

# Ecology of Hendra Virus

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## Abstract

Hendra virus (HeV) is one of four new viruses that recently emerged from *Pteropus species* (otherwise known as flying foxes) in the Australasian region. All reported human cases of HeV infection have resulted from contact with fatally infected horses, which amplify the virus after being infected via an unknown route while grazing in paddocks frequented by flying foxes. HeV is a Biosecurity Level 4 (BSL4) pathogen and has killed two out of four infected people and at least 19 horses.

In this paper we create and parameterize a model that simulates the spatiotemporal dynamics of HeV within structured populations of flying foxes. We use the model to 1) characterize host-viral dynamics and test qualitative patterns in the model against field data; 2) define the critical community structure that explains persistence of HeV in the four Australian species of flying foxes; and 3) explore whether anthropogenically driven changes in flying fox ecology could account for viral emergence.

Persistence of HeV was associated with large numbers of well connected subpopulations, characteristics consistent with *P. alecto* (black flying fox) and *P. scapulatus* (little red flying fox). No reasonable parameter values allowed for persistence of HeV within *P. poliocephalus* (grey headed flying fox) or *P. conspicillatus* (spectacled flying fox) populations, both species characterized by few subpopulations. We hypothesize that interspecific viral dynamics are of a mainland-island nature with *P. alecto* and *P. scapulatus* acting as the mainland with occasional transmission to *P. conspicillatus* and *P. poliocephalus* 'islands'. Fragmentation of flying fox populations had a significant impact on viral dynamics leading to periodic high incidence of infection which could increase the probability of emergence.