

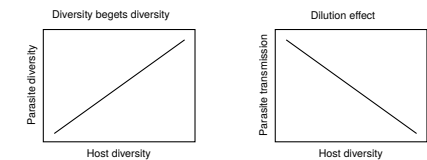
Reconciling divergent effects of diversity on disease: host diversity begets symbiont diversity while inhibiting transmission

Maxwell B. Joseph, Joseph R. Mihaljevic, Pieter T. J. Johnson
University of Colorado Boulder

Introduction

The effect of biodiversity loss on parasite transmission has been the subject of heated controversy lately. Progress in this debate is slowed in part by uncertainty over how transmission rates and parasite diversity relate to disease risk.

Two divergent perspectives have emerged: that disease risk should be high for diverse host communities, because many different parasites ought to be present (**diversity begets diversity**); and disease risk should be low for diverse host communities because of reductions in transmission (**dilution effect**). Using a simple model, we show that this apparent contradiction arises primarily from ambiguous definitions of disease risk rather than any paradox inherent in multi-host, multi-parasite systems.



Results

Host functional diversity mediates symbiont community dynamics through two primary mechanisms:

1. Functional diversity determines whether symbionts attempting to colonize from the regional pool can successfully establish an infection in a host (Figure 1). The relationship between host functional diversity and the niche space of symbionts in a regional pool is shown in Figure 2.

2. Functional diversity determines whether hosts can share symbionts, controlling among-species transmission (Figure 3). With high functional diversity, contacts between infectious and susceptible hosts are less likely to lead to transmission for all but the most generalist symbionts because the within-host environments are less similar.

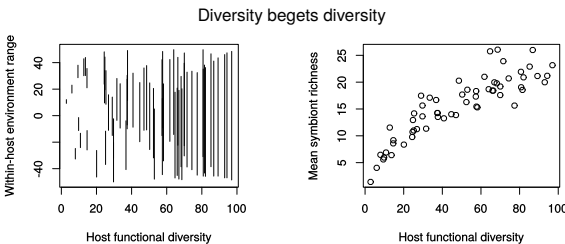


Figure 1: The left panel shows available within-host resource niche space for symbionts across the range of host functional diversity, the length of the vertical line. Short lines indicate a narrow range of host resources available in a local community. The right panel shows an increase in symbiont richness (averaged over time) with host functional diversity. The rate of accumulation decreases due to reductions in transmission that result in more stochastic extinctions (i.e. though more symbionts can now establish locally, persisting is difficult because there are fewer suitable hosts available).

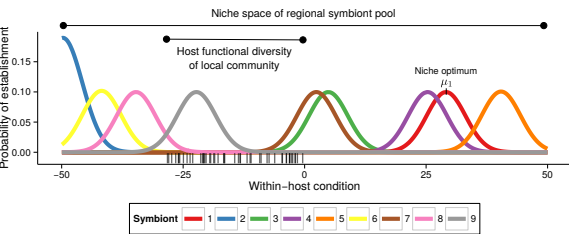


Figure 2: Host functional diversity is defined as the range of within-host conditions represented in a local host community. Individual black vertical lines represent the conditions for individual hosts in a local community. Each symbiont in the regional pool, represented by different colors, has some probability of establishing in each host, conditional on a colonization opportunity. This probability is derived from a Gaussian function of the within-host condition with an optimum (shown for Symbiont 1) and variance representing niche breadth. Symbiont niches are normalized so that all species have equal probabilities of establishment across the entire range of within-host conditions possible (e.g. the left-most niche shown in blue).

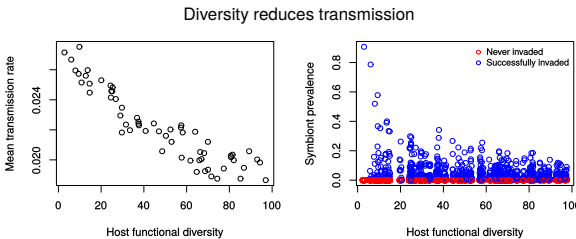


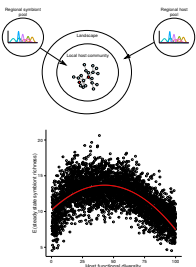
Figure 3: The left panel shows the negative effect of host functional diversity on mean transmission rates (averaged across symbiont species), consistent theoretically with a "dilution" perspective. The right panel depicts the prevalence of each individual symbiont species averaged over time across the same range of host functional diversity. Red points indicate that the symbiont was never able to establish in any local hosts, while blue points indicate at least one successful infection event.

Conclusions

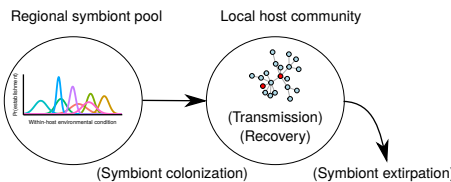
1. Host diversity can increase symbiont diversity while reducing transmission in local communities.
2. The diversity-begets-diversity and dilution persepctives are not contradictory. Rather, they are closely related and emerge from the same processes.
3. Host communities with low functional diversity may maintain fewer symbionts with high transmission, while diverse host communities may have higher symbiont diversity but less transmission.
4. "Disease risk" integrates transmission potential, host susceptibility, and the diversity of infectious agents, raising an interesting question of whether it is advantageous to have fewer agents with high transmission, or more agents with lower transmission.

Future directions

1. Extend model to account for co-infections, treating hosts as patches within a metacommunity (Mihaljevic 2012).
2. Incorporate host dynamics in a landscape model to assess effects of landscape heterogeneity on symbionts.
3. Further assess support for an area-heterogeneity-like trade-off that causes unimodal relationships between host and symbiont diversity (Allouche et al. 2012).



Model structure



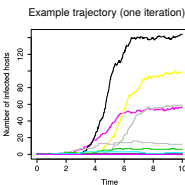
Simplifying assumptions:

- No host births or deaths
- No co-infection
- No symbiont displacement
- Finite host communities
- No cost of infection

Analysis

Iteratively

- Initialize host community with some range of within-host conditions
- Initialize symbiont regional pool & niche space
- Simulate local infection trajectories through time
- Quantify symbiont richness & transmission



References

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Acknowledgments

MBJ and JRM were supported by the NSF GRFP. The idea for this project emerged from discussions with the CU Parasites and Pathogens reading group. This work utilized the Janus supercomputer, which is supported by the National Science Foundation (award number CNS-0821794) and the University of Colorado-Boulder. The Janus supercomputer is a joint effort of the University of Colorado Boulder, the University of Colorado Denver and the National Center for Atmospheric Research.