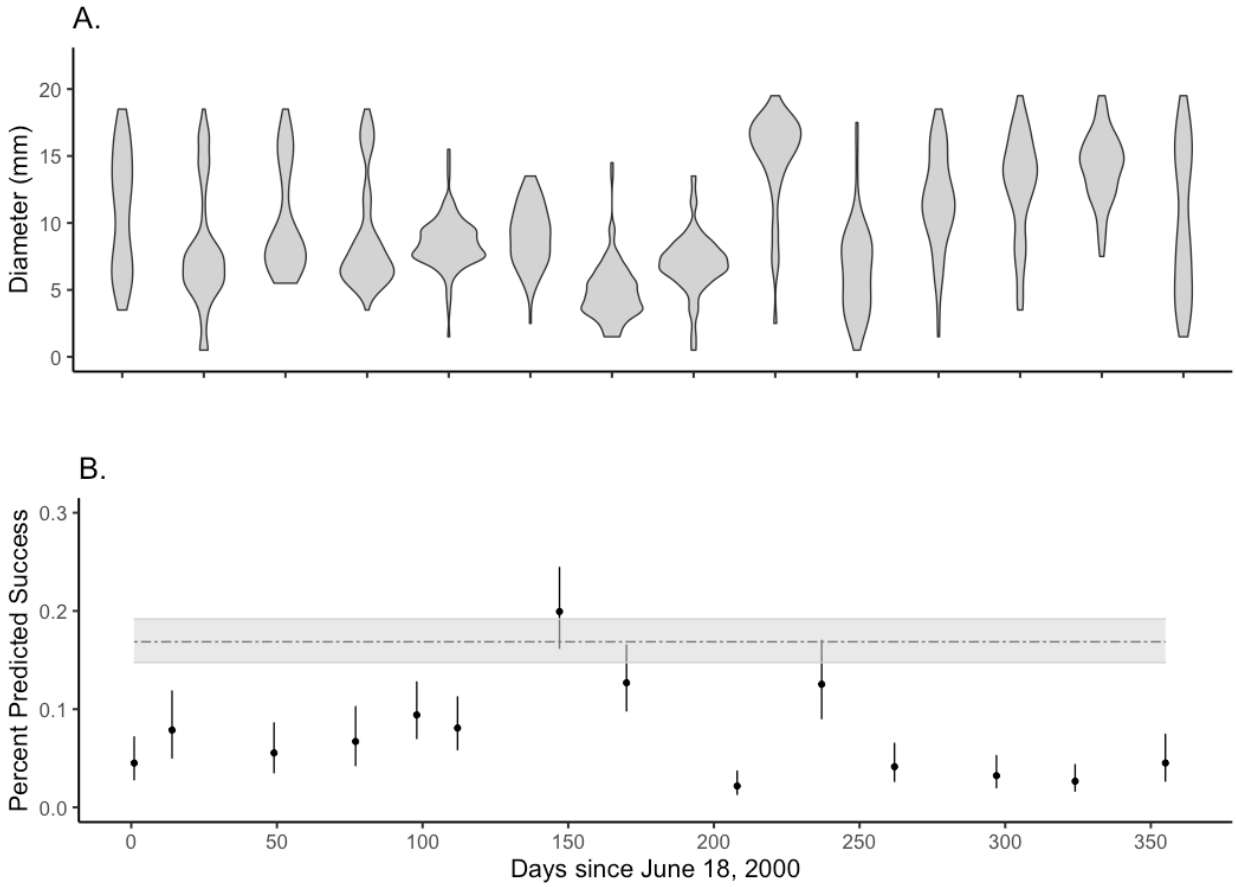

Figure 4. Predicted infection success of a single schistosome parasite given exposure of a snail in a natural population with varying body size structure over time. A) Distribution of body sizes from a population of *Biomphalaria tenagophilia* in del Plata Basin, Argentina from 2000-2001(Rumi *et al.* 2009). Points are the mean ± 95% confidence interval of predicted schistosome success in this snail population from simulated transmission trials using the fully size-dependent model. Grey line is the predicted success from a transmission model that ignores size-based exposure and susceptibility. Substantial changes in snail population size structure cause month-to-month estimates of schistosome success to diverge substantially from predictions that ignore size dependence. In particular, the size-null prediction tends to overestimate schistosome success except at the times in which the population is heavily dominated by small snails.

Discussion

Natural populations are heterogenous, and in order to create ecological theory that can reflect observed dynamics or predict future outcomes we must find tenable ways to address this heterogeneity (Bolnick *et al.* 2011). It is particularly important to include relevant heterogeneity in transmission, because this process shapes the ecological and evolutionary trajectory of disease dynamics (McCallum *et al.* 2001). Transmission models that do not incorporate heterogenous host traits often fit data poorly (Dwyer *et al.* 2010), compromising their applicability to natural populations. Therefore, identifying the traits that drive transmission and the directionality of their effects can improve theoretical predictions for natural dynamics and better assess interventions.

