



HAL
open science

Host diversity and disease prevalence: a case study based on barley and cereal yellow dwarf viruses

Christelle Lacroix, Anna Jolles, Eric W Seabloom, Alison G Power, Charles E Mitchell, Elizabeth T Borer

► To cite this version:

Christelle Lacroix, Anna Jolles, Eric W Seabloom, Alison G Power, Charles E Mitchell, et al.. Host diversity and disease prevalence: a case study based on barley and cereal yellow dwarf viruses. 27. International Congress for Conservation Biology, Society for Conservation Biology Global (SCB). USA., Aug 2015, Montpellier, France. hal-02796146

HAL Id: hal-02796146

<https://hal.inrae.fr/hal-02796146>

Submitted on 5 Jun 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

International Conference of Conservation Biology – Montpellier, France – August 2nd to 6th, 2015
Symposium 151 - Biodiversity and infectious diseases: a role for conservation biology?

SYMPOSIUM 151 - HOST DIVERSITY AND DISEASE PREVALENCE: A CASE STUDY BASED ON BARLEY AND CEREAL YELLOW DWARF VIRUSES

Christelle Lacroix^{1*}, 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*

* *Current address: INRA, UR0407 Plant Pathology, Montfavet Cedex F-84143, France*

Community assembly processes may provide a predictive framework for understanding the mechanisms underlying disease dilution (reduced disease prevalence with increasing biodiversity). The effect of biodiversity on disease prevalence may depend both on a heterogeneity in host traits related to disease spread and on the order of species loss in community disassembly. If host communities decay to a predictable subset of hosts, disease prevalence may reflect the competence of the remaining hosts. To test this hypothesis, we measured local host species abundance and prevalence of four generalist aphid-vectored pathogens (barley and cereal yellow dwarf viruses, Luteoviridae) in a sentinel ubiquitous annual grass host (*Bromus hordeaceus*, Poaceae) at 10 sites spanning 2000 km along the North American West Coast. We measured in laboratory and field trials virus infection, as well as aphid vector fecundity and feeding preferences on several host species. Virus prevalence increased as local host richness declined. Grass community disassembly in this system was non-random: hosts from our ubiquitous sentinel species dominating species-poor assemblages were among the most competent for vector production and virus transmission. These results suggest that non-random biodiversity loss led to predictable increases in disease prevalence, providing a clear mechanism by which disease dilution can occur.

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