

Analyzing the importance of land conversion as a driver of disease emergence in tropical forests

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INTRODUCTION

Human conversion of natural landscapes is one of the major threats to biodiversity, causing loss in species diversity, altering ecosystem services (e.g. water supply) and disrupting biotic interactions such as host-pathogen transmission dynamics¹⁻³. Land conversion is believed to drive zoonotic disease emergence by 1) disrupting disease dynamics and cross-species transmission in multi-host, multi-pathogen systems (“perturbation hypothesis”) and/or 2) increasing exposure of hosts to novel pathogens (“novel pathogen pool hypothesis”) ⁴. Predicting and preventing the emergence of novel diseases is considered a public health, and increasingly a conservation, priority^{5,6}. However, our understanding of the mechanism by which land use change leads to disease emergence is still rudimentary.



METHODS

We examined changes in wildlife host communities (bat, non human primate and rodent) and associated viral diversity along a land use gradient. Biological samples were collected from wildlife and tested for known and novel viral species at sites across the disturbance gradient (low, intermediate, high) during dry and wet seasons between 2012-2015 as part of the Deep Forest project in Sabah. Samples were screened for 17 viral families with PCR assays and were confirmed by sequencing (Tables 1 - 3). Wildlife and viral diversity were compared between sites and disturbance levels.



Releasing of a wild proboscis monkey post sampling. Photo © D. Ramirez

Sampling of a rodent. Photo © J. Lee.

Drawing blood from a bat before releasing it back where it was caught. Photo © J. Lee.

RESULTS & DISCUSSION

Table 1. Percentage of detected viruses in free-ranging NHPs [number of strains]

Virus family	Sabah n=89 animals
Herpesviruses (including <i>Macacine herpesvirus 1</i>)	77.5% [8]* [⊙]
Retroviruses (macaque foamy virus)	20.2% [1] [⊙]
Adenoviruses	3.4% [1]
Paramyxoviruses	1.1% [1] ^Δ
Astroviruses	2.2% [1]

^Δ Human strains
* Co-infection of 2 strains in 20 animals
⊙ Co-infection of 2 inter-family strains in 20 animals
Co-infection of 2 inter-family (herpes/adeno) strains in 1 animal
Co-infection of 3 inter-family (herpes/retro/adeno or paramyxo) strains in 2 animals
Co-infection of 4 inter-family (2 herpes/retro/astro) strains in 1 animal

Table 2. Percentage of detected viruses in wild bats at DF sites [number of viral strains]

Virus family	Low disturbance n=482 animals	Intermediate disturbance n=186 animals	High disturbance n=65 animals
Coronaviruses	0.6% [2]	-	4.6%
Paramyxoviruses	1.2% [4] [†]	-	-
Adenoviruses	0.2% [2]	1.6% [2]	3.1% [1]
Astroviruses	-	0.5% [1]	1.5% [2]
Herpesviruses	0.2% [1]	3.8% [7]	4.6% [3]

[†] Co-infection of 2 strains in 1 animal

Table 3. Percentage of detected viruses in wild rodents at DF sites [number of viral strains]

Virus family	Low disturbance n=64 animals	Intermediate disturbance n=110 animals	High disturbance n=69 animals
Adenoviruses	-	-	1.4%
Astroviruses	-	-	1.4%
Herpesviruses	9.4%	13.6%	23.2%

Host species community structure changed significantly along the land use gradient. Likewise, we found 48 novel and 15 known viruses, and show that high disturbance areas are associated with higher viral diversity. We also discovered 3 new viruses related to known human pathogens, including a SARS-like coronavirus, in pristine forests. The finding of SARS like coronavirus that has public health implications highlights the importance of habitat conservation to protect wildlife species but also to reduce human-animal contact and the risk of disease spill-over.

CONCLUSIONS

Our results indicate the potential for zoonotic viral transmission in areas with NHP-human contact. Certain types of NHP herpes are hazardous to people. The presence of anthrozoönotic transmissions could be a health threat to protected species.

More viruses were found in bats and rodents at high disturbance sites. Low disturbance results were significantly different from the other two disturbance types.

Land use change impacts on zoonotic disease emergence needs to be considered when developing areas to minimize potential viral transmissions and conflict between wildlife and people. Our results can be used to design more effective public health programs in Southeast Asia, and improve land development planning to reduce disease risk and increase conservation.

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