However, we do not suggest that disease ecologists embark on an endless hunt to characterize all heterogenous host traits. Instead, focusing on traits that either integrate numerous aspects of a host's ecology, have the potential to regulate multiple downstream processes impacting transmission, or both, can greatly reduce unexplained variability while still being tenable to include mathematically and empirically. Body size is trait that satisfies both of these criteria for many disease systems, as it profoundly impacts many ecological processes such as predation, resource competition, and reproductive success (Wellborn 1994; Hopcraft *et al.* 2010). Body size has the potential to vary drastically among individuals in a population and can reflect the integration of many processes such as age, nutrition, and environmental stressors (Kooijman, S.A.L.M. 2010).This leads to its utility as a tractable trait to include in transmission models because often an individual's history resulting in their current body size is usually impossible to reconstruct for wild organisms. Body size may interact with transmission via multiple mechanisms: for example, larger individuals may provide a greater target area for vectors (Poulin

2004), may be more apparent to parasites that actively seek out their host using chemical cues (Théron *et al.* 1998), or may encounter a greater abundance and diversity of microparasites if they are exploring larger territories (Han *et al.* 2015). Further exploring the role of body size in other host-parasite systems may reveal correlations and trade-offs between host physiology, behavior, and transmission.

For decades, it has been known that larger *Biomphalaria* snails experience a higher exposure to schistosomes but a lower susceptibility to infection (Niemann & Lewis 1990). However, the relevance of this phenomenon to epidemiological dynamics has not been determined. Here we demonstrate the epidemiological relevance of parasite transmission in size-structured populations. We showed that this individual-level phenomenon can have population-level consequences for schistosome prevalence: differently size-structured populations experienced very different schistosome transmission dynamics in our experimental trials. Populations with a greater proportion of large sized snails had lower schistosome prevalence, while populations of uniformly small snails experienced the greatest prevalence. From the perspective of the snail, the body size of immediate neighbors is also critically important for transmission: small snails had lower prevalence of schistosomes when in populations with a greater proportion of large conspecifics. This observation supports the hypothesis that individuals with relatively high exposure rates to parasites can shield their conspecifics from infection, a form of transmission interference akin to the much-discussed dilution effect that is typically considered in multi-species host communities (Keesing *et al.* 2006; Shaw & Civitello 2021).

Incorporating size structure into schistosome transmission models could also improve our understanding of seasonal variation in schistosome transmission. We found that for a well-characterized natural *B. glabrata* population, temporal variation in size structure was large enough to cause substantial variation in predicted transmission success for schistosomes. Numerous biotic and abiotic factors, such as predation, resource competition, temperature, and nutrient availability, can impact host snail growth and therefore population size structure across space and time. Furthermore, schistosome intervention efforts can be costly and labor-intensive, but characterizing the seasonal patterns in size structure may allow for more targeted approaches at times when the chance of transmission is highest, such as following a large reproductive burst when the population has a large proportion of neonates.

Hosts are not identical, despite the plethora of transmission models that treat them as such. Scaling up the effects of heterogenous host traits on transmission to investigate population-level effects can allow for better inference and prediction, especially when using traits such as body size that are measurable and can reflect correlations between numerous ecological processes. Our work shows the importance of this approach in the snail-schistosome system. Tackling the influence of host heterogeneity in transmission may be key for resolving many unanswered questions in disease ecology.

Acknowledgements: We thank members of the Civitello Lab for their comments on this manuscript. KS was supported by the National Institute of Allergy and Infectious Diseases of the National Institutes of Health under Award Number T32AI138952

and Award Number F31AI147611. DJC was supported by NIH 1R01 AI150774-01. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health.

References

Baer, K.N. & Goulden, C.E. (1998). Evaluation of a High-Hardness COMBO Medium and Frozen Algae forDaphnia magna. *Ecotoxicology and Environmental Safety*, 39, 201–206.

Bolker, B. & R Development Core Team. (2021). bbmle: Tools for General Maximum Likelihood Estimation.

Bolker, B.M. (2008). Likelihood and All That. In: *Ecological Models and Data in R*. Princeton University Press, pp. 169–221.

Bolnick, D.I., Amarasekare, P., Araújo, M.S., Bürger, R., Levine, J.M., Novak, M., *et al.* (2011). Why intraspecific trait variation matters in community ecology. *Trends in Ecology & Evolution*, 26, 183–192.

Dinguirard, N., Heinemann, C. & Yoshino, T.P. (2018). Mass Isolation and In Vitro Cultivation of Intramolluscan Stages of the Human Blood Fluke Schistosoma Mansoni. *JoVE*, e56345.

