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Spatiotemporal dynamics of vector-borne disease risk across human land-use gradients: examining the role of agriculture, indigenous territories, and protected areas in Costa Rica

Brett R. Bayles
Dominican University of California, brett.bayles@dominican.edu

Andria Rusk
Florida International University

Rebecca Christofferson
Louisiana State University at Baton Rouge

Gabriellah Agar
Dominican University of California

Maria Alvarez Pineda
Dominican University of California

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Authors

Brett R. Bayles, Andria Rusk, Rebecca Christofferson, Gabriellah Agar, Maria Alvarez Pineda, Bobin Chen, Kiera Dagy, Emma Kelly, Tyler Hummel, Kira Kuwada, Serena Martin, Alec Murrer, and Carlos Faerron Guzmán

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Abstract

Background Costa Rica has undergone significant changes to its forest ecosystems due, in part, to the proliferation of palm oil and other industrial agriculture operations. However, the country also boasts conservation programmes that are among the most robust in the neotropics. Consequently, gradients of anthropogenic to intact ecosystems are found throughout the country. Forest ecosystems may decrease vector-borne disease (VBD) risk by maintaining insect populations in a state of relative equilibrium; however, evidence suggests that intact forests foster biodiversity and may also amplify VBD risk in some circumstances. As a result, focal points of human-vector contact are likely idiosyncratic. This may be particularly true in indigenous territories, which have been shown to play a vital role in maintaining the ecological integrity of conservation areas. Here, we investigate the relationships between anthropogenic landscapes, indigenous territories, protected areas, and risk of VBD.

Methods We quantified spatial dynamics of risk across three distinct categories of VBD in Costa Rica: emerging flaviviruses (Zika virus disease and dengue); neglected tropical diseases (cutaneous leishmaniasis and Chagas disease); and a disease nearing eradication (malaria). We collected district-level incidence data from between 2006 and 2017 and used spatial statistics to identify hotspots of elevated risk. We then quantified the associations between anthropogenic landscapes, intact forest ecosystems, and indigenous territories with both the presence and persistence of elevated transmission risk over time using multivariate hurdle models.

Findings We detected clear patterns of non-random disease risk across each of the three categories of VBD. Compared with protected areas, districts with higher proportions of human-altered landscapes, particularly agricultural intensification, were at higher risk for VBD across all categories. Districts with the highest proportion of crop cover, compared with the lowest proportion, were significantly associated with the presence of hotspots for Zika virus disease (OR 15·19 [95% CI 6·19–37·26]), dengue (13·00 [7·24–23·35]), leishmaniasis (4·46 [1·18–16·84]), Chagas disease (3·09 [1·47–6·49]), and malaria (8·40 [3·56–19·83]).

Interpretation A set of spatial epidemiology tools within a planetary health framework allowed for a refined understanding of the risk of VBD of global public health significance in a biodiversity hotspot. Our findings may be used to better guide targeted public health disease surveillance, control, and prevention programmes. Additional research to understand the role that socioeconomic factors play in the variating VBD risk would contribute additional context to these findings, as these factors are often also spatially associated.

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Declaration of interests
We declare no competing interests.