

Biodiversity loss and the rise of zoonotic pathogens

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Abstract

The unprecedented loss of biological diversity from anthropogenic causes has profound impacts on human health. One way that biodiversity loss threatens human health is by exacerbating risk and incidence of infectious diseases. This paper briefly reviews two zoonotic diseases – West Nile virus (WNV) illness and Lyme disease (LD) – in which high diversity in the community of vertebrate hosts for arthropod vectors strongly reduces human risk. In both cases, the primary reservoirs for the pathogen are species that dominate in human-impacted, low-diversity communities. As a result, the generalist vectors responsible for transmitting the pathogens to humans have relatively high feeding rates on these reservoirs, leading to high infection prevalence in mosquito (for WNV) and tick (for LD) vectors. In contrast, where native vertebrate diversity is high, mosquito and tick vectors evidently feed from a wider variety of hosts, most of which are poor reservoirs for the pathogens, resulting in lower infection prevalence. Protection of humans against exposure to zoonotic pathogens should be added to the list of utilitarian functions provided by high biodiversity.

Keywords: Dilution effect, ecosystem services, emerging infectious diseases, Lyme disease, West Nile virus

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Introduction

The earth is currently experiencing an extinction crisis that is unprecedented in both magnitude and pace. Although the ability of scientists to ascertain how many species have or will soon become extinct varies considerably among taxonomic groups and ecosystem types, it is clear that the current extinction crisis is pervasive, even universal. At current rates, global extinctions within some classes of vertebrates are predicted to approach 50% within about 100 years [5]. Even more pervasive, yet more poorly documented, are local extinctions of populations and metapopulations. The consequences of this loss of biodiversity for humanity are certainly going to be profound [4].

Many species produce chemical compounds that are usable or adaptable as pharmaceutical agents to the direct benefit of human health. Others provide model systems for biomedical research. Yet others maintain genetic and genomic information vital to improving agricultural productivity and human nutrition [4]. More recently, it has been discovered that high biodiversity can protect human health by reducing the risk of certain infectious diseases [14,15,18].

High biodiversity can buffer against disease transmission by one or more of several mechanisms, including: (i) reducing the population density of an important natural reservoir for pathogens; (ii) reducing the population density of arthropod vectors for pathogens; and (iii) reducing encounter rates between vectors and reservoirs or among reservoirs [7]. The phenomenon by which high diversity reduces disease risk, termed the dilution effect [13,14,18], has been best studied in zoonotic diseases. This article briefly describes two case studies, West Nile virus (WNV) and Lyme disease.

WNV

WNV is a mosquito-borne flavivirus that causes substantial morbidity and mortality in several vertebrate groups [9] including humans [10]. The predominant vectors are *Culex* mosquitoes, although other genera, including *Aedes*, can be vector-competent. The predominant reservoirs are passerine birds, although substantial variation exists among species [8,10]. Historically, WNV was restricted to eastern Europe, the Middle East, and eastern Africa, but it was introduced to the New York City area in 1999. Within several years, the disease had spread to the west coast of North America.

The reservoir status of North American bird species exposed to WNV is still being assessed. However, preliminary data indicate that the most competent reservoirs include the blue jay, western scrub jay, common grackle, house finch,

American crow, house sparrow and American robin [8,10]. All of these species are geographically widespread, common, and highly resilient to anthropogenic disturbances, such as urbanization and suburbanization. As a consequence, these species are expected to predominate in habitats in which avian diversity is low. In contrast, in less disturbed habitats these reservoir species tend to be less common or absent, while the diversity and abundance of non-reservoir species is expected to be considerably higher.