Dwyer, G., Elkinton, J.S. & Buonaccorsi, J.P. (1997). Host heterogeneity in susceptibility and disease dynamics. *The American Naturalist*, 150, 685–707.

Dwyer, G., Elkinton, J.S. & Buonaccorsi, J.P. (2010). The American Society of Naturalists Host Heterogeneity in Susceptibility and Disease Dynamics : Tests of a Mathematical Model Published by : The University of Chicago Press for The American Society of Naturalists Stable URL : http://www.jstor.org/stable/2. *East*, 150, 685–707.

Gryseels, B., Polman, K., Clerinx, J. & Kestens, L. (2006). Human schistosomiasis. *Lancet*, 368, 1106–1118.

Hall, S.R., Sivars-Becker, L., Becker, C., Duffy, M.A., Tessier, A.J. & Cáceres, C.E. (2007). Eating yourself sick: Transmission of disease as a function of foraging ecology. *Ecology Letters*, 10, 207–218.

Han, B.A., Park, A.W., Jolles, A.E. & Altizer, S. (2015). Infectious disease transmission and behavioural allometry in wild mammals. *Journal of Animal Ecology*, 84, 637–646.

Hopcraft, J.G.C., Olff, H. & Sinclair, A.R.E. (2010). Herbivores, resources and risks: alternating regulation along primary environmental gradients in savannas. *Trends in Ecology & Evolution*, 25, 119–128.

Jarne, P., Pointier, J.-P. & David, P. (2011). Biosystematics of Biomphalaria spp. with an Emphasis on Biomphalaria glabrata. In: *Biomphalaria Snails and Larval Trematodes* (eds. Toledo, R. & Fried, B.). Springer New York, New York, NY, pp. 1–32.

Keesing, F., Holt, R.D. & Ostfeld, R.S. (2006). Effects of species diversity on disease risk. *Ecology Letters*, 9, 485–498.

King, K.C., Jokela, J. & Lively, C.M. (2011). Trematode parasites infect or die in snail hosts. *Biology Letters*, 7, 265–268.

Kooijman, S.A.L.M. (2010). *Dynamic Energy Budget Theory For Metabolic Organisation*. Cambridge University Press.

Lloyd-Smith, J.O., George, D., Pepin, K.M., Pitzer, V.E., Pulliam, J.R.C., Dobson, A.P., *et al.* (2009). Epidemic Dynamics at the Human-Animal Interface. *Science*, 326, 1362–1367.

Lloyd-Smith, J.O., Schreiber, S.J., Kopp, P.E. & Getz, W.M. (2005). Superspreading and the effect of individual variation on disease emergence. *Nature*, 438, 355.

McCallum, H., Barlow, N. & Hone, J. (2001). How should pathogen transmission be modelled? *Trends in Ecology & Evolution*, 16, 295–300.

Niemann, G.M. & Lewis, F.A. (1990). Schistosoma mansoni: Influence of Biomphalaria glabrata size on susceptibility to infection and resultant cercarial production. *Experimental Parasitology*, 70, 286–292.

Poulin, R. (2004). Macroecological patterns of species richness in parasite assemblages. *Basic and Applied Ecology*, 5, 423–434.

R Core Team. (2021). R: A language and environment for statistical computing.

Rohatgi, A. (2020). WebPlotDigitizer.

Rumi, A., Gutiérrez Gregoric, D. & Roche, A. (2009). TENDENCIAS DEL CRECIMIENTO INDIVIDUAL EN POBLACIONES NATURALES DE Biomphalaria spp. (GASTROPODA, PLANORBIDAE) EN LA CUENCA DEL PLATA, ARGENTINA. *Comunicaciones de la Sociedad Malacológica del Uruguay*.

Shaw, K.E. & Civitello, D.J. (2021). Re-emphasizing mechanism in the community ecology of disease. *Functional Ecology*, 35, 2376–2386.

Strauss, A.T., Hite, J.L., Civitello, D.J., Shocket, M.S., Cáceres, C.E. & Hall, S.R. (2019). Genotypic variation in parasite avoidance behaviour and other mechanistic, nonlinear components of transmission. *Proceedings. Biological sciences*, 286, 20192164.

Sweeny, A.R. & Albery, G.F. (2022). Exposure and susceptibility: The Twin Pillars of infection. *Functional Ecology*, 36, 1713–1726.

Théron, A., Rognon, A. & Pagès, J.-R. (1998). Host choice by larval parasites: a study of Biomphalaria glabrata snails and Schistosoma mansoni miracidia related to host size. *Parasitology Research*, 84, 727–732.

Wellborn, G.A. (1994). Size-Biased Predation and Prey Life Histories: A Comparative Study of Freshwater Amphipod Populations. *Ecology*, 75, 2104–2117.

White, C.R. (2010). There is no single p. *Nature*, 464, 691–693.

World Health Organization. (2022). Schistosomiasis Fact Sheet.