

# Host diversity increases symbiont diversity while reducing transmission

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## Abstract

## Introduction

Debate around effect of host diversity on disease. Increased availability of microbial data. Need for theoretical framework to make sense of data and predict future observations.

## Methods

### Conceptual model

We consider a local habitat patch that contains populations of hosts that are infected by symbionts. The host populations are open, with deaths, births, emigration and immigration. Symbionts can be transmitted among host individuals, or colonize from outside of the local host population - from a regional pool, for example. There are multiple host species that can colonize the local community, species vary in traits that are relevant to symbiont infection. Specifically, we consider one axis of variation among hosts that could represent some dominant trait that influences the probability of symbiont establishment within or on a host (e.g. pH, immune defenses). We also consider multiple “species” of symbionts, each of which has some optimum or preferred host condition along this axis, and some niche breadth, or variation around the optimum that allows establishment in near-optimal hosts.

Hosts are infected by symbionts at a particular location that can only be occupied by one type of symbiont (no co-infection). Hosts occur in a homogenous landscape, and can colonize the local habitat from the regional pool, reproduce, and die. Offspring attempt to disperse to a random habitat patch, and if it is unoccupied, they successfully colonize.

29 Model formalization

30 Results

31 Discussion

32 See Dunn et al. 2010 for non-linear relationship

33 See Rotstock et al. 2014 for similar resolution of paradox

34 Conclusion

35 Acknowledgments

36 References