The dilution effect hypothesis would predict that mosquitoes occurring in areas of low avian diversity should have a high probability of encountering a competent reservoir for WNV, and therefore a high probability of acquiring infection during blood meals. In contrast, mosquitoes occurring in areas of high avian diversity should have a higher probability of taking a blood meal from one of the many species that are less competent or incompetent as reservoirs for WNV. Consequently, we [2] predicted that counties in the USA with high avian diversity should have a low human incidence of WNV disease, whereas those with low avian diversity should have a high WNV incidence. We were aware that *Culex* mosquitoes show feeding preferences, particularly for American robins, and that strong preferences would reduce the expected importance of total community diversity as a determinant of mosquito or human infection prevalence [8]. We were also aware that the abundance of competent vectors is a potentially strong contributor to host and vector infection prevalence. Strong impacts of feeding preferences and/or vector abundance would undermine the importance of bird diversity in determining WNV prevalence.

For the continental USA, we [2] calculated bird diversity and abundance at the county level from the USGS Breeding Bird Survey raw data (<http://www.mp2-pwrc.usgs.gov/bbs>). We obtained data on all known human cases of WNV disease within each county from the USGS WNV website (<http://westnilemaps.usgs.gov>), and calculated the *per capita* human incidence of WNV for each county (infected persons in county/total persons in county). We determined the year that each state peaked in human incidence for all states with >15 cases from 1999–2004. All states peaked in human incidence in 2002, 2003 or 2004, as the wave of WNV moved westward across the USA, and so we restricted our analyses to these 3 years. Our primary hypothesis was that WNV incidence should be negatively correlated with bird diversity, as measured by the Shannon index, but we also tested the effects of human population density and a community competence index, as well as assessing the importance of spatial autocorrelation (for details, see [2]).

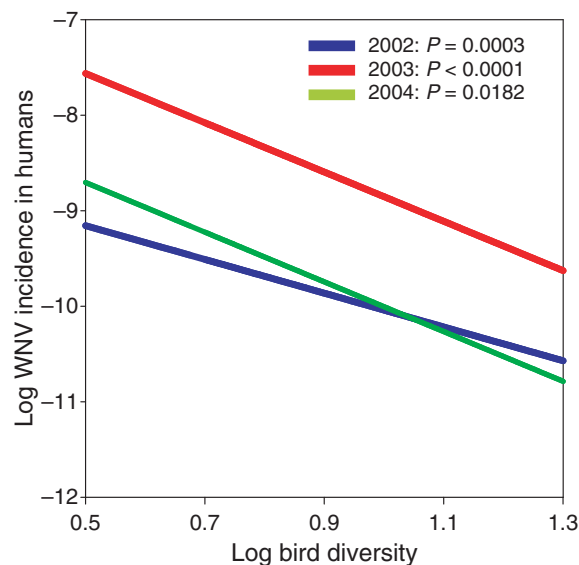


Fig. 1. Relationship between log West Nile virus (WNV) disease incidence in humans and log bird diversity for US counties in the year of peak incidence. The figure is based on multiple regressions that hold constant several other potentially important independent variables, such as human population density and an index of avian community competence. Based on data in Allan *et al.* (unpublished).

For all 3 years, the county-level human incidence of WNV disease was strongly, and significantly, negatively correlated with bird diversity within that county (Fig. 1). Spatial autocorrelation had only a modest effect. Neither of the other two independent variables (human population and community competence index) was consistently correlated with WNV incidence. Therefore, despite the potential for mosquito abundance and feeding preferences to destroy any effect of host diversity, our analysis strongly supported the predictions of the dilution effect hypothesis.

Lyme disease

Lyme disease is a tick-borne bacterial zoonosis caused by the spirochete *Borrelia burgdorferi*. Both the infection prevalence and abundance of the tick vector are critical to determining human exposure rates, and ecological determinants of risk of exposure to Lyme disease show some similarities to those influencing risk of exposure to WNV. In most of North America, the vector is the blacklegged tick, *Ixodes scapularis*, and the primary reservoirs for *B. burgdorferi* are white-footed mice (*Peromyscus leucopus*), eastern chipmunks (*Tamias striatus*), short-tailed shrews (*Blarina brevicauda*), and masked shrews (*Sorex cinereus*) [3,12]. White-footed mice,

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