

# The Effect of Habitat Fragmentation and Species Diversity Loss on Hantavirus Prevalence in Panama

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Habitat fragmentation and diversity loss due to increased conversion of natural habitats to agricultural uses influence the distribution and abundance of wildlife species and thus may change the ecology of pathogen transmission. We used hantaviruses in Panama as a research model to determine whether anthropogenic environmental change is associated with changes in the dynamics of viral transmission. Specifically, we wanted to determine whether hantavirus infection was correlated with spatial attributes of the landscape at both large and small scales or whether these changes are mediated by changes in community composition. When analyzed at coarse spatial scales, hantavirus reservoirs were more commonly found in disturbed habitats and edge habitats than in forested areas. At local scales, reservoir species dominance was significantly correlated with the slope of the terrain. To evaluate the effect of small-mammal diversity loss on infection dynamics, we implemented an experiment with selective species removal at experimental sites. Seroprevalence of hantavirus was higher in the community of small mammals and increased through time in the experimental sites. The higher seroprevalence in experimental plots suggests that greater diversity likely reduces encounter rates between infected and susceptible hosts. Our studies suggest that habitat loss and fragmentation and species diversity loss are altering hantavirus infection dynamics in Panama. Our work represents a multidisciplinary approach toward disease research that includes biodiversity concerns such as environmental change and degradation, human settlement patterns, and the ecology of host and nonhost species, work that may be especially important in tropical countries.

**Key words:** habitat loss; habitat fragmentation; diversity loss; hantavirus; rodent diversity

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## Introduction

Habitat fragmentation and diversity loss are often mentioned as a form of environmental alteration associated with increased disease risks for humans and wildlife. Their relationship with disease dynamics has important implications for human and animal health and conservation biology.<sup>1,2</sup> Extensive global habitat destruction has created a complex array of land cover configurations, fragmenting species distributions and changing the composition of natural communities. These changes can alter the ecology of infectious diseases, leading to new patterns of transmission of endemic pathogens and, in some cases, to emergence and reemergence of infectious diseases, such as hantavirus pulmonary syndrome (HPS).<sup>3,4</sup>

In Panama, as in most tropical countries, deforestation and habitat fragmentation have increased drastically on account of cattle ranching and agriculture, resulting in severe biodiversity loss; currently, less than 44% of Panamanian territory is covered by forests.<sup>5</sup> The break-up of a once continuous vegetation cover has resulted in a variety of large, medium, and small patches of vegetation all over the country, making the Panamanian landscape a series of more numerous and less connected patches of forests. HPS was first documented in the country in 1999 and more than 20 human cases have been detected since then. Sporadic cases are still appearing.<sup>4,6</sup> Since the first outbreak, three new hantaviruses have been described: HPS-causing Choclo virus with *Oligoryzomys fulvescens* as the primary reservoir, Río Segundo virus with *Reithrodontomys mexicanus* and *R. megalotis* as primary reservoirs, and Calabazo virus, associated with *Zygodontomys brevicauda*.<sup>3,6</sup>

We have done a series of studies to evaluate whether anthropogenic environmental change is associated with changes in the transmission dynamics of hantaviruses. Our specific aim has been to determine whether hantavirus infection is correlated with spatial attributes of the land-

scape at both large and small scales or whether these changes are mediated by changes in community composition. Here we summarize the main findings of these studies.<sup>7-9</sup>

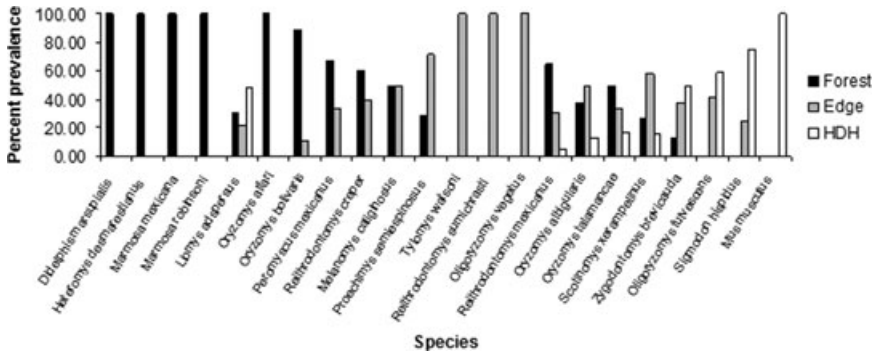
## Materials and Methods

At a coarse scale, we have compared communities of small mammals with trapping grids established in different habitats with varying degrees of anthropogenic fragmentation, including forest, forest edges, and pastures in six national parks and surrounding areas throughout Panama.<sup>7</sup> At the local level, we selected 24 sites that shared similar environmental conditions at edges of small forest fragments; these were distributed along an East–West axis in the southern part of the peninsula.<sup>8</sup> At each site, we established a trapping grid, with the central trap line centered on the edge of the forest. We obtained measures of landscape characteristics (including quantification of characteristics that are relatively common in human-dominated habitats, such as increased edge densities and number of isolated fragments). We used multiple linear regressions to produce a spatial model that would allow a representation of dominance for each species in a rodent community.<sup>8</sup>

