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HAL Authorization

Disease prevalence increases with biodiversity loss through predictable subtraction of host species

Christelle Lacroix¹, Anna Jolles^{2,3}, Eric W. Seabloom^{1,3}, Alison G. Power⁴, Charles E. Mitchell⁵, Elizabeth T. Borer^{1,3}

¹ *Department of Ecology, Evolution, and Behavior, University of Minnesota, Saint Paul, MN 55108, USA*

² *Department of Biomedical Sciences, Oregon State University, Corvallis, OR 97331, USA*

³ *Department of Zoology, Oregon State University, Corvallis, OR 9733, USA*

⁴ *Department of Ecology & Evolutionary Biology, Cornell University, Ithaca, NY 14853, USA*

⁵ *Department of Biology, University of North Carolina, Chapel Hill, NC 27599 USA*

Background/Questions/Methods

Biodiversity loss in communities can degrade ecosystem functions including productivity, resilience and disease regulation. While high species richness is often associated with reduced infectious risk, multiple interacting mechanisms could underlie this ‘dilution’ effect. In particular, community assembly processes may provide a predictive framework for understanding the mechanisms underlying disease ‘dilution’ in communities. The effect of biodiversity on disease prevalence can depend both on the species loss order in community disassembly and on the traits of species left in species-poor communities. If host communities decay to a predictable subset of hosts, infection prevalence by generalist, vector-borne parasites may reflect the competence of the remaining hosts. We measured the distribution and local abundance of grasses at ten sites across 15 degrees of latitude (2000 kilometers) along the North American West Coast. At each site, we monitored the prevalence of four generalist aphid-vectored pathogens, the *Barley* and *Cereal yellow dwarf* viruses (B/CYDVs, *Luteoviridae*), using a widespread species, *Bromus hordeaceus*, as a sentinel host. We used controlled conditions to assess the ability of different hosts to support i) viral infection after inoculation of a BYDV-PAV isolate, ii) secondary infection of new hosts and iii) reproduction and preference of the aphid vector *Rhopalosiphum padi*.

Results/Conclusions

Mean overall prevalence and prevalence of BYDV-PAV per site in *Bromus hordeaceus* declined with local host richness. This relationship was robust to variability in local grass host abundance and abundance of the sentinel host *B. hordeaceus*. Grass community disassembly in this system was non-random: species-poor assemblages represented predictable subsets of the species found in species-rich sites. *Bromus hordeaceus*, present in even the most species-poor grassland communities, was also among the most competent host for transmission of viral particles to new hosts and for the attractiveness to and reproduction of aphid vectors. In summary, our results demonstrate that biodiversity loss in this ecosystem is non-random, leading to predictable increases in the transmission of infectious agents and proliferation of their aphid vectors, thus providing a clear mechanism by which disease dilution can occur.

Keywords: disease dilution effect, vector-borne pathogen, grasslands, B/CYDV, nestedness