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

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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