Dear Senior Editors:

Thank you for considering our article titled, “Abiotic and biotic factors jointly influence the transmission of ranavirus in larval amphibian communities” for publication in *Functional Ecology*.

We study the joint influence of biotic and abiotic factors by focusing on a limited number of factors and the mechanisms underlying their effects on multimodal transmission of ranavirus in larval amphibian communities. By focusing on host community composition, host abundance, and the environmental persistence of the pathogen, we developed a simple mathematical model that can examine each of these factors independently and together. Through our model, we learn that each of these factors can contribute significantly to transmission and that the joint influence of these factors can have synergistic effects. We connect this model to empirical data of ranavirus infections in linked communities of amphibians and find that each of these factors can overlap and appear to contribute to ranavirus prevalence. When host abundance is high, communities are typically dominated by high competence hosts and this typically occurs in cooler months, when lower water temperatures may enhance viral persistence times in the water. Furthermore, we examine the phylogenetic relationship of the host species and find that higher values of competence are moderately spread throughout the phylogeny, potentially enabling coexistence of high competence species. The consideration of both biotic and abiotic factors and the mechanistic rationale that we provide can contribute significantly to our understanding of ranavirus epidemics in natural systems and can also further our understanding of other multimodel multihost pathogens.

We have chosen to submit out article to *Functional Ecology* because of the journal’s strong record of published research regarding biodiversity-disease relationships and the mechanisms underlying these relationships. We intend to contribute to this catalog by expanding theory that focuses on the specific compositions of communities and how these can drive transmission in conjunction with other important abiotic factors. The diversity-disease literature has been dominated by debate regarding species richness patterns and disease metrics. While this debate has generated deep interest in the topic and furthered our understanding of the relationship between biodiversity and disease, it has also been stymied by focusing heavily on the detection of these patterns in lieu of mechanistic understandings. Our study, along with many others, are trending towards developing theory for understanding how abiotic factors influence community composition and how these formulations of host communities relate to disease transmission.

This paper has not been published anywhere else and is not under consideration at any other journals.