We evaluated the effect of small-mammal diversity loss on infection dynamics, by implementing a mark–recapture experiment with selective species removal at experimental sites.<sup>9</sup> We sought to mimic species diversity loss by experimentally removing nonreservoir species. In contrast, none of the captured animals were removed in control sites. We selected 16 experimental and eight control plots distributed along an East–West axis, with environmental conditions similar to those in the Azuero Peninsula in southwestern Panama in 2003.<sup>9</sup>

## Results

As we expected, at coarse scales there were striking differences in small-mammal composition and abundances among habitats, with



**Figure 1.** Habitat preference of 22 rodent species. *Oligoryzomys fulvescens* and *Sigmodontomys brevicauda*, both hantavirus reservoirs, show an inclination for human-dominated habitats (HDHs).

more complex assemblages and higher number of specialist species in forest habitats.<sup>7</sup> The size of forest fragments was relevant to species diversity, with smaller habitat fragments (<5 ha) having significantly fewer species than larger (>5 ha) fragments. We found that both hantavirus reservoirs (*O. fulvescens* and *S. brevicauda*) were more commonly found in both disturbed habitats and edge habitats than in forest (Fig. 1). Forested areas had much lower combined population densities of *O. fulvescens* and *S. brevicauda* than did edges or pastures.<sup>7</sup>

At local scales, we produced a spatial model that allowed a representation of dominance for hantavirus reservoir in rodent communities among the landscape and we used a multiple linear regression model. All variables (three principal factors from landscape metrics principal component analysis and average slope for the site at scale of analysis) were checked for normality using the Kolmogorov–Smirnov test ( $P > 0.05$ ).<sup>8</sup> A sensibility analysis of the regression model (using Cook’s distance) indicated the influence or contribution of each site to the parameters of the model. Topography expressed as slope demonstrated the strongest association with *S. brevicauda* dominance (multiple regression analysis,  $P < 0.05$ ), and although landscape fragmentation characteristics added to the predictive power of regression, they did not significantly improve it. The model predicted the highest abundances

of *S. brevicauda* in flat areas, where humans also dominate. Details of the statistics are presented elsewhere.<sup>8</sup> In the species removal experiment, initial seroprevalence in both control and experimental sites seroprevalence was 8%. At experimental sites, seroprevalence at the community level increased three-fold.<sup>9</sup>

## Concluding Remarks

Habitat fragmentation is broadly accepted as a leading cause of biodiversity loss<sup>10</sup> and it is also frequently mentioned as a type of environmental alteration associated with increased disease risks for humans and wildlife.<sup>1,2</sup> Habitat fragmentation is considered a source of health risks because it alters the distribution and abundance of hosts, vectors, and pathogens. In our study sites, the complexity of human land use that produces a mosaic of various successional stages and patches of forests has resulted in rodent communities dominated by hantavirus reservoir species, such as *S. brevicauda*, and *O. fulvescens*.<sup>7</sup>

When analyzed at a gross scale, decreasing area and increasing patch isolation resulting from fragmentation are seen to lead to variable changes in species diversity, composition, relative abundance, and distribution. At a local scale, human development in the Azuero Peninsula is greater in flat areas, in which crops

can be more easily produced, and we see that generalist species such as *Z. brevicauda* have a marked tendency to dominate these flat lands, where hantavirus outbreaks are reported.<sup>4,8</sup>

Higher levels of biodiversity have been found to act as a buffer against disease prevalence and spread.<sup>11</sup> The relationship between biodiversity and disease is a fundamental issue in need of further assessment in the field of disease ecology. Taken together, our results suggest that biodiversity provides a potentially valuable ecosystem service by buffering the intensity of hantavirus transmission.

Understanding the ecologic relationship between habitat fragmentation, biodiversity loss, and prevalence of pathogens is important for improving our overall comprehension of the links between anthropogenic environmental change and the health of all species. Our studies suggest that habitat loss and fragmentation and species diversity loss are altering hantavirus infection dynamics in Panama. This study represents an approach towards disease research that includes biodiversity concerns, such as environmental change and degradation, human settlement patterns, and the ecology of host and nonhost species. Such an approach may be especially valuable in tropical countries, which are often rich in biodiversity but also experience high rates of environmental alteration and human population growth.

### Conflicts of Interest

The authors declare no conflicts of interest.

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